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OM nucleic - nucleic search, using sw model

Run on: August 30, 2004, 16:58:44 ; Search time 103 Seconds
(without alignments)
6217.605 Million cell updates/sec

Title: US-09-904-584-1

Perfect score: 1154

Sequence: 1 atgagctcccccagatccagat.....ccagatgactagctgtgga 1154

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
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Maximum Match 100%
Listing first 500 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
- 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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- 4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
- 6: /cgn2_6/ptodata/2/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1146	99.3	1182	4	US-09-016-434-1417
2	1143	99.0	1143	4	US-09-341-446B-1
3	1142	99.0	1142	3	US-08-765-743-1
4	1137.8	98.6	1284	4	US-09-341-446B-3
5	1001	86.7	1275	4	US-09-341-446B-5
6	996.2	86.3	1275	4	US-09-341-446B-7
7	910.8	78.9	1408	4	US-09-214-904-5
8	910.8	78.9	1410	4	US-08-147-592A-1
9	910.8	78.9	1410	4	US-08-292-694A-1
10	871.2	75.5	1000	4	US-08-147-592A-11
11	871.2	75.5	1000	4	US-08-292-694A-11
12	448	38.8	2135	3	US-08-430-286A-1
13	446.4	38.7	1618	3	US-08-889-108-1
14	446.4	38.7	1618	3	US-08-889-108-3
15	446.4	38.7	1618	3	US-08-120-601B-1
16	446.4	38.7	1618	3	US-08-120-601B-3
17	446.4	38.7	1618	5	PCT-US94-10358-1
18	446.4	38.7	1618	5	PCT-US94-10358-3
19	434.8	37.7	1610	5	US-08-889-108-7
20	434.8	37.7	1610	5	PCT-US94-10358-7
21	434.8	37.7	2160	4	US-08-188-275A-1
22	434.8	37.7	2162	4	US-09-351-198-1
23	434.8	37.7	2162	4	US-09-113-426-1
24	434.8	37.7	2162	4	US-09-016-434-1379
25	434.8	37.7	2162	4	US-09-355-709C-7
26	432.4	37.5	1334	4	US-09-761-962A-3
27	432.4	37.5	1365	4	US-09-761-962A-11

28	432.4	37.5	1423	4	US-09-761-962A-1	Sequence 1, Appl
29	432.4	37.5	1610	4	US-09-761-962A-16	Sequence 16, Appl
30	432.4	37.5	1729	4	US-09-761-962A-9	Sequence 9, Appl
31	432.4	37.5	2045	4	US-09-761-962A-10	Sequence 10, Appl
32	430.8	37.3	2229	4	US-09-214-904-1	Sequence 1, Appl
33	429.2	37.2	1542	4	US-09-761-962A-4	Sequence 4, Appl
34	429.2	37.2	1981	3	US-08-387-707-15	Sequence 15, Appl
35	429.2	37.2	1981	4	US-08-405-271A-15	Sequence 15, Appl
36	422.6	36.6	1829	2	US-08-411-859-1	Sequence 1, Appl
37	422.6	36.6	1829	3	US-08-387-707-7	Sequence 7, Appl
38	422.6	36.6	1829	3	US-08-405-271A-7	Sequence 7, Appl
39	422.6	36.6	2218	4	US-09-214-904-3	Sequence 3, Appl
40	422.6	36.6	2219	4	US-08-432-174A-1	Sequence 1, Appl
41	422.6	36.6	2272	3	US-08-147-592A-3	Sequence 3, Appl
42	422.6	36.6	2272	4	US-08-292-694A-3	Sequence 3, Appl
43	411	35.6	1346	4	US-09-761-962A-12	Sequence 12, Appl
44	408.6	35.4	1773	4	US-09-016-434-1405	Sequence 1405, Ap
45	399	34.6	998	4	US-08-432-174A-3	Sequence 3, Appl
46	393.4	34.1	1805	4	US-08-405-271A-18	Sequence 18, Appl
47	393.4	34.1	1973	4	US-09-016-434-1391	Sequence 1391, Ap
48	393.4	34.1	1973	4	US-09-023-655-1417	Sequence 1417, Ap
49	393.4	34.1	3205	4	US-09-976-594-171	Sequence 171, App
50	387.6	33.6	1238	4	US-09-761-962A-2	Sequence 2, Appl
51	387.6	33.6	1257	4	US-09-761-962A-5	Sequence 5, Appl
52	377.6	32.7	1567	4	US-08-889-108-16	Sequence 16, Appl
53	377.6	32.7	1567	5	PCT-US94-10358-16	Sequence 16, Appl
54	377.6	32.7	2706	2	US-08-454-549-1	Sequence 1, Appl
55	377.6	32.7	2706	3	US-08-454-552-1	Sequence 1, Appl
56	372.8	32.3	2706	3	US-08-676-351-1	Sequence 1, Appl
57	368	31.9	1452	1	US-08-149-093A-3	Sequence 3, Appl
58	368	31.9	1452	1	US-08-911-245-3	Sequence 3, Appl
59	368	31.9	1452	1	US-08-553-058C-3	Sequence 3, Appl
60	368	31.9	1452	2	US-08-514-451A-3	Sequence 3, Appl
61	368	31.9	1452	3	US-09-170-331-3	Sequence 3, Appl
62	368	31.9	1452	3	US-09-510-473-3	Sequence 3, Appl
63	368	31.9	1452	4	US-09-048-916B-3	Sequence 3, Appl
64	367.8	31.9	1134	4	US-09-743-871B-14	Sequence 14, Appl
65	367.8	31.9	1330	3	US-08-147-592A-5	Sequence 5, Appl
66	367.8	31.9	1330	4	US-08-292-694A-5	Sequence 5, Appl
67	367.8	31.9	2600	4	US-08-986-209A-1	Sequence 1, Appl
68	357	30.9	1177	4	US-09-743-871B-13	Sequence 13, Appl
69	344.8	29.9	2600	1	US-08-147-949A-1	Sequence 1, Appl
70	336.2	29.1	1283	4	US-09-743-871B-11	Sequence 11, Appl
71	336.2	29.1	1283	4	US-09-743-871B-12	Sequence 12, Appl
72	327.4	28.4	2634	4	US-09-743-871B-8	Sequence 8, Appl
73	327	28.3	1256	4	US-09-743-871B-9	Sequence 9, Appl
74	319.6	27.7	830	3	US-08-387-707-13	Sequence 13, Appl
75	319.6	27.7	830	4	US-08-405-271A-13	Sequence 13, Appl
76	243	21.1	2447	3	US-08-387-707-12	Sequence 12, Appl
77	243	21.1	2447	4	US-08-405-271A-12	Sequence 12, Appl
78	242.6	21.0	1317	4	US-09-016-434-1446	Sequence 1446, Ap
79	229.6	19.9	1205	1	US-08-417-103-13	Sequence 13, Appl
80	229.6	19.9	1634	1	US-07-816-283-1	Sequence 1, Appl
81	229.6	19.9	1634	1	US-08-417-103-1	Sequence 1, Appl
82	229.6	19.9	1634	4	US-09-016-434-1302	Sequence 1302, Ap
83	226.6	19.6	1265	1	US-07-816-283-3	Sequence 3, Appl
84	226.6	19.6	1265	1	US-08-417-103-3	Sequence 3, Appl
85	221.2	19.2	1244	1	US-07-816-283-7	Sequence 7, Appl
86	221.2	19.2	1244	1	US-08-417-103-7	Sequence 7, Appl
87	219.4	19.0	2518	4	US-09-743-871B-10	Sequence 10, Appl
88	214.8	18.6	1147	1	US-08-417-103-15	Sequence 15, Appl
89	214.8	18.6	1351	1	US-07-816-283-5	Sequence 5, Appl
90	214.8	18.6	1351	1	US-08-417-103-5	Sequence 5, Appl
91	214.8	18.6	1351	4	US-09-016-434-1303	Sequence 1303, Ap
92	210.4	18.2	1002	4	US-09-170-496D-15	Sequence 15, Appl
93	210.4	18.2	1518	1	US-08-148-215A-3	Sequence 3, Appl
94	210.4	18.2	1518	4	US-09-016-434-1480	Sequence 1480, Ap
95	207.2	18.0	1002	4	US-09-170-496D-171	Sequence 171, App
96	204.8	17.7	441	4	US-09-530-880-5	Sequence 5, Appl
97	175.6	15.2	987	4	US-09-170-496D-11	Sequence 11, Appl
98	175.6	15.2	1054	1	US-08-148-215A-1	Sequence 1, Appl
99	175.6	15.2	1596	4	US-09-016-434-1479	Sequence 1479, Ap
100	172.4	14.9	987	4	US-09-170-496D-169	Sequence 169, App

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102	162.2	14.1	1296	1	US-07-816-283-9	Sequence 9, Appli	175	92.6	8.0	1679	1	US-08-076-093A-5	Sequence 5, Appli
103	162.2	14.1	1296	1	US-08-417-103-9	Sequence 9, Appli	176	92.6	8.0	1679	1	US-08-701-265-5	Sequence 5, Appli
104	162.2	14.1	1413	4	US-09-016-434-1361	Sequence 1321, Ap	177	92.6	8.0	1679	2	US-08-284-586-5	Sequence 5, Appli
105	156.2	13.5	1796	1	US-07-816-283-11	Sequence 11, Appl	178	92.6	8.0	1679	2	US-08-805-478-5	Sequence 5, Appli
106	156.2	13.5	1796	1	US-08-417-103-11	Sequence 11, Appl	179	92.6	8.0	1679	2	US-08-802-627A-5	Sequence 5, Appli
107	123.4	10.7	1219	4	US-08-981-700A-3	Sequence 3, Appli	180	92.6	8.0	1679	2	US-08-801-238-5	Sequence 5, Appli
108	123.4	10.7	1365	4	US-08-899-1102A-27	Sequence 27, Appl	181	92.6	8.0	1679	2	US-08-801-228-5	Sequence 5, Appli
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110	122.4	10.6	1164	4	US-08-993-424B-6	Sequence 6, Appli	183	92.6	8.0	1679	3	PCT-US94-06380-3	Sequence 3, Appli
111	122.4	10.6	1164	4	US-09-603-680-6	Sequence 6, Appli	184	92.6	8.0	2818	3	US-08-982-493-7	Sequence 7, Appli
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115	119	10.3	1495	4	US-09-023-655-1021	Sequence 1021, Ap	188	92	8.0	1088	4	US-09-077-674-6	Sequence 6, Appli
116	119	10.3	2156	1	US-08-012-988A-1	Sequence 1, Appli	189	92	8.0	1101	4	US-09-016-434-1148	Sequence 1148, Ap
117	119	10.3	2156	1	US-09-023-655-1247	Sequence 1247, Ap	190	92	8.0	1101	4	US-09-170-496D-87	Sequence 87, Appl
118	108	9.4	1116	3	US-08-993-088A-18	Sequence 18, Appl	191	92	8.0	1101	4	US-09-364-425B-44	Sequence 44, Appl
119	108	9.4	1116	3	US-08-993-088A-18	Sequence 18, Appl	192	92	8.0	2111	2	US-08-966-316-6	Sequence 6, Appli
120	108	9.4	1116	4	US-08-993-424B-18	Sequence 18, Appl	193	91.8	8.0	1083	4	US-09-131-827A-19	Sequence 19, Appli
121	108	9.4	1116	4	US-09-603-680-18	Sequence 18, Appl	194	91.6	7.9	1122	3	US-09-077-675A-9	Sequence 9, Appli
122	108	9.4	1116	4	US-09-603-680-19	Sequence 19, Appl	195	91.6	7.9	1122	3	US-09-077-674-9	Sequence 9, Appli
123	108	9.4	1116	2	US-08-626-685A-7	Sequence 7, Appli	196	90.8	7.9	1068	4	US-09-170-496D-129	Sequence 129, App
124	108	9.4	1193	3	US-08-899-112B-7	Sequence 7, Appli	197	90.8	7.9	1068	4	US-09-170-496D-231	Sequence 231, App
125	107.2	9.3	248	3	US-08-513-974B-300	Sequence 300, App	198	90.8	7.9	1161	1	US-08-153-848-31	Sequence 31, Appl
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129	105.6	9.2	1047	4	US-08-540-650B-6	Sequence 6, Appli	202	90.8	7.9	2254	4	US-09-088-337B-27	Sequence 27, Appl
130	102.2	8.9	1053	4	US-09-016-434-1423	Sequence 1423, Ap	203	90.8	7.9	2254	5	PCT-US93-11153-27	Sequence 27, Appl
131	102.2	8.9	1882	4	US-08-540-650B-11	Sequence 11, Appl	204	90.8	7.9	3100	4	US-09-016-434-1442	Sequence 1442, Ap
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136	101.2	8.8	1293	4	US-08-720-565-3	Sequence 3, Appli	209	90.2	7.8	1979	3	US-08-446-669-3	Sequence 3, Appli
137	101.2	8.8	1201	4	US-09-016-434-1085	Sequence 1085, Ap	210	90.2	7.8	1979	4	US-09-023-655-1419	Sequence 1419, Ap
138	101.2	8.8	1201	4	US-09-023-655-905	Sequence 905, App	211	90.2	7.8	2232	5	PCT-US95-00476-3	Sequence 1, Appli
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141	101.2	8.8	1315	3	US-08-575-967A-3	Sequence 3, Appli	214	90.2	7.8	2232	4	US-09-016-434-1392	Sequence 1392, Ap
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144	100.4	8.7	1953	4	US-09-016-434-1096	Sequence 1096, Ap	217	89.6	7.8	4009	4	US-09-743-475-1	Sequence 1, Appli
145	100.4	8.7	2608	4	US-09-023-655-955	Sequence 955, App	218	89	7.7	1572	1	US-08-041-219A-5	Sequence 5, Appli
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148	97.2	8.4	1209	3	US-09-170-496D-51	Sequence 51, Appli	221	88	7.6	1225	4	US-09-016-434-1235	Sequence 1235, Ap
149	97.2	8.4	1269	3	US-09-224-426-1	Sequence 1, Appli	222	88	7.6	1317	1	US-08-153-848-45	Sequence 45, Appl
150	97.2	8.4	1269	3	US-09-478-602-1	Sequence 1, Appli	223	88	7.6	1317	3	US-09-299-843A-45	Sequence 45, Appl
151	97.2	8.4	1269	3	US-09-478-602-1	Sequence 1, Appli	224	88	7.6	1317	4	US-09-088-337B-45	Sequence 45, Appl
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153	97.2	8.4	1316	5	PCT-US95-16472-1	Sequence 1, Appli	226	88	7.6	1664	4	US-09-582-224A-5	Sequence 5, Appli
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156	94	8.1	1143	4	US-09-170-496D-61	Sequence 61, Appl	229	88	7.6	1737	1	US-08-202-056-4	Sequence 4, Appli
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165	93.6	8.1	1101	1	US-09-170-496D-209	Sequence 209, App	238	88	7.6	1737	5	PCT-US94-06380-2	Sequence 2, Appli
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169	93.4	8.1	2126	3	US-09-233-857-1	Sequence 1, Appli	242	87.8	7.6	1225	4	US-09-023-655-967	Sequence 967, App
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172	92.6	8.0	1119	4	US-09-170-496D-65	Sequence 65, Appl	245	87.8	7.6	1376	4	US-09-796-202-2	Sequence 2, Appli
173	92.6	8.0	1119	4	US-09-170-496D-199	Sequence 199, App	246	87.8	7.6	1378	1	US-08-759-848-2	Sequence 2, Appli

247	87.8	7.6	1378	4	US-08-148-708-6	Sequence 6, Appl1	320	82	7.1	1107	4	US-09-595-549-3	Sequence 3, Appl1
248	87.8	7.6	1378	4	US-09-016-434-1123	Sequence 1123, Ap	321	82	7.1	1417	4	US-09-199-737-3	Sequence 3, Appl1
249	87.8	7.6	1378	5	PCT-US95-09383-2	Sequence 2, Appl1	322	82	7.1	1417	4	US-09-058-333A-3	Sequence 3, Appl1
250	87.8	7.6	1414	4	US-09-502-785A-1	Sequence 1, Appl1	323	82	7.1	1607	3	US-08-513-974B-341	Sequence 341, App
251	87.8	7.6	1477	4	US-08-833-752-2	Sequence 2, Appl1	324	81.8	7.1	1068	4	US-09-170-496D-1	Sequence 1, Appl1
252	87.8	7.6	1383	3	US-08-861-105-13	Sequence 13, Appl1	325	81.8	7.1	1068	4	US-09-016-434-126	Sequence 163, App
253	87.8	7.6	3383	3	US-08-575-967A-1	Sequence 1, Appl1	326	81.8	7.1	1438	4	US-09-016-434-1426	Sequence 1426, Ap
254	87.8	7.6	3383	4	US-09-023-655-951	Sequence 951, App	327	81.8	7.1	2582	2	US-08-480-994-6	Sequence 6, Appl1
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256	87.6	7.6	1764	4	US-08-313-553-12	Sequence 12, Appl1	329	81.8	7.1	2582	2	US-08-599-654-6	Sequence 6, Appl1
257	87.6	7.6	1764	1	US-08-767-993-12	Sequence 12, Appl1	330	81.8	7.1	2582	2	US-08-485-573-6	Sequence 6, Appl1
258	87.6	7.6	3472	4	US-09-016-434-1328	Sequence 1328, Ap	331	81.8	7.1	2582	3	US-08-944-868A-6	Sequence 6, Appl1
259	87.6	7.6	3480	1	US-07-657-769B-68	Sequence 68, Appl1	332	81.8	7.1	2582	3	US-08-944-433A-6	Sequence 6, Appl1
260	87.6	7.6	3480	1	US-07-789-184-219	Sequence 219, App	333	81.8	7.1	2582	3	US-08-925-743-6	Sequence 6, Appl1
261	87.6	7.6	3480	1	US-08-475-263-219	Sequence 219, App	334	81.8	7.1	2582	3	US-08-944-446-6	Sequence 6, Appl1
262	87.6	7.6	3480	1	US-08-485-886-219	Sequence 219, App	335	81.8	7.1	2582	3	US-08-925-767-6	Sequence 6, Appl1
263	87.6	7.6	3480	2	US-08-477-362-219	Sequence 219, App	336	81.6	7.1	1029	3	US-09-077-675A-4	Sequence 4, Appl1
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265	87.6	7.6	3480	3	US-08-473-489A-219	Sequence 219, App	338	81.4	7.1	2100	4	US-09-495-050A-289	Sequence 289, App
266	87.6	7.6	3480	3	US-08-485-695-219	Sequence 219, App	339	81.4	7.1	3129	3	US-09-077-675A-14	Sequence 14, Appl1
267	87.6	7.6	3480	3	US-08-018-760-219	Sequence 219, App	340	81.4	7.1	3129	4	US-09-077-674-14	Sequence 14, Appl1
268	86.8	7.5	1766	5	PCT-US92-06532-2	Sequence 2, Appl1	341	81.2	7.0	563	1	US-07-915-966C-2	Sequence 2, Appl1
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270	86.6	7.5	1063	4	US-09-077-674-1	Sequence 1, Appl1	343	81.2	7.0	563	3	US-08-853-194-2	Sequence 3, Appl1
271	86.6	7.5	1128	4	US-09-517-605-8	Sequence 193, App	344	81.2	7.0	1140	4	US-09-016-434-750	Sequence 750, App
272	86.2	7.5	1059	4	US-09-867-915-2	Sequence 2, Appl1	345	81.2	7.0	1301	2	US-08-467-948A-7	Sequence 7, Appl1
273	85.8	7.4	1080	4	US-09-016-434-1187	Sequence 1187, Ap	346	81.2	7.0	1301	3	US-08-467-947A-7	Sequence 7, Appl1
274	85.8	7.4	1829	4	US-09-016-434-1187	Sequence 1187, Ap	347	81	7.0	1176	5	PCT-US95-03032-2	Sequence 2, Appl1
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276	85.8	7.4	2632	4	US-09-867-915-1	Sequence 1, Appl1	349	81	7.0	1214	3	US-09-478-601-3	Sequence 3, Appl1
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287	84.6	7.3	1020	4	US-09-170-496D-181	Sequence 181, App	360	81	7.0	1933	2	US-08-410-456A-2	Sequence 2, Appl1
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296	83.6	7.2	1280	3	US-09-199-737-1	Sequence 1, Appl1	369	80.8	7.0	183	3	US-08-513-974B-307	Sequence 307, App
297	83.6	7.2	1280	4	US-08-900-230-1	Sequence 1, Appl1	370	80.2	6.9	1098	4	US-09-503-219B-7	Sequence 7, Appl1
298	83.6	7.2	1280	4	US-09-058-333A-1	Sequence 1, Appl1	371	80	6.9	2234	4	US-08-993-088A-8	Sequence 8, Appl1
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301	83.6	7.2	1607	4	US-08-540-650B-17	Sequence 17, Appl1	374	79.6	6.9	1110	4	US-08-462-509B-3	Sequence 3, Appl1
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477 70.4 6.1 2858 4 US-09-976-594-912 Sequence 912, App

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487 68.8 6.0 1535 4 US-09-016-434-1051 Sequence 1051, Ap

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496 67.4 5.8 1414 3 US-08-486-673B-62 Sequence 62, Appli

497 67.2 5.8 1110 4 US-09-170-496D-177 Sequence 177, App

498 66.8 5.8 1551 4 US-09-016-434-1239 Sequence 1239, Ap

499 66.8 5.8 1551 4 US-09-023-655-1186 Sequence 1186, Ap

500 66.8 5.8 1866 4 US-09-016-434-1205 Sequence 1205, Ap

RESULT 1

US-09-016-434-1417

Sequence 1417, Application US/09016434

Patent No. 6500938

GENERAL INFORMATION:

APPLICANT: Janice Au-Young

APPLICANT: Jeffrey J. Sellhammer

TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING

TITLE OF INVENTION: PATHWAY GENE EXPRESSION

NUMBER OF SEQUENCES: 1490

CORRESPONDENCE ADDRESSES:

ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

STREET: 3174 PORTER DRIVE

CITY: PALO ALTO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

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ATTORNEY/AGENT INFORMATION:

NAME: Zeller, Karen J.

REGISTRATION NUMBER: 37,071

REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1417:
SEQUENCE CHARACTERISTICS:
LENGTH: 1182 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: 9532059
US-09-016-434-1417

Query Match 99.3%; Score 1146; DB 4; Length 1182;
Best Local Similarity 99.6%; Pred. No. 7.7e-271;
Matches 1149; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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QY 1 ATGGAATCCCGGATCCAGATCTTCCGCGGGGAGCGGGGCTTACCTGGGCGCCGAGCGGC 60
DB 14 ATGGAATCCCGGATCCAGATCTTCCGCGGGGAGCGCTTGGCCCTTACCTGGGCGCCGAGCGGC 73
QY 61 TGCCTGCCCCCAAGCAGCAGCGCGCTGGTTCCCGGCTGGGCGGAGCGCCGAGCAAGCGGC 120
DB 74 TGCCTGCCCCCAAGCAGCAGCGCGCTGGTTCCCGGCTGGGCGGAGCGCCGAGCAAGCGGC 133
QY 121 AGCGCGCGCTGGAGAGCGCGGAGCTGGAGCGCGGACATCTCCCGGCGCATCCCGGCTC 180
DB 134 AGCGCGCGCTGGAGAGCGCGGAGCTGGAGCGCGGACATCTCCCGGCGCATCCCGGCTC 193
QY 181 ATCATCAGGCGGCTTACTCCGCTAGTGTCTGCTGGGCTTGGTGGGCAATCCGCTGCTC 240
DB 194 ATCATCAGGCGGCTTACTCCGCTAGTGTCTGCTGGGCTTGGTGGGCAATCCGCTGCTC 253
QY 241 ATGTTCTGATCATCCGATACACAAAGATGAAGACAGCAACCAATTTACATATTAAAC 300
DB 254 ATGTTCTGATCATCCGATACACAAAGATGAAGACAGCAACCAATTTACATATTAAAC 313
QY 301 CTGGCTTTGGGAGATGCTTACTACTACATCAACCATGCTTCAAGATGAGGCTTACTTTC 360
DB 314 CTGGCTTTGGGAGATGCTTACTACTACATCAACCATGCTTCAAGATGAGGCTTACTTTC 373
QY 361 ATGAATTCCTGGGCTTTGGGAGATGCTGCTGGGCAAGATTAATTTCCATTGATTAAC 420
DB 374 ATGAATTCCTGGGCTTTGGGAGATGCTGCTGGGCAAGATTAATTTCCATTGATTAAC 433
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QY 481 TGGCAACCCCGTAGAGGCTTTGGAGCTTCCGACACCTTTGAAGGCAAGATCAATATTC 540
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QY 541 TGCATCTGGGCTGCTGCTGATCTGTTGGCACTCTTGCAATAGTCTTTGAGAGGCAACAA 600
DB 554 TGCATCTGGGCTGCTGCTGATCTGTTGGCACTCTTGCAATAGTCTTTGAGAGGCAACAA 613
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DB 614 GTCAAGGAAAGAGTGAATGCTATTGAGTCTCTTGAAGTCCAGATGATGATCACTAC 673
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QY 721 ATCATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
DB 734 ATCATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 793
QY 781 GGCCTCCGAGAGAAAGATGCAACCTGCTAGATCAACAGAGCTGCTGCTGCTGCTGCTGCTG 840
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DB 794 GGCCTCCGAGAGAAAGATGCAACCTGCTAGATCAACAGAGCTGCTGCTGCTGCTGCTG 853
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DB 914 AGCACTCCCAAGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 973
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DB 1094 CGAAATACAGTTCAAGATCTGCTTACCTGAGAGGACATGATGGATGATTAACCACTA 1153
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RESULT 2
US-09-341-446B-1
; Sequence 1, Application US/09341446B
; Patent No. 6518480
; GENERAL INFORMATION:
; APPLICANT: Conklin, Bruce R.
; TITLE OF INVENTION: Selective Target Cell Activation By
; TITLE OF INVENTION: Expression of A G Protein-Coupled Receptor Activated
; FILE REFERENCE: UCAL-049CIP
; CURRENT APPLICATION NUMBER: US/09/341,446B
; CURRENT FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US97/05334
; PRIOR FILING DATE: 1997-03-25
; PRIOR APPLICATION NUMBER: US 08/622,348
; PRIOR FILING DATE: 1996-03-26
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq For Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1143
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-341-446B-1

Query Match 99.0%; Score 1143; DB 4; Length 1143;
Best Local Similarity 100.0%; Pred. No. 4.1e-270;
Matches 1143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ATGGAATCCCGGATCCAGATCTTCCGCGGGGAGCGGGGCTTACCTGGGCGCCGAGCGGC 60
QY 61 TGCCTGCCCCCAAGCAGCAGCGCGCTGGTTCCCGGCTGGGCGGAGCGCCGAGCAAGCGGC 120
DB 61 TGCCTGCCCCCAAGCAGCAGCGCGCTGGTTCCCGGCTGGGCGGAGCGCCGAGCAAGCGGC 120
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DB 121 AGCGCGCGCTGGAGAGCGCGGAGCTGGAGCGCGGCAATCTCCCGGCGCATCCCGGCTC 180
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DB 181 ATCATCAGGCGGCTTACTCCGCTAGTGTCTGCTGGGCTTGGTGGGCAATCCGCTGCTC 240
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Db 241 ATGTCGTGATCATCCGATACAAAGATGAAAGACAGCAACCAATTATATTAC 300
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Db 301 CTGGCTTTGGAGATGCTTACTTACTAACAACGCTTTCAGAGTACGGTCTACTG 360
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Db 421 AACGATTTACCAAGCATCTTACCTTGACCAATGATGAGCGGTACACTGCGGTG 480
Qy 421 AACGATTTACCAAGCATCTTACCTTGACCAATGATGAGCGGTACACTGCGGTG 480
Db 421 AACGATTTACCAAGCATCTTACCTTGACCAATGATGAGCGGTACACTGCGGTG 480
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Db 481 TGGCAACCCCGTGAAGGCTTTGGACCTTCGACACACCTTGAAGGCAAAAGTCAATATC 540
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Db 541 TGCATCTGGCTGCTGTGCTGATCTGTGGCATCTCTGAATATGCTCTTGAAGGCAACAA 600
Qy 601 GTCAAGGGAAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
Db 601 GTCAAGGGAAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
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Db 661 TGGTGGGAGCTTTTCAATGAAAGTGTGCGCTTTCATCTTTGCTTGTGATGCTTCTTC 720
Qy 721 ATCATCATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
Db 721 ATCATCATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
Qy 781 GGCCTCCGAGAGAAAGATGCAACCTGGGTAGATGCAACGATGCTGCTGCTGCTGCTG 840
Db 781 GGCCTCCGAGAGAAAGATGCAACCTGGGTAGATGCAACGATGCTGCTGCTGCTGCTG 840
Qy 841 GCAGTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
Db 841 GCAGTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
Qy 901 AGCAGCTTCCACAGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
Db 901 AGCAGCTTCCACAGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
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Db 1081 CGAATATACAGTTGAGATGCTGCTTACCTGAGGAGCATGATGAGATGAGATGAGATG 1140
Qy 1141 TGA 1143
Db 1141 TGA 1143

RESULT 3

US-08-765-743-1

; Sequence 1, Application US/08765743

; Patent No. 6146835

; GENERAL INFORMATION:

; APPLICANT: KIEFER, Brigitte

; APPLICANT: SIMONIN, Frederic

; TITLE OF INVENTION: HUMAN KAPPA OPIOID RECEPTOR, NUCLEIC

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765,743
; FILING DATE: 11-FEB-1997
; CLASSIFICATION: 536
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: FR 94/08531
; FILING DATE: 11-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR95/00912
; FILING DATE: 07-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: NX 1758-1P US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 521-2297
; TELEFAX: (703) 685-0573
; TELEX: 248425 EMBON
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1142 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1142
; US-08-765-743-1
Query Match 99.0%; Score 1142; DB 3; Length 1142;
Best Local Similarity 100.0%; Pred. No. 7,2e-270;
Matches 1142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGAGCTCCCGGATCCGATCTTCCGCGGAGCGGAGCCCTTACCTGCGCCCGAGCGCC 60
Db 1 ATGAGCTCCCGGATCCGATCTTCCGCGGAGCGGAGCCCTTACCTGCGCCCGAGCGCC 60
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1081 CGAATTAAGTTCAGGATCTGCTTACCTGAGGAGCATGATGGATGAATTAACCAAGTA 1140
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RESULT 4

US-09-341-446B-3

Sequence 3, Application US/09341446B

Patent No. 6518480

GENERAL INFORMATION:

APPLICANT: Conklin, Bruce R.

TITLE OF INVENTION: Selective Target Cell Activation By

TITLE OF INVENTION: Expression of A G Protein-coupled Receptor Activated

FILE REFERENCE: USAL-049CIP

CURRENT APPLICATION NUMBER: US/09/341,446B

PRIOR APPLICATION NUMBER: PCT/US97/05334

PRIOR FILING DATE: 1997-03-25

PRIOR APPLICATION NUMBER: US 08/622,348

NUMBER OF SEQ ID NOS: 12

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 3

LENGTH: 1284
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: modified KOR
US-09-341-446B-3

Query Match 98.8%; Score 1137.8; DB 4; Length 1284;
Best Local Similarity 99.8%; Pred. No. 8e-269; Mismatches 2; Indels 0; Gaps 0;
Matches 1139; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

2 TGGAATCCCGATCCAGATCTTCCGCGGGAGCCGGGCTTACCTGCGCCCGAGAGCT 61
113 TGGAATCCCGATCCAGATCTTCCGCGGGAGCCGGGCTTACCTGCGCCCGAGAGCT 172
62 GCTGCGCCCGATCCAGATCTTCCGCGGGAGCCGGGCTTACCTGCGCCCGAGAGCT 121
173 GCTGCGCCCGATCCAGATCTTCCGCGGGAGCCGGGCTTACCTGCGCCCGAGAGCT 232
122 GCGCGCGCTCGAGAGAGCGGAGCTGAGCCCGGAGATCTCCCGGAGATCCCGGCTCA 181
233 GCGCGCGCTCGAGAGAGCGGAGCTGAGCCCGGAGATCTCCCGGAGATCCCGGCTCA 292
182 TCATCAAGCGGATCTACCTCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 241
293 TCATCAAGCGGATCTACCTCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 352
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653 GCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 712
602 TCAGGAAAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 661
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662 GGTGGAGCTTCTTCAATGAAGATCTGCTTCAATCTTGGCTTGTGATTCCTGCTGCTCA 721
773 GGTGGAGCTTCTTCAATGAAGATCTGCTTCAATCTTGGCTTGTGATTCCTGCTGCTCA 832
722 TCATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 781
833 TCATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 892
782 GCTCCCGAGAGAGATGCGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 841
893 GCTCCCGAGAGAGATGCGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 952
842 CAGTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 901
953 CAGTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1012
902 GCACCTCCACAGACAGCTGCTCTCCAGCTATTAATTCTGATGCTGCTGATGCTGCTGATA 961

Db 1013 GCACCTCCACAGACAGAGCTGCTCTCTCCAGCTATTACTTTCGATTCGCTTAGGCTATA 1072
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Db 1073 CCAACAGTACCTGTAATCCCATTTCTTACGCTTTTGTATGAAAATTGACGGGTGT 1132
Qy 1022 TCCGGGACTTCTGCTTTCAGTGAAGATGAGTGGAGCGGACATACAGAGTCC 1081
Db 1133 TCCGGGACTTCTGCTTTCAGTGAAGATGAGTGGAGCGGACATACAGAGTCC 1192
Qy 1082 GAAATACAGTTGAGATCTGCTTACCTGAGGACATCGATGAGTGAATTAACAGTAT 1141
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Qy 1142 G 1142
Db 1253 G 1253

RESULT 5

US-09-341-446B-5
; Sequence 5, Application US/09341446B
; Patent No. 6518480
; GENERAL INFORMATION:
; APPLICANT: Conklin, Bruce R.
; TITLE OF INVENTION: Selective Target Cell Activation By
; TITLE OF INVENTION: Expression of A G Protein-Coupled Receptor Activated
; TITLE OF INVENTION: Superiority By Synthetic Ligand
; FILE REFERENCE: UCAL-049CIP
; CURRENT APPLICATION NUMBER: US/09/341,446B
; CURRENT FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US97/05334
; PRIOR FILING DATE: 1997-03-25
; PRIOR APPLICATION NUMBER: US 08/622,348
; PRIOR FILING DATE: 1996-03-26
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1275
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: RASL ORI
US-09-341-446B-5

Query Match 86.7%; Score 1001; DB 4; Length 1275;
Best Local Similarity 93.1%; Pred. No. 2.2e-235;
Matches 1062; Conservative 0; Mismatches 70; Indels 9; Gaps 1;

Qy 2 TGAATCTCCCGATCCAGATCTTCCGCGGAGAGCCGGGCTTACCTGAGCCCGGAGCGCT 61
Db 113 TCGACTCCCGATCCAGATCTTCCGCGGAGAGCCGGGCTTACCTGAGCCCGGAGCGCT 172
Qy 62 GCTGCCCCCAACAGAGCGCTGTGTTCCGCGTGGGCGAGCCGACAGCAAGCGCA 121
Db 173 GCTGCCCCCAACAGAGCGCTGTGTTCCGCGTGGGCGAGCCGACAGCAAGCGCA 232
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Qy 362 TGAATCTCCCGATCCAGATCTTCCGCGGAGAGCCGGGCTTACCTGAGCCCGGAGCGCT 421
Db 473 TGAATCTCCCGATCCAGATCTTCCGCGGAGAGCCGGGCTTACCTGAGCCCGGAGCGCT 532
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Qy 602 TCAAGGAAAGCTGATGATCTGATGATCTGATGATCTGATGATGATGATGATGATGAT 661
Db 713 CCGCGGATGAGAGAGTGTATGACAGCTCCAGTTCGCCAGCCC-----CAGCTGCT 763
Qy 662 GGTGGACCTCTTCATGAAAGATCTGCGTCTTATCTTGTGCTTGTGATCCGTCTCA 721
Db 764 ACTGGGACACTGTGACCAAGATCTGCGTCTTATCTTGTGCTTGTGATCCGTCTCA 823
Qy 722 TCAATCATGCTGCTGATACCTGATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 781
Db 824 TCAATCATGCTGCTGATACCTGATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 883
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Qy 902 GCACCTCCCAAGAGAGCTGCTCTCCAGCTTATTAATCTGATGCTTGGGCTATA 961
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Db 1064 CCAACAGTACCTGTAATCCCATTTCTTACGCTTTTGTATGAAAATTGACGGGTGT 1123
Qy 1022 TCCGGGACTTCTGCTTTCAGTGAAGATGAGTGGAGCGGACATACAGAGTCC 1081
Db 1124 TCCGGGACTTCTGCTTTCAGTGAAGATGAGTGGAGCGGACATACAGAGTCC 1183
Qy 1082 GAAATACAGTTGAGATCTGCTTACCTGAGGACATCGATGAGTGAATTAACAGTAT 1141
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Qy 1142 G 1142
Db 1244 G 1244

RESULT 6

US-09-341-446B-7
; Sequence 7, Application US/09341446B
; Patent No. 6518480
; GENERAL INFORMATION:
; APPLICANT: Conklin, Bruce R.
; TITLE OF INVENTION: Selective Target Cell Activation By
; TITLE OF INVENTION: Expression of A G Protein-Coupled Receptor Activated
; TITLE OF INVENTION: Superiority By Synthetic Ligand
; FILE REFERENCE: UCAL-049CIP
; CURRENT APPLICATION NUMBER: US/09/341,446B
; CURRENT FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US97/05334
; PRIOR FILING DATE: 1997-03-25
; PRIOR APPLICATION NUMBER: US 08/622,348
; PRIOR FILING DATE: 1996-03-26

/ NUMBER OF SEQ ID NOS: 12
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO: 7
/ LENGTH: 1275
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: RASSL OR2
US-09-341-446B-7

Query Match 86.3%; Score 996.2; DB 4; Length 1275;
Beet Local Similarity 92.8%; Pred. No. 3.3e-234;
Matches 1059; Conservative 0; Mismatches 73; Indels 9; Gaps 1;

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QY 2 TGGACCTCCCGATCCAGATCTTCCGCGGGAGCCCGGCTTACCTGCGCCCGAGCGGCT 61
DB 113 TCGACCTCCCGATCCAGATCTTCCGCGGGAGCCCGGCTTACCTGCGCCCGAGCGGCT 172
QY 62 GCTGCCCCCAACAGACAGCGCGCTGGTTCCCGGCTGGGCGGAGCCGAGCAAGGCA 121
DB 173 GCTGCCCCCAACAGACAGCGCGCTGGTTCCCGGCTGGGCGGAGCCGAGCAAGGCA 232
QY 122 GCGCGCGCTCGAGAGACGCGAGCTGGAGCCCGGCAATCTCCCGGCAATCCGCTCA 181
DB 223 GCGCGCGCTCGAGAGACGCGAGCTGGAGCCCGGCAATCTCCCGGCAATCCGCTCA 292
QY 182 TCATACAGCGCGCTACCTCCGATAGTTCGTGTGGGCTTGGTGGGCACTGGCTGTCA 241
DB 293 TCATACAGCGCGCTACCTCCGATAGTTCGTGTGGGCTTGGTGGGCACTGGCTGTCA 352
QY 242 TGTTCGTGATCATCCGATACCAAGATGAGAGACAGCAACATTTACATATTAAAC 301
DB 353 TGTTCGTGATCATCCGATACCAAGATGAGAGACAGCAACATTTACATATTAAAC 412
QY 302 TGGCTTTGGCAGATCTTTAGTTACTACCAACATGCTTTGAGAGTACGTTCTACTGA 361
DB 413 TGGCTTTGGCAGATCTTTAGTTACTACCAACATGCTTTGAGAGTACGTTCTACTGA 472
QY 362 TGAATTCCTGGCTTTTGGGGATGTGCTGTGCAAGATAGTATTTCCATGTTACTACA 421
DB 473 TGAATTCCTGGCTTTTGGGGATGTGCTGTGCAAGATAGTATTTCCATGTTACTACA 532
QY 422 ACATGTTACACAGCATCTTCACTTGACCATGATGAGCGGTGACGCTACGCTGT 481
DB 533 ACATGTTACACAGCATCTTCACTTGACCATGATGAGCGGTGACGCTACGCTGT 592
QY 482 GCCACCCCGTGAAGCTTTGACCTTCCGACACCTTGAAGGCAAGATCATCATATCT 541
DB 593 GCCACCCCGTGAAGCTTTGACCTTCCGACACCTTGAAGGCAAGATCATCATATCT 652
QY 542 GCATCTGGCTGTGCTGATCTTGTGGCATCTTGCAATAGTCTTTGAGGACCAAG 601
DB 653 GCATCTGGCTGTGCTGATCTTGTGGCATCTTGCAATAGTCTTTGAGGACCAAG 712
QY 602 TCAGGAGAGAGCTGATGATGATGATGCTCTTGCAGTTCACAGATGATGATGATGAT 661
DB 713 TCAGGAGAGAGCTGATGATGATGATGCTCTTGCAGTTCACAGATGATGATGATGAT 763
QY 762 GGTGGAGACCTTTCATGAGATCTGCTTTCATCTTGGCTTCTGTGATCTCTGTCTCA 721
DB 874 ACTGGAGACCTGATGAGATCTGCTTTCATCTTGGCTTCTGTGATCTCTGTCTCA 823
QY 722 TCATCATGCTGTGCTACACCTGATGATCTGCTGTCTCAAGAGCTTCGGCTCTTTCTG 781
DB 834 TCATCATGCTGTGCTACACCTGATGATCTGCTGTCTCAAGAGCTTCGGCTCTTTCTG 883
QY 782 GCTCCGAGAGAAAGTGCACACCTGAGATGATGATGATGATGATGATGATGATGATG 841
DB 884 GCTCCGAGAGAAAGTGCACACCTGAGATGATGATGATGATGATGATGATGATGATG 943
QY 842 CAGTCTGTGCTGTGCTGATCTCCATTCATATTCATCTGTGTGAGAGCTGTGGGGA 901
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QY 902 GCACCTCCCAACAGACAGCTGCTCTCCAGCTATTTACTTGTGATCGGCTTAGGCTATA 961
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DB 1064 CCACAGTAGGCTGATATCCATCTCTACGCTTTCTTGATGAAAACTTCAAGCGGTGT 1123
QY 1022 TCCGGAGCTTCTGCTTTCCATGTAAGATGAGATGAGAGCGGAGCACTAGCAAGTTC 1081
DB 1124 TCCGGAGCTTCTGCTTTCCATGTAAGATGAGATGAGAGCGGAGCACTAGCAAGTTC 1183
QY 1082 GAATATACGTTCAAGATCTGCTTACCTGAGGAGCATGATGAGTGAATTAACAGTAT 1141
DB 1184 GAATATACGTTCAAGATCTGCTTACCTGAGGAGCATGATGAGTGAATTAACAGTAT 1243
QY 1142 G 1142
DB 1244 G 1244
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RESULT 7
US-09-214-904-5
Sequence 5, Application US/09214904
Patent No. 6632977
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: TRANSGENIC ANIMAL IN WHICH THE EXPRESSION
TITLE OF INVENTION: OF OPIATE RECEPTORS IS MODIFIED
NUMBER OF SEQUENCES: 6
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/214,904
FILING DATE:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/FR97/01282
FILING DATE:
APPLICATION NUMBER: FR 96.08810
FILING DATE: 15-JUL-1996
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1408 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 184..1323
US-09-214-904-5
Query Match 78.9%; Score 910.8; DB 4; Length 1408;
Beet Local Similarity 86.8%; Pred. No. 2.6e-213;
Matches 1002; Conservative 0; Mismatches 152; Indels 0; Gaps 0;
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QY 1 ATGAGCTCCCGATCCAGATCTTCCGCGGGAGCCCGGCTTACCTGCGCCCGAGCGGC 60
DB 184 ATGAGCTCCCGATCCAGATCTTCCGCGGGAGCCCGGCTTACCTGCGCCCGAGCGGC 243
QY 61 TGCCTGCCCCCAACAGACAGCGCGCTGGTTCCCGGCTGGGCGGAGCCCGAGCAAGCGGC 120
DB 244 TGCCTGCCCCCAACAGACAGCGCGCTGGTTCCCGGCTGGGCGGAGATCCGAGATATGCG 303
QY 121 AGCGCGCGCTGAGAGAGCGCGAGCTGGAGCCCGGCGACATCTCCCGGCAATCCCGGTC 180
DB 304 AGTGTGGCTGAGAGAGATCAACAGCTGGAGTCCCGGCGACATCTCCCGGCAATCCCGGTC 363
QY 181 ATCATACAGGGGCTACTCCGATAGTGTTCGTGTGGGCTTGTGTGGGCAACTCCGTGCTC 240
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Qy	301	TTGGCTTTGGGAGATGCTTTAGTACTCTCAACACGAGCCCTTTCAGATGAGCTCTACTTG	360
Db	486	CTGGCTTTGGGAGATGCTTTGGTATCTACACACTATGCCCTTTACAGATGCTCTACTTG	545
Qy	361	ATGAATTCCTGACCTTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC	420
Db	546	ATGAATTCCTGACCTTTTGGAGATGTGCTATGCAAGATTGTCATTTCATTGACTACTAC	605
Qy	421	AACATGTTACACAGATCTTCAACCTTGACATGATGAGACGGTGAACGGCTACATTGCCGTG	480
Db	606	AACATGTTACACAGATCTTCAACCTTGACATGATGATGAGACGGCTGACATTGCTGTG	665
Qy	481	TGCCACCCCGTGAAGAGCTTTGGACTTTCGGCACACCTTTGAAGGCAAAATCATCAATATC	540
Db	666	TGCCACCCCGTGAAGAGCTTTGGACTTTCGGACACTTTGAAAGCAAAATCATCAACATC	725
Qy	541	TGCATCTGGGCTGCTGTGCTCATCTGTGTGGCATCTTGCATATAGTCTTTGGAGGACCAAA	600
Db	726	TGCATTTGGGCTCTGGGCATCATCTGTGTGTATATAGGAGATAGTCTTTGGAGGACCAAA	785
Qy	601	GTCAGGGAGAAGTGTGATGTCATTGATGATGCTCTTGACAGTTCCAGATGATGATCACTCC	660
Db	786	GTCAGGGAGAAGTGTGATGTCATTGATGATGCTCTTGACAGTTCTCGATGATGATCACTCC	845
Qy	661	TGTTGGGACCTCTTCTATGATGATCTGCGTCTTTCATCTTTGCCCTTCTGTATCCCTGCTC	720
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Qy	721	ATCATCATGCTGTGCTGTACACCCGTATGATCCGCGGCTCAAGAGGCTCGGCTCTTCTCT	780
Db	906	ATCATCATGCTGTGCTGTACACCCGTATGATCCGCGGCTGAAAGTGTCCGGCTCTGCTCT	965
Qy	781	GAGTCCCGAGAAAGATCGCAACCTGCGTAGATCACACAGCTGTCTGTGTGTGTG	840
Db	966	GAGTCCCGAGAAAGATCGCAAACTCGCGGCATCACCAAGCTGTGTGTGTGTGTG	1025
Qy	841	GCAGTCTTCGCTGTGCTGTGATCTCCCATTCACATATCATCTGTGTGTGTGTGTGTG	900
Db	1026	GCAGTCTTCATCATCTGTGTGTGACCCCATTCACATCTTATCTGTGTGTGTGTGTGTG	1085
Qy	901	AGCACTTCCACAGACAGCTGCTCTCTCCAGCTTATCTTGTGATGAGCTGAGCTAT	960
Db	1086	AGCACTTCCACAGACAGCTGCTCTCTCCAGCTATATTTCTGTATGTGCTGTGTGTAT	1145
Qy	961	ACCAACAGTATGCTGTATATCCATTTCTTACGCTTTTCTTGATGAAAATTCAAGCGGTGT	1020
Db	1146	ACCAACAGTATGCTGTATATCCATTTCTTATGCTTTTCTTGATGAAAATTCAAGCGGTGT	1205
Qy	1021	TTCCGGGACTTCTGTCTTCCACTGAAATGAGATGAGACGGCAGAGCACTTACAGAGATC	1080
Db	1206	TTTATGGGACTTCTGTCTTCCCTTATTTAAGATGCGAATGAGACGGCAGAGCACTTATGAGTT	1265
Qy	1081	CGAAATACAGTTACAGATCTGTCTTACCTGAGGGAATCATGATGGATGAATTAACAGTA	1140
Db	1266	AGAAATACAGTTACAGATCTGTCTTCCATGAGAGATGTGGAGGGATGAATTAAGCACTA	1325
Qy	1141	TGACTAGTCGTGGA 1154	
Db	1326	TGACTAGTCGTGGA 1339	

RESULT 9
 US-08-292-694A-1
 : Sequence 1, Application US/08292694A
 : Patent No. 6319686
 : GENERAL INFORMATION:
 : APPLICANT: BELL, GRAEME
 : APPLICANT: REISINGE, TERRY
 : APPLICANT: YASUDA, KAZUKI
 : TITLE OF INVENTION: OPIOID RECEPTORS: COMPOSITIONS AND METHODS
 : NUMBER OF SEQUENCES: 46
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Arnold, White & Durkee

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1 STREET: P. O. Box 4433
2 CITY: Houston
3 STATE: Texas
4 COUNTRY: USA
5 ZIP: 77210
6
7 COMPUTER READABLE FORM:
8 MEDIUM TYPE: Floppy disk
9 OPERATING SYSTEM: IBM PC compatible
10 SOFTWARE: Patentin Release #1.0, Version #1.25
11
12 CURRENT APPLICATION DATA:
13 APPLICATION NUMBER: US/08/292,694A
14 FILING DATE: August 19, 1994
15
16 CLASSIFICATION: 435
17
18 PRIOR APPLICATION DATA:
19 APPLICATION NUMBER: 08/066,296
20 FILING DATE: 20 May 1993
21 CLASSIFICATION: 435
22 APPLICATION NUMBER: 08/100,694
23 FILING DATE: 30 July, 1993
24
25 CLASSIFICATION: 435
26 APPLICATION NUMBER: 08/147,592
27 FILING DATE: 5 No. 6319686ember 1993
28 CLASSIFICATION: 435
29 APPLICATION NUMBER: PCT/US94/05747
30 FILING DATE: 20 May 1994
31
32 CLASSIFICATION: 435
33
34 ATTORNEY/AGENT INFORMATION:
35 NAME: MARK B. WILSON
36 REGISTRATION NUMBER: 37,259
37 REFERENCE/DOCKET NUMBER: ARCD.140/WIM
38 TELECOMMUNICATION INFORMATION:
39 TELEPHONE: (512) 418-3000
40 TELEFAX: (713) 789-2679
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42 TELEX: 79-0924
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44 INFORMATION FOR SEQ ID NO: 1:
45
46 SEQUENCE CHARACTERISTICS:
47 LENGTH: 1410 base pairs
48 TYPE: nucleic acid
49 STRANDEDNESS: single
50 TOPOLOGY: linear
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52 MOLECULE TYPE: genomic DNA
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54 FEATURE:
55 NAME/KEY: CDS
56 LOCATION: 186..1325
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58 US-08-292-694A-1
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486 CTGGCTTTGGCAGATGCTTTGGTTACTACCACTATGCCCTTTGAGATGCTGCTACTTTG 545
QY 361 ATGAATTCCTGGCTTTTGGGGATGCTGTGCAAGATAGTAATTTCCATTGATTCTAC 420
Db 546 ATGAATTCCTGGCTTTTGGAGATGCTATGCAAAATTTGCTATTTCCATTGACTAC 605
QY 421 AACATGTTACCGACGATCTTTCACCTTGCACCATGATGAGGTGAGCCGCTACATTGCGGTG 480
Db 606 AACATGTTACCGACGATTTTCACTTGCACCATGATGAGGTGAGCCGCTACATTGCTGTG 665
QY 481 TGGCACCCTGTAAGGCTTTGACCTTCCGACACCTTTGAAGGCAAAATCATCAATATC 540
Db 666 TGGCACCCTGTAAGCTTTGACCTTCCGACACCTTTGAAGGCAAAATCATCAATATC 725
QY 541 TGCATCTGAGCTGCTGTCTCATCTGTTGGCATCTGCAAAATGCTCTTGAAGGCAACCA 600
Db 726 TGCATTTGAGCTCTTGGCATCTGTTGGATATCAGCAATGCTCTTGAAGGCAACCA 785
QY 601 GTCAAGGAAGACGTCGATGTCATTTGAGTCTCTTGCAGTTCCAGATGATGACTACTCC 660
Db 786 GTCAAGGAAGATGTGATGTCATTTGAAATGCTCTTGCAGTTCTGATGATGATTAATTC 845
QY 661 TGTGAGGACCTCTTTCATGAAAGATGCGCTCTTTCATTTTGGCTTGTGATCTCTGTCTC 720
Db 846 TGTGAGGATCTCTTTCATGAAAGATGCTGTCTTTCATTTTGGCTTGTGATCTCTGTCTC 905
QY 721 ATCATCATCTGCTGCTACACCTGATGATCTGCGCTCTGCAAGAGGCTCGGCTCTTCT 780
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QY 781 GGCTCCCGAGAGAAAGATGCAACCTGCGTGAATTCACCAAGCTGCTGTGTGTGTG 840
Db 966 GGCTCCCGAGAGAGCAAGAAATCTCCGCGCATCACCAAGCTGCTGTGTGTGTG 1025
QY 841 GCAATCTTCTGCTGCTGCTGCACTCCCATTTCAATTTCACTCTGTGTGTGTGTG 900
Db 1026 GCAATCTTCTGCTGCTGCTGCACTCCCATTTCACTCTGTGTGTGTGTGTG 1085
QY 901 AGCACCCTCCACAGACAGCTCTCTCTCAGCTATTAATTTTGCATGCGCTTGAAGCTAT 960
Db 1086 AGCACCCTCCACAGACAGCTCTCTCTCAGCTATTAATTTTGTATGCTTGTGTGTAT 1145
QY 961 ACCAAGATGAGCTTGAATCTCTCTCTGAGCTTTTGTATGAAGAACTTCAAGCGGTG 1020
Db 1146 ACCAAGATGAGCTTGAATCTCTCTCTGAGCTTTTGTATGAAGAACTTCAAGCGGTG 1205
QY 1021 TTCGGGACCTTCTGCTTCCACTGAAGATGAGAGGCGGCGACAGCATAGCAGATC 1080
Db 1206 TTTAGGACCTTCTGCTTCCACTGAAGATGAGAGGCGGCGACAGCATAGCAGATC 1265
QY 1081 CGAAATACAGTTCAAGATCTGCTTACCTGAGGAGCATTCGATGGAGTAATTAACAGTA 1140
Db 1266 AGAAACACAGTTCAAGATCTGCTTCCATGAGAGATGTGGAGGAGTAATTAACAGTA 1325
QY 1141 TGACTAGTCGTGGA 1154
Db 1326 TGACTAGTCGTGGA 1339

RESULT 10
US-08-147-592A-11
Sequence 11, Application US/08147592A
Patent No. 6096513
GENERAL INFORMATION:
APPLICANT: Bell, Graeme I
APPLICANT: Reisine, Terry
APPLICANT: Yasuda, Kazuki
TITLE OF INVENTION: Opioid Receptor Genes,
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433

CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 72210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/147,592A
FILING DATE: 05-NOV-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/100,694
FILING DATE: 30-JUL-1993
CLASSIFICATION: 435
APPLICATION NUMBER: 08/066,296
FILING DATE: 20-MAY-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: ARCD:105
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
TELEX: N/A
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1000 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: N
LOCATION: 607-608, 642-643, 896, 906
IDENTIFICATION METHOD: N = A, C, G or T
FEATURE:
NAME/KEY: CDS
LOCATION: 102..986
FEATURE:
NAME/KEY: Xaa
LOCATION: 169, 181, 265, 269
IDENTIFICATION METHOD: Xaa = unknown
US-08-147-592A-11

Query Match 75.5%; Score 871.2; DB 3; Length 1000;
Best Local Similarity 97.6%; Pred. No. 1.1e-203;
Matches 892; Conservative 0; Mismatches 19; Indels 3; Gaps 1;

QY 244 TTCTGTATCATCCGATACCAAGATGAGAGCAACCAATTTCATATTTAACTTG 303
Db 87 TTCTTTCTTTTGTAGTACCAAAAGATGAGAGCAACCAATTTCATATTTAACTTG 146
QY 304 GCTTGGCAGATGCTTAACTTAACTTCAACCATGCGCTTGAAGTACGCTACTTGATG 363
Db 147 GCTTGGCAGATGCTTAACTTAACTTCAACCATGCGCTTGAAGTACGCTACTTGATG 206
QY 364 AATTCTGAGCTTTTGGGAGTGTGCTGTGCAAGATAGTAATTTCAATGATTACTACAC 423
Db 207 AATTCTGAGCTTTTGGGAGTGTGCTGTGCAAGATAGTAATTTCAATGATTACTACAC 266
QY 424 ATGTTACCGACGATCTTTCACCTTGCACCATGATGAGGTGAGCCGCTACATTGCGGTGC 483
Db 267 ATGTTACCGACGATCTTTCACCTTGCACCATGATGAGGTGAGCCGCTACATTGCGGTGC 326
QY 484 CACCCGTAAGGCTTTGACCTTCCGACACCTTGAAGGCAAAAGATCATCAATATCTGC 543
Db 327 CACCCGTAAGGCTTTGACCTTCCGACACCTTGAAGGCAAAAGATCATCAATATCTGC 386
QY 544 ATCTGCTGTGTGCTATCTGTGATCTGTGACATCTGCAATATGCTCTTGAAGGCAACCAAGTC 603

DB 1058 TCACGAGTGTCTTCAAGAGAGTCTTGATCCACACCTGCTCCAGATCGAAGCAAAACT 1117
QY 1070 CTAGCAGAGTCCGAATATACAGTTACAGATCTGCTTAC 1107
DB 1118 CCATCGAGTCCGTGAGAACACTAGGGAACATCCCTCC 1155

RESULT 13

US-08-889-108-1
; Sequence 1, Application US/08889108
; Patent No. 6103492
; GENERAL INFORMATION:
; APPLICANT: Yu, Lei
; TITLE OF INVENTION: Mu Opioid Receptors: Compositions and Methods
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/889,108
; FILING DATE:
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/305,518
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: INDA005\WIM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-474-7577
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1618 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (cDNA)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 214..1410
; US-08-889-108-1

Query Match 38.7%; Score 446.4; DB 3; Length 1618;

Best Local Similarity 66.9%; Pred. No. 9.2e-100; Matches 668; Conservative 0; Mismatches 321; Indels 9; Gaps 2;

QY 110 ACAGCAACGCGACGCCGCGCTCGAGGACGCGACAGCTGGAGCCGCGACATCTCCCGG 169
DB 350 ACCGACCGGGCTTGGCGGGAACGACAGCTGTGCGCTCAAGACCGGAGCCCTTCATCG 409
QY 170 CCATCCGGGTATCATCAACGCGGCTCTACTCCGTAGTGTTCGTCTGGGCTTGGTGGCA 229
DB 410 TCACAGCCATATACCATATGAGCCCTCTACTATGCTGTGTAGTGGGCTCTTCGGAA 469
QY 230 ACTGCTGGTATGATGATCCGATCCGATACAAAGATGAAGCAGACCAACATTT 289
DB 470 ACTTCTGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 529
QY 290 ACATATTTAAGCTGCTTGGCAGATGCTTTAGTTACTACACCATGACCTTTGAGAGTA 349
DB 530 ACATTTCAAGCTTCTCTGCGGAGAGGCTTAGGACCAAGTACACTGCGCTTTGAGAGTG 589

QY 350 CGGTCTACTGTATGATTCCTGGCCCTTTGGGAGATGTGCTGTGCAAGATAGTAATTTCCA 409
DB 590 TCAACTACTGTATGAGGAATGGAATGCGCTTGGAAACATCTCTGCAAGATGATGATCTCA 649
QY 410 TTGATTTACTACAACATGTTCAACAGATCTTCACTTGAACATGATGAGCGTGAACCGCT 469
DB 650 TAGATTTACTACAACATGTTCAACAGATTTACCTCTGCAACATGAGCGTGAACCGCT 709
QY 470 ACATTCGGGTGTGCAACCCCGTGAAGCTTGGACTTCCGCAACACCTTTGAAGCAAGA 529
DB 710 ACATTCGTGTGCGACCAACGATCAAAAGCCCTGATTCGTATCCGCCCAATGCAAAA 769
QY 530 TCATCAATATTCGATCTGCGCTGTGTGTATCTTTGGGCAATCTCTGAATAGTCTTG 589
DB 770 TCGTCAAGCTGTGCAACTGATCTCTCTTCCATCGCTGTGCTGTAATGTTATG 829
QY 590 GAGGACCAAAAGTCAAGGGAAGACGTGATGTATGATGAGTCTCTTGCAGTTCCAGATG 649
DB 830 CAACCAAAATACAGGAGGAGGCTC-----CATGATTTGCAACCTCAGTTCTCCAC 883
QY 650 ATGACTACTCTGTGAGGACCTTTCAATGAGATCTGCGCTTTCATCTTTGCTTCGTA 709
DB 884 CAACCTGGTACTGGGAGAACTGCTC-----AAATCTGTGTCTTTATCTTCGCTTCATCA 940
QY 710 TCCCTGTCTCTATCATCATCTGTCTGTACACCCGTATGATCTGCTGCTCAAGAGCTTC 769
DB 941 TCCCATCTCTCATCATCACTGTGTGTACGGCTGTATGATCTTACGACTCAAGAGGCTTC 1000
QY 770 GGCCTCTTCTTGTGCTCCGAGAAAGATTCGCAACCTGCTGATGATTCACAGCTGCTCC 829
DB 1001 GCATGCTATCGGCTCTCCAAAGAAAGACAGAAATCTGGGACGATCAACCGGATGTGTC 1060
QY 830 TGTGTGTGTGTGCACTCTTCTGTCTGTGAGCTTCCATTCATCATTCATCTGTGTCG 889
DB 1061 TGTGTGTGTGTGCTGTATTTATGCTGTGTGAGACCCCATCACTATCTGTCATCATCA 1120
QY 890 AGGCTGTGGGAGACCTTCCACAGACAGCTGCTCTCTCCAGCTATTAATCTTGTGATG 949
DB 1121 AAGCGCTATATCAAGATTCAGAAACCATATTCAGACCGTTTCTGGGCACTTCTGTGATG 1180
QY 950 CCTTAGGCTATATCAACAGTATGACCTGAATCCATTCCTTCAAGCTTTCTTGAAGAAACT 1009
DB 1181 CTTTGGGTATACAGAAACAGCTGCTGAAATCCAGTTCTTTAGCCCTTCTCGATGAAACT 1240
QY 1010 TCACGCGGTGTTTCCGGAATCTTCTGCTTTCATGAAGATGAGATGAGCGGACAGACA 1069
DB 1241 TCACGCGATGCTTCAAGAGGTTCTGATTCACCACTCGTCCACGATCGAAGCAAGAAACT 1300
QY 1070 CTAGCAGAGTCCGAATATACAGTTCAAGATCTGCTTAC 1107
DB 1301 CCATCGAGTCCGTGAGAACACTAGGGAACATCCCTCC 1338

RESULT 14

US-08-889-108-3
; Sequence 3, Application US/08889108
; Patent No. 6103492
; GENERAL INFORMATION:
; APPLICANT: Yu, Lei
; TITLE OF INVENTION: Mu Opioid Receptors: Compositions and Methods
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

QY 350 CGGTCTACTGTATGATTCCTGGCCCTTTGGGAGATGTGCTGTGCAAGATAGTAATTTCCA 409
DB 590 TCAACTACTGTATGAGGAATGGAATGCGCTTGGAAACATCTCTGCAAGATGATGATCTCA 649
QY 410 TTGATTTACTACAACATGTTCAACAGATCTTCACTTGAACATGATGAGCGTGAACCGCT 469
DB 650 TAGATTTACTACAACATGTTCAACAGATTTACCTCTGCAACATGAGCGTGAACCGCT 709
QY 470 ACATTCGGGTGTGCAACCCCGTGAAGCTTGGACTTCCGCAACACCTTTGAAGCAAGA 529
DB 710 ACATTCGTGTGCGACCAACGATCAAAAGCCCTGATTCGTATCCGCCCAATGCAAAA 769
QY 530 TCATCAATATTCGATCTGCGCTGTGTGTATCTTTGGGCAATCTCTGAATAGTCTTG 589
DB 770 TCGTCAAGCTGTGCAACTGATCTCTCTTCCATCGCTGTGCTGTAATGTTATG 829
QY 590 GAGGACCAAAAGTCAAGGGAAGACGTGATGTATGATGAGTCTCTTGCAGTTCCAGATG 649
DB 830 CAACCAAAATACAGGAGGAGGCTC-----CATGATTTGCAACCTCAGTTCTCCAC 883
QY 650 ATGACTACTCTGTGAGGACCTTTCAATGAGATCTGCGCTTTCATCTTTGCTTCGTA 709
DB 884 CAACCTGGTACTGGGAGAACTGCTC-----AAATCTGTGTCTTTATCTTCGCTTCATCA 940
QY 710 TCCCTGTCTCTATCATCATCTGTCTGTACACCCGTATGATCTGCTGCTCAAGAGCTTC 769
DB 941 TCCCATCTCTCATCATCACTGTGTGTACGGCTGTATGATCTTACGACTCAAGAGGCTTC 1000
QY 770 GGCCTCTTCTTGTGCTCCGAGAAAGATTCGCAACCTGCTGATGATTCACAGCTGCTCC 829
DB 1001 GCATGCTATCGGCTCTCCAAAGAAAGACAGAAATCTGGGACGATCAACCGGATGTGTC 1060
QY 830 TGTGTGTGTGTGCACTCTTCTGTCTGTGAGCTTCCATTCATCATTCATCTGTGTCG 889
DB 1061 TGTGTGTGTGTGCTGTATTTATGCTGTGTGAGACCCCATCACTATCTGTCATCATCA 1120
QY 890 AGGCTGTGGGAGACCTTCCACAGACAGCTGCTCTCTCCAGCTATTAATCTTGTGATG 949
DB 1121 AAGCGCTATATCAAGATTCAGAAACCATATTCAGACCGTTTCTGGGCACTTCTGTGATG 1180
QY 950 CCTTAGGCTATATCAACAGTATGACCTGAATCCATTCCTTCAAGCTTTCTTGAAGAAACT 1009
DB 1181 CTTTGGGTATACAGAAACAGCTGCTGAAATCCAGTTCTTTAGCCCTTCTCGATGAAACT 1240
QY 1010 TCACGCGGTGTTTCCGGAATCTTCTGCTTTCATGAAGATGAGATGAGCGGACAGACA 1069
DB 1241 TCACGCGATGCTTCAAGAGGTTCTGATTCACCACTCGTCCACGATCGAAGCAAGAAACT 1300
QY 1070 CTAGCAGAGTCCGAATATACAGTTCAAGATCTGCTTAC 1107
DB 1301 CCATCGAGTCCGTGAGAACACTAGGGAACATCCCTCC 1338


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QY 110 ACAGCAAGGCGAGCGCGGCTGGAGAGACCGCAGCTGGAGCGCGGCGACATCTCCCGG 169
DB 350 ACCGCAACCGGCTTGGCGGGAACGACACCTTGCCTTACAGACGGGACCTTTCATG 409
QY 170 CCATCCCGGTCAATCAACGCGGCTTCTAGTCTGTCGTGCGGCTTGGGCGCA 229
DB 410 TCACAGCCATTACATCATGCGCCTTACTATCTGTGTGTAGTGGGCTTGTGGAA 469
QY 230 ACTCGGTGATCATCTTGTGATCATCCGATACCAAGATGAAAGACGACCAACATTT 289
DB 470 ACTTCGTGTGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 529
QY 290 ACATATTTAACTGGCTTGGCGAGATGCTTTAGTTACTAACCCAGCCCTTTCAGAT 349
DB 530 ACATTTTCAACCTTGTCTTGGCGAGCGCTTTCAGACGATGACCTTTCAGATG 589
QY 350 CGGTCTACTGTGATGATTCCTGCTTGGGAGTGTGTGTGTGTGTGTGTGTGTGT 409
DB 590 TCACACTGATGATGGGACATGGCCCTTGGAAACATCTCTGTGTGTGTGTGTGTGT 649
QY 410 TTGATTACTACAAATGTTTACACAGATCTTCACTTGAACATGATGAGCGTGG 469
DB 650 TAGATTACTACAAATGTTTACACAGATCTTCACTCTGTGTGTGTGTGTGTGTGT 709
QY 470 ACATGCGGTGGCGACCGCGGAGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGT 529
DB 710 ACATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 769
QY 530 TCATCAATATCTGATCTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 589
DB 770 TGTGTACAGCTGTGCACTGTGATCTTCTTGTGTGTGTGTGTGTGTGTGTGTGT 829
QY 590 GAGGCAACAAAGTCAGGAAAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 649
DB 830 CAACCAACAAATGACAGGAGGAGGCTC-----CATGATGTGACCCCTCAGTGTCTCCACC 883
QY 650 ATGATCTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 709
DB 884 CAACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 940
QY 710 TCCGTGTCTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 769
DB 941 TCCGTGTCTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 1000
QY 770 GGCCTCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 829
DB 1001 GCATGCTATCGGAGCTCCTCAAAAGAAAGACAGGATCTGCGCAGGATCACCCGATG 1060
QY 830 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 889
DB 1061 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1120
QY 890 AGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 949
DB 1121 AAGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1180
QY 950 CCTTGAAGCTATACCAACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1009
DB 1181 CTTTGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1240
QY 1010 TCAGGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1069
DB 1241 TCAGGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1300
QY 1070 CTAGCAGAGTCCGAATATGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1107
DB 1301 CCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1338

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RESULT 16
US-08-120-601B-3
; Sequence 3, Application US/08120601B

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; Patent No. 6235496
; GENERAL INFORMATION:
; APPLICANT: Yu, Lei
; TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/120,601B
; FILING DATE: 13-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: INDA:002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1618 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 339..1232
; US-08-120-601B-3

Query Match 38.7%; Score 446.4; DB 3; Length 1618;
Best Local Similarity 66.9%; Pred. No. 9, 2e-100;
Matches 668; Conservative 0; Mismatches 321; Indels 9; Gaps 2;

QY 110 ACAGCAAGGCGAGCGCGGCTGGAGAGACCGCAGCTGGAGCGCGGCGACATCTCCCGG 169
DB 350 ACCGCAACCGGCTTGGCGGGAACGACACCTTGCCTTACAGACGGGACCTTTCATG 409
QY 170 CCATCCCGGTCAATCAACGCGGCTTCTAGTCTGTCGTGCGGCTTGGGCGCA 229
DB 410 TCACAGCCATTACATCATGCGCCTTACTATCTGTGTGTAGTGGGCTTGTGGAA 469
QY 230 ACTCGGTGATCATCTTGTGATCATCCGATACCAAGATGAAAGACGACCAACATTT 289
DB 470 ACTTCGTGTGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 529
QY 290 ACATATTTAACTGGCTTGGCGAGATGCTTTAGTTACTAACCCAGCCCTTTCAGAT 349
DB 530 ACATTTTCAACCTTGTCTTGGCGAGCGCTTTCAGACGATGACCTTTCAGATG 589
QY 350 CGGTCTACTGTGATGATTCCTGCTTGGGAGTGTGTGTGTGTGTGTGTGTGTGT 409
DB 590 TCACACTGATGATGGGACATGGCCCTTGGAAACATCTCTGTGTGTGTGTGTGT 649
QY 410 TTGATTACTACAAATGTTTACACAGATCTTCACTTGAACATGATGAGCGTGG 469
DB 650 TAGATTACTACAAATGTTTACACAGATCTTCACTCTGTGTGTGTGTGTGTGTGT 709
QY 470 ACATGCGGTGGCGACCGCGGAGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGT 529
DB 710 ACATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 769
QY 530 TCATCAATATCTGATCTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 589

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Qy	950	CTTAGGGGTATACCAACAGTAGACCTGGATCCATCTCTAGAGCCCTTCTGATGAAACT	1009
Db	1181	CTTTGGGTAAACGACACAGCTGCTCGAATCCAGTTCCTTAGCGCTCTCGATGTAACCT	1240
Qy	1010	TCAAGCGGTGTTTCCGGAGACTTCTGCTTCCACTGAATGAGATGAGCGCGAGAGCA	1068
Db	1241	TCAAGCGATGCTTCAGAGAGTTCTGCAATCCCACTCGTCCACGATCGAACGCAAACT	1300
Qy	1070	CTAGCAGATCCGAATAACAGTTCAGATTCCTGTTC	1107
Db	1301	CCACTCGAGTCCGTCAGAACACTAGGGAACATCCCTCC	1338

RESULT 18
PCT-US94-10358-3

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1  TITLE OF INVENTION:  MU OPIOID RECEPTORS: COMPOSITIONS AND METHODS
2  NUMBER OF SEQUENCES:  17
3  CORRESPONDENCE ADDRESS:
4  ADDRESSEE:  Arnold, White & Durkee
5  STREET:  P. O. Box 4433
6  CITY:  Houston
7  STATE:  Texas
8  COUNTRY:  USA
9  ZIP:  77210
10 COMPUTER READABLE FORM:
11 MEDIUM TYPE:  floppy disk
12 COMPUTER:  IBM PC compatible
13 OPERATING SYSTEM:  PC-DOS/MS-DOS/ASCII
14 SOFTWARE:  PATENTIN RELEASE #1.0, VERSION #1.25
15 CURRENT APPLICATION DATA:
16 APPLICATION NUMBER:  PCT/US94/10358
17 FILING DATE:  Concurrently herewith
18 CLASSIFICATION:
19 PRIOR APPLICATION DATA:
20 APPLICATION NUMBER:  08/120,601
21 FILING DATE:  13 SEPTEMBER 1993
22 ATTORNEY/AGENT INFORMATION:
23 NAME:  WILSON, MARK B. 37,259
24 REGISTRATION NUMBER:  37,259
25 REFERENCE/DOCKET NUMBER:  INDA005P--
26 TELECOMMUNICATION INFORMATION:
27 TELEPHONE:  (512) 418-3000
28 TELEFAX:  (713) 789-2679
29 TELEX:  79-0924
30 INFORMATION FOR SEQ ID NO: 3:
31 SEQUENCE CHARACTERISTICS:
32 LENGTH:  1618 base pairs
33 TYPE:  nucleic acid
34 STRANDEDNESS:  single
35 TOPOLOGY:  linear
36 MOLECULE TYPE:  CDNA
37 FEATURE:
38 NAME/KEY:  CDS
39 LOCATION:  339..1235
40 PCT-US94-10358-3

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	Query Match	38.7%	Score 446.4	DB 5	Length 1618
	Best Local Similarity	66.9%	Pred. No. 9,2e-100		
	Matches 668	Conservative 0	Mismatches 321	Indels 9	Gaps 2
QY	110 ACAGAACGGCAGCGCCGCGTGGAGAGACGGCAGCTGAGGCCCGCGCATTCTCCCGG	169			
DB	350 ACCGACCGGGCTTGGCCGGAAAGACAGCCTGTGCTTCAGACCCGACCCCTTCATGG	409			
QY	170 CCATCCCGGTATCATACAGCGGGGTATTCCGTAGTCTTCGTCGGGCTTGTGTGGGA	229			
DB	410 TCACAGCCATTCCATCATGAGGCCCTCTACTCTATCTGTGTGTAGTGGGCTCTTGGAA	469			
QY	230 ACTGCTGTATCTTTCTGATCATCTCCGATTACCAAGATGGAAGACGACCAATTT	289			

Db	470	ACTTCGTCGATGATGTGATTGTAATGATACCAACCAATGAAAGCTGCACCAACATCT	522
Oy	290	ACATATTTAACCTGGCTTTGGCAGATGCTTTATGTTATCTACACCAATGCGCTTTGAGAGTA	349
Db	530	ACATTTTCMACCTTGCTCTGGCAGACGCTTAGCGACACAGTACACTGCGCTTTTCAGAGTG	589
Oy	350	CGGTCTACTTATGTAATTCCTGGCCCTTTTGGGGATGTCGTGTCGAAGATAGTAATTTCCA	409
Db	590	TCAACTACTGATGGAACATGCGCCCTTCGGAACCATCTCTGCAAGATCGTGAATCTCA	649
Oy	410	TTGATTACTACAAATGTTTCAACAGCATCTTTCACCTTGAACATGATGAGCTGACCGCT	469
Db	650	TAGATTACTACAAATGTTTCAACAGCATATTTACACCTCTGCAACATGAGCTGAGACCGCT	709
Oy	470	ACATTTCCGTCGTCACCCCGGTGAAGGCTTTGGAATTCGCGACACCTTTGAAGGCAANA	529
Db	710	ACATTTGCTGTGCGCACCCAGTCGAAAGCCTTGATTTCCGTAACCCCGAATATGCGAANA	769
Oy	530	TCATCAATATCTGCATCTGCGTGTGTCGTATCTGTTGGCATCTCTGCAATAGTCTTG	589
Db	770	TCGTCAAGCTGTGCAACTGATTCCTCTTCTGCATCGGTGTGCTGTGATATGTTTCATGG	829
Oy	590	GAGGCACCAAAAGTCAGGGAAGACGTGCATGTCATTTGAGTGTCTCTTGGCAGTTCCAGATG	649
Db	830	CAACCACAAAAATACAGGACGGGGTC-----CATGATTGACCCCTCACGTTCTCCACCC	883
Oy	650	ATGACTACTCTGTCGGGGACCTCTTCATGAGAAGATCTGCGTCTTCATCTTTGCGCTTGTA	709
Db	884	CAACTGCTACTGGGAAGAACCTGCTC---AAATGTGTGTTTATCTTTCGCTTTCATCA	940
Oy	710	TCCCTGTCTCATCATCATCTGTCGTCTGCTACACCCCTGATATCTCGCTCTCAAGAGCTCC	769
Db	941	TGCCGATCTCATATCACTGTGTGTTTACGGCTGTGATATCTTACGACTCAAGAGACGTTTC	1001
Oy	770	GGCTTCCTTTCTGSGCTCCCGGAGAGAAGATCGCAACTGCGTATGATACACCAACTGTGTC	829
Db	1001	GCATGCTATCGGGCTCCAAAGAAAAGACAGAAATCTGCGCAGATCACCGGATGTGTC	1061
Oy	830	TGCTGTGTGTGGACGTCTTCGTGTCGTCTGCTGGACTCCGATTCACATATTCATCTGTGTGG	889
Db	1061	TGCTGTGTGTGGCTGTATTTATTCGCTGTGGAACCCCATCAACATTCACGTCAATCATCA	1121
Oy	890	AGGCTTGGGGAGACCTCCACAGACAGACGTCTCTCCAGCATTAATCTCTGATGCG	949
Db	1121	AAGGCTGTATCCAGATTCAGAAACACATTTACAGACGTTTCTGGGACCTTCTGTGATGG	1181
Oy	950	CCTTAGGCTATACCAACAGTAGCGCTGAATCCCATCTCTACGCTTTTCTTGATGAAAATCT	1001
Db	1181	CTTTGTGGTTACACGAACAGCTGCGTGATTCAGTTCTTTATGCGCTTCCGTGATGAAAATCT	1241
Oy	1010	TCAAACGGGTGTTTCGGGACTTTCTGTCTTCCACTGAAGATGAGATGGAAGCGGCAAGACA	1061
Db	1241	TCAAACGGATGCTTACAGAGATTTCTGCAATCCCAACCTGTGTCACGATCGAATCGAACAATCT	1301
Oy	1070	CTAGAGAGTCCGAAATACAGTTACAGATTCAGATTCGCGTTAC	1107
Db	1301	CACTCTGAGTCCGTACGAACACTAGGGAACATCTCTCC	1338

RESULT 19
US-08-889-108-7
Sequence 7, Application US/08889108
Patent No. 6103492
GENERAL INFORMATION:
APPLICANT: Yu, Lei
TITLE OF INVENTION: Mu Opioid Receptors: Compositions and Methods
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA

```

ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/889,108
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/305,518
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: INDA005\WIM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1610 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-889-108-7

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Query Match      37.7%; Score 434.8; DB 3; Length 1610;
Best Local Similarity 66.3%; Pred. No. 6.3e-97;
Matches 660; Conservative 0; Mismatches 327; Indels 9; Gaps 2;

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QY 92 CCGGCTGGGCGGAGCCGAGCAAGCAAGCGGCGGCTGGAGAGCCGAGCTGAGC 151
DB 363 CCGAGCCATGCGGTCCGACCGCAGCCAGCTGGGCGGAGAGCAGCCTGCTCCGA 422
QY 152 CCGGCGCATCTCCCGGCGCATCCGCTCATCATCAGGCGGCTACTCCGTAGTGTG 211
DB 423 CCGGCGATCCTCTCATATATACGCGCCATCAGATCATGCGCTCTACTCATGTGTGCG 482
QY 212 TCGTGGGCTGTGGGCACTCGCTGTATGTTGCTGATCATTCGATACACAAAGATGA 271
DB 483 TGGTGGGGCTCTTCGAAACTCTCGGTGATGATGTTGTCAGATACACCAAGATGA 542
QY 272 AGACAGAACCAATTTATATTTAACTGCTTGGGAGATGCTTATGTTACTACAA 331
DB 543 AGACTGCAACCAATTTATATTTTCAACTGCTGCGAGATGCTTATGCGACAGTA 602
QY 332 CCAATGCCCTTTAGAGTACGCTCTACTTGAATTCCTGGCTTTTGGGATGTGCTGT 391
DB 603 CCTGCGCTTCCAGAGTGAATTTAATCTATATGGAACATGCGCATTTGGAACATCTTT 662
QY 392 GCAAGATGATTAATTTTCATTGATTTACTACAACTGTTACACAGCATCTTCACTTACCA 451
DB 663 GCAAGATGATGATCTCATGATTTACTATTAACATGTTACACAGCATTTACCTCTGCA 722
QY 452 TGATGAGCGTGAACCGCTATATTCGCTGTCGCAACCCCGGAGGCTTTGGAATTCGCA 511
DB 723 CCAATGATGTTGATTCATATATGAGTCTGCAACCTGTCAGAGGCTTATGATTTCCGA 782
QY 512 CACCTTGAAGGCAAGATCATATATTCATCTGCTGCTGTGCTCATCTGTTGGA 571
DB 783 CTCCTCCGAAATGCAAAATATATCATGTCTGCAACTGATGATCTCTTCAAGCATTTGCTC 842
QY 572 TCTCTGATATGCTCTTGGAGGCAACAAAGTCAAGGAAAGCTGATGTCATTGAGTGTCT 631
DB 843 TTCCTTAAATGTTCAATGCTGACAAACAAATATACAGCAAGG-----TTCATATGATTGTA 896
QY 632 CCTTGAGTTCCAGATGATGATCTACTCCCTGTCGTCGAGGACCTTTCATGATGATGCTGCT 691
DB 897 CACTAATATTTCTCTCATTCACACTGCTACTGGGAAACCTGCG---TGAAGATCTGTGTTT 953

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QY 692 TCAATCTTGGCTTCGTGATCCCTGTCTCATATCATATCTGTGCTACACCTGATGATCC 751
DB 954 TCAATCTTGGCTTCATATATGCTCAGTCTCATATCAATCCGTTGCTATGACTGATATCT 1013
QY 752 TGGGTCCAAAGAGCGTCCGCTCTCTTTCGCTCCCGAGAGAAAGATTCGCAACCTGCTGA 811
DB 1014 TGGGCTCCAAAGATGTCCTGATGCTCTCTGCTCCAAAGAAAGAGACAGAAATCTTTCGAA 1073
QY 812 GATACCAAGACTGTGCTGTCGTGTCGTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 871
DB 1074 GATACCAAGAGATGTCGTGTCGTGTCGTGTCGTGTCGTGTCGTGTCGTGTCGTGTCGTC 1133
QY 872 ACATATTCATCTCTGTGTCGTGTCGTGTCGTGTCGTGTCGTGTCGTGTCGTGTCGTGTC 931
DB 1134 ACATATTCATCTCTGTCGTGTCGTGTCGTGTCGTGTCGTGTCGTGTCGTGTCGTGTCGTC 1193
QY 932 GCATATTCATCTCTGTCGTGTCGTGTCGTGTCGTGTCGTGTCGTGTCGTGTCGTGTCGTC 991
DB 1194 CTGGGCACTTCTGTCATTCCTCTGTCGTGTCGTGTCGTGTCGTGTCGTGTCGTGTCGTGTC 1253
QY 992 CTTTCTTATGAAAACTTCAAGCGGTGTTTCCGGGACTTCTGCTTTCGACTGAAAGATGA 1051
DB 1254 CATTCTGATGAAAACTTCAACGATGCTTCAAGAGATTCGTGTCGTGTCGTGTCGTGTCGTC 1313
QY 1052 GATGAGGCGGACGACACTAGCAGATGTCGGAATTA 1087
DB 1314 ACATGAGCAACAAACTCCACTCGAATTCGTGTCGAG 1349

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RESULT 20
PCT-US94-10358-7
Sequence 7: Application PC/TUS9410358
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10358
FILING DATE: Concurrently herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/120,601
FILING DATE: 13 SEPTEMBER 1993
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARK B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: INDA005P--
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1610 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
PCT-US94-10358-7
Query Match      37.7%; Score 434.8; DB 5; Length 1610;

```

Best Local Similarity 66.3%; Pred. No. 6.3e-97;
Matches 660; Conservative 0; Mismatches 327; Indels 9; Gaps 2;

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QY 92 CCGGCTGGGCGGAGCCGACGACGACGAGCGCGGCTCGGAGGAGCGCGACGCTGGAGC 151
DB 363 CCGACCCCAATCGGCTCGGAACCCGACCGACCTGGGGGAGAGACGACCTGTGCTCCGA 422
QY 152 CCGGCGACATCTCCCGGCGCATCCGGGTATCATACGGCGGCTCACTCCGAGTGTG 211
DB 423 CCGGAGTCTCTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 482
QY 212 TCGTGGGCTTGGTGGGCAACTGCGTGTGATGATGATGATGATGATGATGATGATGATG 271
DB 483 TGTGGGGGCTTGGGAAACTTCTGGTGTATGATGATGATGATGATGATGATGATGATGATG 542
QY 272 AGACGACCAACCAATTTACATTTTACCTGGCTTGGCAGATGCTTTAGTTACTACA 331
DB 543 AGACTGCCACCAACATTTACATTTTACCTGGCTTGGCAGATGCTTTAGTTACTACA 602
QY 332 CCATGCCCTTTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 391
DB 603 CCTGCCCCCTTCAGAGTGTGAATTAATGGAATGGAACATGGCCATTTGGAACCATCTTT 662
QY 392 GCAAGATGATATTTCCATTTGATTTACTACACATGTTCCAGACATCTTCACTTGACCA 451
DB 663 GCAAGATGATGATTTCTCCATGATGATTTACTACACATGTTCCAGACATTTCACTTCTG 722
QY 452 TGATAGCGCTGGACCGCTACATTTGCTGTGTCACCCCGTGAAGGCTTTGACCTTCCGA 511
DB 723 CCATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 782
QY 512 CACCTTTGAAGGCAAAAGATCATCATTTGATGATGATGATGATGATGATGATGATGATG 571
DB 783 CTCCCGAAATGCAAAATTTATCAATGCTGCAACATGATCTCTTTCATGACCATTTGGTC 842
QY 572 TCTGTCAATAGTCTTGGAGGACCAAAAGTCAAGGAAAGACGTCATGATGATGATGATG 631
DB 843 TTCCTGATATGTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 896
QY 632 CTTTGACGTTCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 691
DB 897 CACTTAACATTTCTCATCCACCTGATGATGATGATGATGATGATGATGATGATGATGATG 953
QY 692 TCATCTTGGCTTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 751
DB 954 TCATCTTGGCTTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1013
QY 752 TGGCTCTCAAGAGCGTCCGCTCTTTCGCTCCGAGAGAAAGTCCGACCTGCGTA 811
DB 1014 TGGCTCTCAAGAGTCCGCTCTTTCGCTCCGAGAGAAAGTCCGACCTGCGTA 1073
QY 812 GGATACACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 871
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QY 872 ACATTTATATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 931
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QY 932 GCTATTATCTTGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 991
DB 1194 CTTGACATCTTGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1253
QY 992 CTTTCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1051
DB 1254 CATTCTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1087
QY 1052 GGATGAGGCGGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1313
DB 1314 ACATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1349

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RESULT 21

US-08-188-275A-1
Sequence 1, Application US/08188275A

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; Patent No. 6258556
; GENERAL INFORMATION:
; APPLICANT: Unl, George R.
; APPLICANT: Wang, Jia-Bei
; APPLICANT: Johnson, Peter S.
; APPLICANT: Persico, Antonio
; TITLE OF INVENTION: CDNA and Genomic Clones Encoding Human
; TITLE OF INVENTION: Mu Opiate Receptor and the Purified Gene Product
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESS: Birch, Stewart, Kolasch & Birch
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22040-3487
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/188,275A
; FILING DATE: 28-JAN-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy Jr., Gerald M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 1173-449P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-241-1300
; TELEFAX: 703-241-2848
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2160 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..2160
; OTHER INFORMATION: /label= cDNA
; OTHER INFORMATION: /note= "cDNA encoding human mu opiate receptor"
US-08-188-275A-1

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Query Match 37.7%; Score 434.8; DB 3; Length 2160;

Best Local Similarity 66.3%; Pred. No. 7e-97;
Matches 660; Conservative 0; Mismatches 327; Indels 9; Gaps 2;

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QY 92 CCGGCTGGGCGGAGCCGACGACGACGAGCGCGGCTCGGAGGAGCGCGACGCTGGAGC 151
DB 337 CCGACCCCAATCGGCTCGGAACCCGACCGACCTGGGGGAGAGACGACCTGTGCTCCGA 396
QY 152 CCGGCGACATCTCCCGGCGCATCCGGGTATCATACGGCGGCTCACTCCGAGTGTG 211
DB 397 CCGGAGTCTCTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 456
QY 212 TCGTGGGCTTGGTGGGCAACTGCGTGTGATGATGATGATGATGATGATGATGATGATG 271
DB 457 TGTGGGGGCTTGGGAAACTTCTGGTGTATGATGATGATGATGATGATGATGATGATGATG 516
QY 272 AGACGACCAACCAATTTACATTTTACCTGGCTTGGCAGATGCTTTAGTTACTACA 331
DB 517 AGACTGCCACCAACATTTACATTTTACCTGGCTTGGCAGATGCTTTAGTTACTACA 576
QY 332 CCATGCCCTTTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 391
DB 577 CCTGCCCCCTTCAGAGTGTGAATTAATGGAATGGAACATGGCCATTTGGAACCATCTTT 636

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QY 392 GCAAGATGATTAATTTCCATTGATTACTACAAATGTTACACGACATCTTACCTTGACCA 451
DB 637 GCAAGATGATGATCTCATATGATTACTATATACATGTTCAACGACATATTCACCTCTGCA 696
QY 452 TGATAGCGTGAGACCGCTACATGCGGTGGCCACCCCGGAGAGCTTTGGACCTCCGCA 511
DB 697 CCATAGGTGTGATTCATATCATATGACGTCTGCCACCCCTGTCAAGGCGCTTATGATTCGGA 756
QY 512 CACCTTTGAAGGCAAAATCATATATCTGATCTGGCTGTGTGTCATCTGTGGCA 571
DB 757 CTCGCCGAATGCGCAAAATTTATCATATGTCGCAATGATGATCTCTCTTCAGCATTTGTC 816
QY 572 TCTCTGCAATAGCTTGTGAGGACCAAGTACAGGAAACGTCATCTGTGTCATCTGTGGCA 631
DB 817 TTCCTTAATGTTCAATGCTACAACAAAATACAGGCAAGG-----TTCATATGATTGTA 870
QY 632 CCTTGAGTTCCTCAGATGATGATGATCTCTGCTGGGAGACCTTTCAATGAGATCTGGTCT 691
DB 871 CACTAACATTTCTCTCATTCGACCTGCTACTGGGAAAACCTCG---TGAAGATCTGTGTT 927
QY 692 TCATCTTGGCTTGTGATCTCTGTCTCTCATCATCTGTCTGTCAACCTGTATGATCC 751
DB 928 TCATCTTGGCTTGTGATCTCTGTCTCTCATCATCTGTCTGTCAACCTGTATGATCT 987
QY 752 TGGGTCTCAAGAGCGCTCGGCTCTTTCTGGCTCCCGAGAGAAATGCGCACTGGCTTA 811
DB 988 TGGGCTCAAGAGTGTCTCGGCTCTCTGTCTCGGCTCCCGAGAGAAATGCGCACTGGCTTA 1047
QY 812 GGATCACGACGATGCTGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 871
DB 1048 GGATCACGAGATGCTGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1107
QY 872 ACATTTATCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 931
DB 1108 ACATTTATGCTATCATTTAAAGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1167
QY 932 GCTATTACTTCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 991
DB 1168 CTGGCACTTCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1227
QY 992 CTTTCTTGTATGAAACTTCAAGCGGTGTTCCGGAATCTTCTGCTTCTCACTGAAGATGA 1051
DB 1228 CATTTCTGATGAAACTTCAAGCGGTGTTCCGGAATCTTCTGCTTCTCACTGAAGATGA 1287
QY 1052 GGATGAGGCGGAGACGCTAGCAGATGCCGAAATA 1087
DB 1288 ACATTTAGCAACAAATCTCAGTCTGCAATTCGTCAGA 1323

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RESULT 22
US-09-351-198-1
; Sequence 1, Application US/09351198
; Patent No. 6335168
; GENERAL INFORMATION:
; APPLICANT: Kireek, Mary J
; APPLICANT: Laforge, Karl S
; APPLICANT: Yu, Lei
; APPLICANT: Tischfield, Jay A.
; TITLE OF INVENTION: ALLELES OF THE HUMAN MU OPIOID RECEPTOR, DIAGNOSTIC
; TITLE OF INVENTION: METHODS OF USING SAID ALLELES, AND METHODS OF TREATMENT
; TITLE OF INVENTION: BASED THEREON
; FILE REFERENCE: 600-1-226N
; CURRENT APPLICATION NUMBER: US/09/351,198
; CURRENT FILING DATE: 1999-07-09
; EARLIER APPLICATION NUMBER: 60/092,402
; EARLIER FILING DATE: 1998-07-10
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2162
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

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; NAME/KEY: misc feature
; LOCATION: (2063)
; OTHER INFORMATION: No. 6335168feature for this position in GeneBank.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2091)
; OTHER INFORMATION: No. 6335168feature for this position in GeneBank.
US-09-351-198-1

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Query Match 37.7% Score 434.8; DB 4; Length 2162;
Beet Local Similarity 66.3%; Pred. No. 7e-97;
Matches 660; Conservative 0; Mismatches 327; Indels 9; Gaps 2;

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QY 92 CCGGCTGGGCGGAGCCGACAGCAACGCGCGGCTCGAGAGAGCGCGGAGCTGAGC 151
DB 337 CCGAACCATGGGCGGCTCGAACCGGCAACCTGGGCGGAGAGAGAGCGCTGCGCTCGA 396
QY 152 CCGGACATTTCCCGGCGCATCCCGGTATCATCAGCGGCTTACTCGGTATGTTGG 211
DB 397 CCGGACATCTCTCATATCATACGCGCATCATCATGATCATGCGCTCTCATCTCATCTGTGCG 456
QY 212 TCGTGGGCTTGTGGGCACTCGGTGATGTTGTTGATCATCCGATACCAAAAGATGA 271
DB 457 TGGTGGGCTCTTGGAACTTCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 516
QY 272 AGACAGCAACCAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTA 331
DB 517 AGACTGCGACCAACATCATCATTTTCAACCTTGTGTGAGATGCTTGTGCGACGATGA 576
QY 332 CCATGCCCTTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 391
DB 577 CCGTCCCTTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 636
QY 392 GCAAGATGATTAATTTCCATTTGATTTACTACAAATGTTCAACAGATCTTACCTTGACCA 451
DB 637 GCAAGATGATGATTTCCATTTGATTTACTACAAATGTTCAACAGATTTACCTTGTGCA 696
QY 452 TGATGACGCTGAGACCGCTTACATGCTGCTGTCACACCCGTTGAAGCTTGTGACTTCGCA 511
DB 697 CCATGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 756
QY 512 CACCTTTGAAGGCAAAAGATCATCAATATTCGATCTGGGCTGCTGCTGCTGCTGCTGCTGCTG 571
DB 757 CTCGCCGAATGCGCAAAATTTATCAATGTCTGCAATCTGATCTCTTCAAGCATTTGCTC 816
QY 572 TCTCTGCAATAGTCTTGAAGGCAACCAAGTCAAGGAGAGAGATGATGATGATGATGATG 631
DB 817 TTCCTGTAATGTTCATGCTTACCAAAATATACAGGCAAGG-----TTCATATGATTGTA 870
QY 632 CTTTGAAGTCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 691
DB 871 CACTTAATTTCTTCTTCAACCTGTGTATCTGGGAAAAACCTCG---TGAAGATCTGTGTT 927
QY 692 TCATCTTGGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 751
DB 928 TCATCTTGGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 987
QY 752 TGGGTCTCAAGAGCGCTCGGCTCTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 811
DB 988 TGGGCTCAAGAGTGTCTCGGATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1047
QY 812 GGATCACGACGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 871
DB 1048 GGATCACGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1107
QY 872 ACATTTATCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 931
DB 1108 ACATTTATGCTATCATTTAAAGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1167
QY 932 GCTATTACTTGTGATGCTTGTGATGCTTGTGATGCTTGTGATGCTTGTGATGCTTGTGATG 991
DB 1168 CTGGCACTTGTGATGCTTGTGATGCTTGTGATGCTTGTGATGCTTGTGATGCTTGTGATG 1227

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Qy	Db	Qy	Db
992	1228	1052	1087
CCCTTCTGTGATGAAAACTTCCAGCGGATGTTCCGGAGCTTCGCTTCCACGAAAGATGA	CATTCTCGATGAAAACTTCAAACGATCCTTCAGAGAGTTCTGTATCCCAACCTTTCCA	GGATGAGACGGCAGACACTAGACAGATGCCAATAA	ACATTGAGCAACAAAATCTCACTCGAATTCGTCAGA
1323	1323	1323	1323

RESULT 23
US-09-113

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Sequence 1 Application US/09113426
Patent No. 6337207
GENERAL INFORMATION:
APPLICANT: Kreek, Mary J
APPLICANT: Laforge, Karl S
APPLICANT: Yu, Lei
APPLICANT: Tischfield, Jay A.
TITLE OF INVENTION: ALLELES OF THE HUMAN MU OPIOID RECEPTOR, DIAGNOSTIC
TITLE OF INVENTION: METHODS OF USING SAID ALLELES, AND METHODS OF TREATMENT
FILE REFERENCE: 600-1-226
CURRENT APPLICATION NUMBER: US/09/113,426
CURRENT FILING DATE: 1998-07-10
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 2162
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (2063)
OTHER INFORMATION: No. 6337207feature for this position in GeneBank.
FEATURE:
NAME/KEY: misc feature
LOCATION: (2091)
OTHER INFORMATION: No. 6337207feature for this position in GeneBank.
US-09-113-426-1

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Query Match	37.7%	Score 434.8	DB 4	Length 2162
Best Local Similarity	66.3%	Pred. No. 76-97		
Matches	660	Conservative	0	Mismatches 327, Indels 9, Gaps 2
QY	92	CCGGCTGGGGCCGAGCCCGACAGCAACGGCAGCGCCGGCTCGGAGGACGCGCAGCTGGAGC	151	
Db	337	CCGACCCCATGCGGCTCGGACCGCACCAACTGGGGGGAGAGACAGCCTGTGCTCCCTCCGA	396	
QY	152	CCGGGCAATCTCCCGGGCCATCCGGGATCATCAGCGCGGCTCTACTCCGATGGTCC	211	
Db	397	CCGGCAGTCCCTCCATGATTCAGCGGCATCAGCATATGGCCCTCTACTCCTCATCGTGTGG	456	
QY	212	TCGTGGGCTTGGTGGCACTCGCTGATCTGTGATTCATCCGATACACAAGATGA	271	
Db	457	TGTGGGGGCTCTTCGGAAACTTCTGTGTCATGTATGTATGTGTGATGATACCAAGATGA	516	
QY	272	AGACAGCAACCAACTTTACATTTTAACTCGGCTTTGGCAGATGCTTTAGTACTACAA	331	
Db	517	AGACTGCCACCAACATCTACATTTTTCACCTTGTGCTGTGGCAATGCTTTAGCCACAGTA	576	
QY	332	CCATGCCCCCTTCAGAGTACGCGTCTACTTGATGAATTCCTGGCGCTTTGGGGAGTGTGCTG	391	
Db	577	CCCTGCCCCCTTCAGAGTGTGAATTACCTAATGTGGAACATGGCCATTTGGAACCATTCCTTT	636	
QY	392	GCAAGATAGTAAATTTCCATTGATTTACTACACAATGTTCCACGAGATCTTACCTTGAACA	451	
Db	637	GCAAAATAGTATCTCCATAGATTATCTMAAATGTTCACCGACATATTCACCCCTCTGCA	696	
QY	452	TGATAGAGTGGACCGCTACATTTGCGGTGGCCACCCGCTGAAGGCTTTGAACCTTCGCA	511	
Db	697	CCATGAGCTTGTATGTATACATTCATTCGACAGCTGCGCACCCCTGTCAAGGCTTTAGATTTCGTA	756	
QY	512	CACCTTGAAGCAAGATCATCAATATCTGCATCTGGCTGCTGTGTCATCTGTTGGCA	571	

[illegible]

RESULT 24
US-09-016-434-1379

Sequence 1379, Application US/09016434
Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Sellhammer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1450
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071

REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1379:
SEQUENCE CHARACTERISTICS:
LENGTH: 2162 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: 9452072
US-09-016-434-1379

Query Match 37.7%; Score 434.8; DB 4; Length 2162;
Best Local Similarity 66.3%; Pred. No. 7e-97;
Matches 660; Conservative 0; Mismatches 327; Indels 9; Gaps 2;

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QY 92 CCGGCTGGGCGGAGCCGACAGCAAGGAGCGCGCTCGAGAGACGGCAGCTGGAGC 151
DB 337 CCGACCCATGCGGTCCGAAACCGACCACTGGCGGAGAGACAGCTGTGCTCCGA 396
QY 152 CCGGCAATCTCCCGGCAATCCGGTATATCAAGCGGCTTAATCTCGTAGTGTGG 211
DB 397 CCGGAGTCCCTCCATGATCAAGGCATCAATGAGCCCTTAATCTCAATCGTGTGG 456
QY 212 TCGTGGGCTTGGTGGCACTGCTGTGATGTGTGATCAATCGGATCAAGAGTGA 271
DB 457 TGGTGGGCTCTTGGAACTTCTGTGTATGTGTGTGTGTGTGTGTGTGTGTGTGT 516
QY 272 AAGACAGCAACCAATTTAATATTTAACTGTGTGTGTGTGTGTGTGTGTGTGTGT 331
DB 517 AGACTGCGCAACCAATCTTCAATTTTCACTTGTGTGTGTGTGTGTGTGTGTGTGT 576
QY 332 CCATGCGCTTTGAGTGAAGGTCTATGATGAATTTCTGCGCTTTTGGAGTGTGCT 391
DB 577 CCGTCCCTTCCAGAGTGTGAATTAATGGAATGGAACATGGCATTTGGAACCATCT 636
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DB 637 GCAAGATAGTATCTTCAATTTACTTCAATGTCACAGCATCTTCACTTGAACCA 696
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DB 697 CCATGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 756
QY 512 CACCTTTGAGGCAAGATCATATTTGATGATGATGATGATGATGATGATGATGATG 571
DB 757 CTTCCCGAAATGCCAAATTTATCAATGTCGACATGATCTCTTCAAGCATTTGTC 816
QY 572 TCTTGCATAGTCTTGTGAAGCACAAAGTCAGGAGAGAGTGCATGATGATGATG 631
DB 817 TTTCTGTATGTTTCAATGCTACAAACAAATACAGCAAG-----TTCCATATG 870
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DB 871 CACTAACATTTCTTCAATCAACCTGTGATCTGTGAAACCTG---TGAAGATCTGT 927
QY 692 TCATTTTGGCTTGTGATCTGCTGCTCATCATCATCATCATCATCATCATCATCAT 751
DB 928 TCATTTTGGCTTGTGATCTGCTGCTCATCATCATCATCATCATCATCATCATCAT 987
QY 752 TGGCTTCAAGAGCGTCCGCTCTTTTGTGCTCCGAGAGAAAGATGCAACCTGTG 811
DB 988 TGGCTTCAAGAGCGTCCGCTCTTTTGTGCTCCGAGAGAAAGATGCAACCTGTG 1047
QY 812 GGATCAACAGATGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 871
DB 1048 GGATCAACAGATGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1107
QY 872 ACATATTCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 931
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DB 1108 ACATTTAGTATCTATTAAGCTTTGTTAATTCAGAAACTAAGTTCAGACTGTT 1167
QY 932 GCTATTACTTTCATGCGCTTAAAGCTTATACCAACAGTAGCTGATTCCTTACG 991
DB 1168 CTGGACATCTTGCATGCTCTCTAGGTTACAAACAGCTGCTCAACCAATCTTTATG 1227
QY 992 CTTTCTTGATGAAAACTTCAAGGGGTCTTCCGAGATTTGCTTCTTCACTGAAGTGA 1051
DB 1228 CATTTGTGATGAAAACTTCAAGGGGTCTTCCGAGATTTGCTTCTTCACTGAAGTGA 1287
QY 1052 GGATGAGCGGCGAGAGCACTAGAGAGTCCGAATA 1087
DB 1288 ACATTTAGCAACAAACTCCACTGGAATTCGTGACA 1323
```

RESULT 25
US-09-355-709C-7
Sequence 7, Application US/09355709C
Patent No. 6538120
GENERAL INFORMATION:
APPLICANT: Max-Debrunck-Centrum fur Molekulare Medizin
TITLE OF INVENTION: Genomic Sequences of Human -opioid Receptor Gene ...
FILE REFERENCE: 101195-15
CURRENT APPLICATION NUMBER: US/09/355,709C
CURRENT FILING DATE: 1999-09-27
PRIOR APPLICATION NUMBER: DE 197 03 925.1
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 2162
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Human Genomic
OTHER INFORMATION: Clone
OTHER INFORMATION: cDNA encoding human opiate receptor
NAME/KEY: unsure
LOCATION: (2063)
OTHER INFORMATION: n = unknown
NAME/KEY: unsure
LOCATION: (2091)
OTHER INFORMATION: n = unknown
US-09-355-709C-7

Query Match 37.7%; Score 434.8; DB 4; Length 2162;
Best Local Similarity 66.3%; Pred. No. 7e-97;
Matches 660; Conservative 0; Mismatches 327; Indels 9; Gaps 2;

```
QY 92 CCGGCTGGGCGGAGCCGACAGCAAGGAGCGCGCTCGAGAGACGGCAGCTGGAGC 151
DB 337 CCGACCCATGCGGTCCGAAACCGACCACTGGCGGAGAGACAGCTGTGCTCCGA 396
QY 152 CCGGCAATCTCCCGGCAATCCGGTATATCAAGCGGCTTAATCTCGTAGTGTGG 211
DB 397 CCGGAGTCCCTCCATGATCAAGGCATCAATGAGCCCTTAATCTCAATCGTGTGG 456
QY 212 TCGTGGGCTTGGTGGCACTGCTGTGATGTGTGATCAATCGGATCAAGAGTGA 271
DB 457 TGGTGGGCTCTTGGAACTTCTGTGTATGTGTGTGTGTGTGTGTGTGTGTGTGT 516
QY 272 AAGACAGCAACCAATTTAATATTTAACTGTGTGTGTGTGTGTGTGTGTGTGTGT 331
DB 517 AGACTGCGCAACCAATCTTCAATTTTCACTTGTGTGTGTGTGTGTGTGTGTGTGT 576
QY 332 CCATGCGCTTTGAGTGAAGGTCTATGATGAATTTCTGCGCTTTTGGAGTGTGCT 391
DB 577 CCGTCCCTTCCAGAGTGTGAATTAATGGAATGGAACATGGCATTTGGAACCATCT 636
QY 392 GCAAGATAGTATTTTCAATTTACTTCAATGTCACAGCATCTTCACTTGAACCA 451
DB 637 GCAAGATAGTATCTTCAATTTACTTATATATGTTTCAAGCAATATTCACCTTGTGA 696
```

Qy	452	GATAGTAGGTCGACCGCTCATTCGCGTGGACACCCGGTGAAGGGCTTTGAACTTCGGA	512
Db	637	CCATAGAGTTCATGATGATACATTGCAAGCTGCGACCCCTGTCAAGGCTTATGATTTCCGTA	756
Qy	512	CACCCCTTGAAGGCAAAAGATCATCAATATCTGCATCTGAGCTGTGTCATCTGTTGGCA	571
Db	757	CTCCCCGAAATTCGCAAAATATTAATCAATGTCTGGCAACTGGATTCCTCTTCAAGCATTTGGTC	816
Qy	572	TCTCTGCAATAGTCTCTTGGAGGACCCAAAGTCAGGGAAGACGTGCATGTTCATTGAGTGTCT	631
Db	817	TTCCCTGATATGTTCAATGGCTACACAAATATACAGGGAAG-----TTCCATATGATTTGA	870
Qy	632	CCTTGACAGTCCCAAGATGATGACTACTCCTGGGAGGACCTCTTATGAAGATGTGAGTCT	691
Db	871	CACHTAACATTTCTCTCATCTCCAACTGGTACTGGGAAAACTTCG---TGAAATTTGTGTTT	927
Qy	692	TCATCTTTCCTTTCGTGATCCCTGTCTCTCATCATCTGTCGTCTACACCTGATGATCC	751
Db	928	TCATCTTCGCTTTCATTTATGCGCAGTGTCTCATCTATTAACCGTGTGTATATGACCTGATGATCT	987
Qy	752	TGCGCTCTCAAGAGCGTCCGCGCTCCTTTCTTGTGCTCTCCGAGAGAAAGATGCGAACCTGCGTA	811
Db	988	TGCGGCTCAAGAGTGTCCGCAAGCTCTCTGCGCTCCAAAGGACAGAAATCTTCGAA	1044
Qy	812	GGATCACCAGACCTGGCCCTGT	871
Db	1048	GGATACACAGAGATGCTGT	110
Qy	872	ACATATTCATCTCTGTGTGAGGCTCTGTGGGAGCACCTCCACAGCAGCTGTCTCTTCCA	931
Db	1108	ACATTTAGTATCATTTAAAGCTTGTGTTAAATCCCAAAATCAATGCTTCAGACGTGTTT	116
Qy	932	GCTATTACTTCTGTGCATTCGCTTTAAGCTTATACCAACATGAGCTGAATCCCATTTCTTACG	991
Db	1168	CTTGGACATTCCTGCATGTCTCTAGGTTACAAACAGCGCTCTCAACCCAGTCTTTATG	122
Qy	992	CCTTTCTTGATGAAACTCAAGCGGTGTTCCGGGACTTCTGCTTCCACTGAAAGATGA	105
Db	1228	CATTTCTGATGAAAACTTCAAACCATGCTTTCAAGAGAGTTCTGTATCCAACTCTTCCA	128
Qy	1052	GGATGAGCGCGCAGACACTAGACAGAGTCCGAATA	1087
Db	1288	ACATGAGCAACAAATCTCCATCTGATTCGTACAG	1323

RESULT 26
US-09-761-962A-3
; Sequence 3, Application US/09761962A
; Patent No. 6500927
GENERAL INFORMATION:
APPLICANT: Memorial Sloan-Kettering Cancer Center
TITLE OF INVENTION: MULTIPLE SPLICED VARIANTS OF THE MU-OP101D RECEPTOR GENE
FILE REFERENCE: 830002-2000.2
CURRENT APPLICATION NUMBER: US/09/761,962A
CURRENT FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/743,872
PRIOR APPLICATION NUMBER: PCT/US99/15974
PRIOR FILING DATE: 1999-07-15
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3
LENGTH: 1334
TYPE: DNA
ORGANISM: Mus musculus
US-09-761-962A-3

Query Match	37.5%	Score 437.41	DB 4	Length 1334
Best Local Similarity	65.8%	Pred. No. 2.3e-96		
Matches	663	Conservative	0	Mismatches 336; Indels 9; Gaps 2

Oy	92	CCGGCTGGAGCCGACGCCGACAGCAAGCGACGCCGCGCTCGAGAGACGCGGACAGCTTGAGAC	151
Ob	185	CCGACCCATGCGCGTCTTAACCGCACGGGGCTTTGGCGGAGCCACAGCCTGTGCTTCAAA	244

QY	152	CCGGGACATATCCCGGCGCCATCCCGGATCATCAACGGAGGTCTACTCCGTAAGTTCG	211
Db	245	CCGGGACGCCCTTCATGGTCAACGCATCAACATATGCCCCCTATTTCTATCGTGTG	304
QY	212	TCGTGGGCTTGGTGGGCACTCGTGGTCATGTTCTGTATCATCCGATACCAAGATGA	271
Db	305	TATGGGGCTCTTTGGAACTTCTGGTCATGTATGTGATTGTGAAGATATACAAATATGA	364
QY	272	AGACAGCAACCAACTTATTAATTTAACTGGCTTTGGCAGATGCTTTAGTTACTACA	331
Db	365	AGACTGCACCAACATTTACATTTTCAACCTTGTCTGGCAGATGCCCTTACCCACTACGA	424
QY	332	CCATGGCCCTTCAAGTACGGGTCTACTGTATGAATTCCTGGACCTTTTGGGATGTCGT	391
Db	425	CGTGCCTTTCAAGTGTTTACTACTGATGGGAAGTGGCCCTTTGGAAACATCTCT	484
QY	392	GCAAGATAGTATTTTCATTTGATTTACTACAACATGTTTCAACGAGCATCTTCACTTGAACA	451
Db	485	GCAAGATCGTATCTCAATAGACTATACATCAACATGTTTCAACGATATCTTCAACCTCTGCA	544
QY	452	TGATGAGCGTGGACCGCTCACTTGGCGTGTGCCACCCCGTGAAGGCTTTGGACTTCCGCA	511
Db	545	CCATGAGTGTATAGACCGGTACTATCCCGTCTGCCACCCGCGTAAAGGCCCTGTGATTTTCCGTA	604
QY	512	CACCTTGAAGGGCAAGATCATCAATATATCTGATCTGGCGTGTGTCATCTGTGGCA	571
Db	605	CCCCCGCAATATCCCAAAATGTCTCAATGTCTGGAACTGGATCTCTCTTCTGCCATTGGTTC	664
QY	572	TCTCTGCATATAGTCTCTTGGAGGCCAACAAAGTCAGGGAAGAGTCGATGTCAATTAGTGTCT	631
Db	665	TGCCCGTATGTTTATGTGGCAACCAACAAATATACAGGAGGGGTCTC-----CATATATGGCA	718
QY	632	CTTTGCAATTCAGATGATGACTATCTCTGTGTGGAACTCTTTCATGAAGATCTGCGTCT	691
Db	719	CCCTCAAGTCTCTCATCTCCACATAGTATCTGGGGAACCTGCTC---AAATCTGTGTCT	775
QY	692	TCATCTTGGCCTTGATCCCTGTCCGTCCGTATCATCATCTGTGTGCATCAACCTGTATGATCC	751
Db	776	TCATCTTGGCCTTATCATGTCCGATCCCTCATCATCACTGTGTGTTATGTATGAGCTGATGATCT	835
QY	812	GGATCACCAAGCTGTCTGTGTGTGTGGCAGTCTTCTGTCTGTCTGCTGCACTCCCATTC	871
Db	896	GGATCACCCGAGTGTCTGTGTGTCTGTGTGTATTTATTTATGTCTGTGTGCAACCCCATTC	955
QY	872	ACATATTCATCTGTGTGGAAGGCTCTGGGAGACCTCCACAGACAGCTGCTCTTCCA	931
Db	956	ACATCTATGTATCATCAAGCACTGTATCAAGATTCAGAAACCACTTTCAGACTGTT	1015
QY	932	GCTATTAATCTTGATCGCTTGAAGCTATACCAACAGTAGCGTGAATCCATTCCTACG	991
Db	1016	CTTGGCACTTCTGATGTGCTTGGGTTTACAAACAGCTGCTTGAACCCAGTTCTTTATG	1075
QY	992	CTTTCTTGTATGAAAACTTCAAGCGGTGTTCCGGGACTTCTGCTTTCCACTGAAGATGA	1051
Db	1076	CGTTCCTGATGAAAACTTCAAAAGATGTTTATGAGAGTTCTGCATCCCACTTCTCTCA	1135
QY	1052	GGATGAGCGCGAGAGCACTAGCAGATCCGAATATACAGTTCAAGATC	1099
Db	1136	CAATCGAAGCAAACTCTGCTCAATCCGTCAAAACACTAGGGAAC	1183

RESULT 27
US-09-761-962A-11
Sequence 11, Application US/09761962A
Patent No. 6508927
GENERAL INFORMATION:
APPLICANT: Memorial Sloan-Kettering Cancer Center
TITLE OF INVENTION: MULTIPLE SPICE VARIANTS OF THE MU-OPIOD RECEPTOR GENE


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; FILE REFERENCE: 830002-2000.2
; CURRENT APPLICATION NUMBER: US/09/761,962A
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/743,872
; PRIOR APPLICATION NUMBER: PCT/US99/15974
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 1365
; TYPE: DNA
; ORGANISM: Mus musculus
; US-09-761-962A-11

Query Match      37.5%; Score 432.4; DB 4; Length 1365;
Best Local Similarity 65.8%; Pred. No. 2.3e-96;
Matches 663; Conservative 0; Mismatches 336; Indels 9; Gaps 2;

QY 92 CCGGCTGGGCGGAGCCGAGCAAGAGCGGCGCTCGGAGGACGGCAGCTGGAGC 151
   |||
DB 185 CCGACCCATGCGGTCTTAACCGGAGGCGCTTGGCGGAGCCAGCCTGTGCTCAGA 244
   |||
QY 152 CCGGCAATCTCCCGGCGCATCCGGTCAATCAAGCGGCTTAATCCGAGTGTTCG 211
   |||
DB 245 CCGGAGCCCTTCAATGATCAGAGCCATCACCATATGCGCTTATCTATCGTGTG 304
   |||
QY 212 TGGTGGCTTGGTGGCAATCGCTGTGATGTGTGATCAATCCGATACAAAGATGA 271
   |||
DB 305 TGGTGGCTTGGTGGCAATCGCTGTGATGTGTGATCAATCCGATACAAAGATGA 364
   |||
QY 272 AGACAGCAACAACTTATCATATTTAACTGGCTTGGAGAGCTTATGATCAAA 331
   |||
DB 365 AGACTGCCAACAACTTATCAATTTCAACTTGTCTGGAGATCCCTTAGCACTAACA 424
   |||
QY 332 CCATGCCCTTTAGAGTACGGCTTACTTGTATGAATTCCTGGCTTTGGGAGTGTGCT 391
   |||
DB 425 CGCTCCCTTTCAGAGTGTAACTTACCTGATGGGAACGGGCGCTTGGAAACATCTCT 484
   |||
QY 392 GCAAGATAGTAAATTTCCATTTGATTAATAAGATGTAACAGGACCTTCACTTGAACA 451
   |||
DB 485 GCAAGATAGTAAATTTCCATTTGATTAATAAGATGTAACAGGACCTTCACTTGAACA 544
   |||
QY 452 TGATGAGCGTGAACCGCTAATTTGCGTGTGCAACCGGCTGAAGGCTTGAACCTTCGCA 511
   |||
DB 545 CCATAGAGTGAACCGCTAATTTGCGTGTGCAACCGGCTGAAGGCTTGAACCTTCGCA 604
   |||
QY 512 CACCTTGAAGGCAAGATCAATATTTGCTATGTGCTGTGTCTGTCATCTGTGGCA 571
   |||
DB 605 CCCCCGAAATGCCAAATTTGTCATGTCTGCACTGATCTCTCTTCTGCAATGTGCTC 664
   |||
QY 572 TCTGTCAATAGTCTTGTGAAGGACCAAAAGTCAGGGAAGAGCGTGAATGTCATTTAGTGT 631
   |||
DB 665 TGCCTGTATGTCTTATGCGAACCAAAATACAGGAGAGGCTC-----CATAGTTGCA 718
   |||
QY 632 CTTTGAAGTTCAGATGATGATCTCTCTGGTGGGACCTTCTTCAATGAAGTCTGCGCT 691
   |||
DB 719 CCTTCAAGTCTCTCTATCCCATGATGATCTGGAGAACTGTCTC---AAATCTGTGTCT 775
   |||
QY 692 TCAATCTTGGCTTGTGATTCCTGTGCTCAATCAATGCTGTGCAACCTGATGATCC 751
   |||
DB 776 TCAATCTTGGCTTGTGATTCCTGTGCTCAATCAATGCTGTGATGATGATGATGATGAT 835
   |||
QY 752 TGCCTTCAAGAGCGTCCGAGCTCTTCTTGTGCTCCGAGAGAAAGATGCAACCTGTGTA 811
   |||
DB 836 TACGATCAAGAGTGTCCGAGTGTGTGGGCTCCAAAGAAAGAGAGCAAGAACTGTGCGCA 895
   |||
QY 812 GGAATCAACAGACTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 871
   |||
DB 896 GGAATCAACAGACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 955
   |||
QY 872 ACATATTCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 931
   |||
DB 956 ACATATTCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1015

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QY 932 GCTATTAATCTTGTGATGCGCTTAAAGCTTAAATACCAAGATAGCTGAATCCATTTCTTACG 991
   |||
DB 1016 CTTGGCACTTCTGATGATGCTTGGGATTAACAAACAGCTGTGCAACCCAGCTTCTTATG 1075
   |||
QY 992 CTTTCTTGAATGAATCAATCAAGGCTTCCGAGCTTGTGCTTGTTCACCTGAAGATGA 1051
   |||
DB 1076 GCTTCTGATGAATCAATCAAGGCTTCCGAGCTTGTGCTTGTTCACCTGAAGATGA 1135
   |||
QY 1052 GAATGAGCGGCGAGAGCACTAGAGAGTCCGAATTAAGTTCAAGATC 1099
   |||
DB 1136 CAATGGAACAGCAAAATCTGTGCTGAATCCGTCAAAACCTAGGGAAC 1183
   |||

RESULT 28
US-09-761-962A-1
; Sequence 1, Application US/09761962A
; Patent No. 650927
; GENERAL INFORMATION:
; APPLICANT: Memorial Sloan-Kettering Cancer Center
; TITLE OF INVENTION: MULTIPLE SPLICE VARIANTS OF THE MU-OP10ID RECEPTOR GENE
; FILE REFERENCE: 830002-2000.2
; CURRENT APPLICATION NUMBER: US/09/761,962A
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/743,872
; PRIOR APPLICATION NUMBER: PCT/US99/15974
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 1423
; TYPE: DNA
; ORGANISM: Mus musculus
; US-09-761-962A-1

Query Match      37.5%; Score 432.4; DB 4; Length 1423;
Best Local Similarity 65.8%; Pred. No. 2.3e-96;
Matches 663; Conservative 0; Mismatches 336; Indels 9; Gaps 2;

QY 92 CCGGCTGGGCGGAGCCGAGCAAGAGCGGCGCTCGGAGGACGGCAGCTGGAGC 151
   |||
DB 185 CCGACCCATGCGGTCTTAACCGGAGGCGCTTGGCGGAGCCAGCCTGTGCTCAGA 244
   |||
QY 152 CCGGCAATCTCCCGGCGCATCCGGTCAATCAAGCGGCTTAATCCGAGTGTTCG 211
   |||
DB 245 CCGGAGCCCTTCAATGATCAGAGCCATCACCATATGCGCTTATCTATCGTGTG 304
   |||
QY 212 TGGTGGCTTGGTGGCAATCGCTGTGATGTGTGATCAATCCGATACAAAGATGA 271
   |||
DB 305 TGGTGGCTTGGTGGCAATCGCTGTGATGTGTGATCAATCCGATACAAAGATGA 364
   |||
QY 272 AGACAGCAACAACTTATCATATTTAACTGGCTTGGAGAGCTTATGATCAAA 331
   |||
DB 365 AGACTGCCAACAACTTATCAATTTCAACTTGTCTGGAGATCCCTTAGCACTAACA 424
   |||
QY 332 CCATGCCCTTTAGAGTACGGCTTACTTGTATGAATTCCTGGCTTTGGGAGTGTGCT 391
   |||
DB 425 CGCTCCCTTTCAGAGTGTAACTTACTGATGGAAGCGGCTTGTGAAACATCTCT 484
   |||
QY 392 GCAAGATAGTAAATTTCCATTTGATTAATAAGATGTAACAGGACCTTCACTTGAACA 451
   |||
DB 485 GCAAGATAGTAAATTTCCATTTGATTAATAAGATGTAACAGGACCTTCACTTGAACA 544
   |||
QY 452 TGATGAGCGTGAACCGCTAATTTGCGTGTGCAACCGGCTGAAGGCTTGAACCTTCGCA 511
   |||
DB 545 CCATAGAGTGAACCGCTAATTTGCGTGTGCAACCGGCTGAAGGCTTGAACCTTCGCA 604
   |||
QY 512 CACCTTGAAGGCAAGATCAATATTTGCTATGTGCTGTGTGTGTGTGTGTGTGTGTGT 571
   |||
DB 605 CCCCCGAAATGCCAAATTTGTCATGTCTGCACTGATCTCTCTTCTGCAATGTGCT 664
   |||
QY 572 TCTGTCAATAGTCTTGTGAAGGACCAAAAGTCAGGGAAGAGCGTGAATGTCATTTAGTGT 631
   |||

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[illegible]

RESULT 32

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US-09-214-904-1
: Sequence 1, Application US/09214904
: Patent No. 6632977
: GENERAL INFORMATION:
: APPLICANT:
: TITLE OF INVENTION: TRANSGENIC ANIMAL IN WHICH THE EXPRESSION
: TITLE OF INVENTION: OF OPIATE RECEPTORS IS MODIFIED
: NUMBER OF SEQUENCES: 6
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/214,904
: FILING DATE:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/FR97/01282
: FILING DATE:
: APPLICATION NUMBER: FR 96.08610
: FILING DATE: 15-JUL-1996
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2229 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 256..1449
: US-09-214-904-1

```

	Query Match	37.3%	Score 430.8	DB 4	Length 2229
	Best Local Similarity	65.7%	Pred. No. 6	7e-96	
	Matches 662	Conservative 0	Mismatches 337	Indels 9	Gaps 2
QY	92	CCGCGTGGGGCCGAGCCGACACAGCAACGAGGCGCGCTCGGAGAGCAGCGGACGCTGGAGC	151		
DB	374	CCGACCCATGCGGTCCTTAACCGCACGGGGCTTGGCGGAGCCACAGCCTGTGCTTCAGAA	433		
QY	152	CCGGCCACATCTCCCCCGGCGCATCCGGGTATATACAGGCGGCTACTCCGTAAGTTCG	211		
DB	434	CCGGAGCCCTTCCATGTGCACAGGCATCACCATCAGTCCCTCATTTATTCGTGTG	493		
QY	212	TCGTGGGCTTGGTGGGCACTGCTGTGTATTTGTATCATCCGATACAAAGATGA	271		

[illegible]

RESULT 33

```

US-09-761-962A-4
; Sequence 4, Application US/09761962A
; Patent No. 650927
; GENERAL INFORMATION:
; APPLICANT: Memorial Sloan-Kettering Cancer Center
; TITLE OF INVENTION: MULTIPLE SPICE VARIANTS OF THE MU-OPIOD RECEPTOR GENE
; FILE REFERENCE: 830002-2000.2
; CURRENT APPLICATION NUMBER: US/09/761,962A
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/743,872
; PRIOR APPLICATION NUMBER: PCT/US99/15974
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 46

```

SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 1542
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-761-962A-4

Query Match 37.2%; Score 429.2; DB 4; Length 1542;
Best Local Similarity 65.6%; Pred. No. 1.4e-95;
Matches 661; Conservative 0; Mismatches 338; Indels 9; Gaps 2;

QY 92 CCGGCTGGGCCGAGCCCGACAGCAACGCGAGCGCGCTCGAGAGACGCGACGTGAGC 151
DB 185 CCGAGCCAGTGGGGTCTTAACCGGAGCGGGCTTGGGGAGGCCACAGCCTGTGCTCAGA 244
QY 152 CCGGCAATCTTCCCGGCGCATCCGGTCATCATCAAGCGCGGTCTACTCCGTAGTGTTCG 211
DB 245 CCGGAGCGCTTCCAGTGTCAAGCGCATCACCATCATGCGCTCTATTTCTATCGTGTG 304
QY 212 TCGTGGGCTTGGTGGCAACTGCGTGTATGTGTATCAATCGATACCAAGATGA 271
DB 305 TAGTGGGCTCTTTGAAATCTTCTGTGTATGTATGTATGAATATACCAAAATGA 364
QY 272 AGACAGCAACCAACATTTATACATATTTAACTGGCTTGGCAGAGTCTTATGTTACTACA 331
DB 365 AGACTGCCAACCAATCTAATTTTCAACCTTGTCTGGCAGATGCTTATGCACTAGCA 424
QY 332 CCATCCCTTTTCAAGTACGAGTCTACTGATGAATTTCTGCGCTTTTGGGAGTGTCTGT 391
DB 425 CGCTCCCTTTTCAAGTGTATTAATCTGATGGAAACGCGCTTTTGGAAACATCTCT 484
QY 392 GCAAGATGATATTTCCATTTGATTTACTAACAATGTTACAGCATCTTCACTTGAACA 451
DB 485 GCAATATGATATCTCAATAGACTTACTACACATTTTCAACGATTTCTTACCTCTGCA 544
QY 452 TGATGAGGTGAGCGGTACATTTGCGTGTGCGACCCCGTGAAGGCTTTGACCTTCCGA 511
DB 545 CCATGAGTGTAGACGGTACATTTGCGTGTGCGACCCCGTGAAGGCTTTGAGTTCCGTA 604
QY 512 CACCTTGAAGGCAAGATCATCATATCTGATGTGCTGTCTGTCTGATCTGTGCA 571
DB 605 CCCCCGAAATGCAAAATTTGTCATGTCTGACATGATCTCTCTTCTGCAATTTGTC 664
QY 572 TCTGTCAATAGTCTTGGAGGACCAAAAGTCAAGGAAAGACGTGATCTATGAGTGTCT 631
DB 665 TGCCGTATATGTTATGCAACACCAAAATACAGGAGGGGTC-----CATAGTTGCA 718
QY 632 CTTGACGTTCCAGATGATGACTACTCTGCTGGGAGCTCTTCAATGAAGTCTGCTCT 691
DB 719 CCTTACGTTCTCTCATCCACATGTTACTGGAGAACCTGTCTC---AAATCTGTGCT 775
QY 692 TCAATTTTGGCTTGTGATCTCTGTCTCTCATCATATGTGTCTGTACACCTGATGATCC 751
DB 776 TCAATTTTGGCTTGTGATCTCTGTCTCTCATCATATGTGTGTATGAGTGTGATCT 835
QY 752 TGGCTCTAAGAGGCTCGGCTCTTCTGTGCTCCGAGAGAAAGATGCAACCTGCGTA 811
DB 836 TACGACTAAGAGTGTCCGATGCTGTGGGCTCCAAAGAAAGAGAGAAACCTGCGCA 895
QY 812 GGAATCAACGAAGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 871
DB 896 GGAATCAACCGAGT 955
QY 872 ACATATTCATCTGT 931
DB 956 ACATATTCATCTGT 1015
QY 932 GCTATTAATCTTGTGATCGCTTGAAGCTATACCAAGAGGCTGATCCATCTCTACG 991
DB 1016 CTTGCACTTGTGATGCTTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1075
QY 992 CTTTCTTGTGAAACTTCAAGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1051

DB 1076 GCTTCTGATGATAAACTTCAAAAGATGTTTATAGAGTTCGATCCCACTTCTTCA 1135
QY 1052 GATGAGCGGCGAGAGCATAGCAGAGTCCGAAATPACATTTACAGATC 1099
DB 1136 CAATCGAACAGCAAAACTGTCTGTAATCTGTCAAAACACTAGGAAC 1183

RESULT 34
US-08-387-707-15
; Sequence 15, Application US/08387707
; Patent No. 6265563
; GENERAL INFORMATION:
; APPLICANT: EVANS, CHRISTOPHER J.
; APPLICANT: KEITH, DUANE E.
; TITLE OF INVENTION: OPIOID RECEPTOR GENES
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESS: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, N.W. Suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/387,707
; FILING DATE: 10-SEP-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: MORASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22000-20526.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1981 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-387-707-15

Query Match 37.2%; Score 429.2; DB 3; Length 1981;
Best Local Similarity 65.6%; Pred. No. 1.6e-95;
Matches 661; Conservative 0; Mismatches 338; Indels 9; Gaps 2;

QY 92 CCGGCTGGGCCGAGCCCGACAGCAACGCGAGCGCGCTCGAGAGACGCGACGTGAGC 151
DB 374 CCGAGCCAGTGGGGTCTTAACCGGAGCGGGCTTGGGGAGGCCACAGCCTGTGCTCAGA 433
QY 152 CCGGCAATCTTCCCGGCGCATCCGGTCATCATCAAGCGCGGTCTACTCCGTAGTGTTCG 211
DB 434 CCGGAGCGCTTCCAGTGTCAAGCATCAATCAATGCGCTCTATTTCTATCGTGTG 493
QY 212 TCGTGGGCTTGGTGGCAACTGCGTGTCTGATGTTGCTGATCATCGATACCAAAAGTGA 271
DB 494 TAGTGGGCTCTTTGAAATCTTCTGTGTATGTATGTATGAATATACCAAAATGA 553
QY 272 AGACAGCAACCAATTTATACATTTTAACTGCTTGGAGAGTCTTTAGTTACTACAA 331
DB 554 AGACTGCCAACCAATCTAATTTTCAACCTTGTCTGCGAGATGCTTATGCGCACTAGCA 613
QY 332 CCATGCGCTTTCAGAGTACGCTACTGATGAATTTCTGCGCTTTTGGGAGTGTGCTGT 391
DB 614 CGCTGCCCTTTCAAGTGTTAATCTATGATGAGAAAGTGTGCGCTTTTGGAAACATCTCT 673
QY 392 GCAAGATGATTAATTTCCATGATTAATCTATCAACATGTTCAACAGCATCTTACCTTGACA 451

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Db      674 GCAAGATCGTGAATCTCAATAGACTACTACAAACATGTTCAACAGTATCTTCAACCCCTGCA 733
Qy      452 TGATAGCGCTGAGACCGCTACATTTGCGGTGGCCACCCCGTGAAGGCTTGAAGCTTCCGA 511
Db      734 CCATGAGTGTAGACCGCTACATTTGCGGTGGCCACCCCGTGAAGGCTTGAAGCTTCCGA 793
Qy      512 CACCCCTTGAAGCAAGATCATCAATATCTGCACTGGCTGTGCTGTGATCTGTTGGA 571
Db      794 CCCCCGGAATGCCAAATTTGTCAATGTCTGCACTGGAATCTCTCTTTGTCATTTGGTC 853
Qy      572 TCTTGCAATAGTCTTGGAGGACCAAAAGTCAGGGAAGACGTGATGATTAAGTGTCT 631
Db      854 TCCCGGTATGTTACATGAGCAACCAAAATACAGGAGGGGTC-----CATAGATTGA 907
Qy      632 CTTTGCAATGTTCCCAATGATGACTACTCTGCTGGGAGACCTTTTCATGAAGATCTGGCT 691
Db      908 CCTCAACGTTCTCTCAATCCCAACATGATGATGAGGAAACCTGCTC---AAAATCTGTGCT 964
Qy      692 TCATCTTTCCTTCCGATCCCTGTGCTGATCATCATGCTGCTCAACCCCTGATGATCC 751
Db      965 TCATCTTTCCTTCCGATCCGCTGATCATCATCTGTGTATGATGATGATGATCT 1024
Qy      752 TCCGCTCAAGACCGTCCGCTCTTCTGCTCCGAGAGAAAGATCCCACTGCGTA 811
Db      1025 TACAGCTCAAGAGTGTCCGATGCTGTGCGGGCTCAAAAGAAAGACAGAAACCTGCGCA 1084
Qy      812 GGATCAACCAAGATGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 871
Db      1085 GGATCAACCGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1144
Qy      872 ACATATTCATCTCGGTGGAGGCTCTGGGAGACCTCCACAGACAGCTGCTCTCA 931
Db      1145 ACATCTATATCTCATCAAAAGCATGATCAAGATTCAGAAACCATTTTCCAGATGTTT 1204
Qy      932 GCTATTAATCTTGCATGCTGCTTGAAGCTATACCAACAGTACCTGATCCCATTTCTCTAG 991
Db      1205 CTTGGACATCTTGCATGCTGCTTGAAGCTATACCAACAGTACCTGATCCCATTTCTCTAG 1264
Qy      992 CTTTCTTGTATGAAATCTTCAAGCGGTGTTCCGGGACCTTCTGCTTCCACTGAAAGATA 1051
Db      1265 CTTTCTTGTATGAAATCTTCAAGCGGTGTTCCGGGACCTTCTGCTTCCACTGAAAGATA 1324
Qy      1052 GGATGAGGCGGAGAGCACTAGAGAGTCCGAAATCAGTTCAAGATC 1099
Db      1325 CAATGACAGCAAACTCTGCTCGATCGTCAAAACACTAGGGAAC 1372

RESULT 35
US-08-405-271A-15
Sequence 15, Application US/08405271A
Patent No. 6432652
GENERAL INFORMATION:
APPLICANT: EVANS, CHRISTOPHER J.
APPLICANT: KEITH, DUANE E.
TITLE OF INVENTION: OPIOID RECEPTOR GENES
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESS: MORRISON & FOERSTER
STREET: 2000 PENNSYLVANIA AVENUE, NW, Suite 5500
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/405,271A
FILING DATE: 14-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

```

```

NAME: MORASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 22000-20526.22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030 MRSPFOERSWSH
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 1981 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-405-271A-15

Query Match      37.2%; Score 429.2; DB 4; Length 1981;
Best Local Similarity 65.6%; Pred. No. 1.6e-95;
Matches 661; Conservative 0; Mismatches 338; Indels 9; Gaps 2;

Qy      92 CCGGCTGGGCGGAGCCCGACAGCAACGGAGCGCGGCTCGAGAGACGGGCAAGCTGAGAC 151
Db      374 CCGACCCATGCGGTCTTAACCCGACGGGCTTGGCGGGAAGACAGACCTGTGCTTCA 433
Qy      152 CCGGCAATCTCCCGGCGCATCCGATCATCAACGCGGTCTACTCCGTAAGTGTG 211
Db      434 CCGGCAAGCCCTTCATGTCACAGCATACCATATGACCTCTATTTCTATCTGTGTG 493
Qy      212 TGTGGGCTTGTGGGCAACCTGCTGTGATGTTGTGTATCATCCGATACAGAAAGATA 271
Db      494 TAGTGGGCTCTTGTGAAACCTTCTGTGATGATGATGATGATGATGATGATGATGATGATGAT 553
Qy      272 AGACGACCAACCAATTTATATTAATTAACCTGCTTGGCAATGTTAGTTACATCA 331
Db      554 AGACTGCCACCAACATCTAATTTCAACCTTGTCTGCAATGCTTGAACATGCTTGAACATGCA 613
Qy      332 CCATCCCTTTGAGAGTACGCTCTACTGATGATTAATTCCTGAGCTTGGGAGTGTGCT 391
Db      614 CCGTCCCTTTGAGAGTGTATCTAATCTGATGGAACGTTGCTTGGAAACATCTCT 673
Qy      392 GCAAGATGTAATTTTCATGATTAATCAACATGTTCAACAGATCTTCACTTGAACA 451
Db      674 GCAAGATGTAATTTTCATGATTAATCAACATGTTCAACAGATCTTCACTTGAACA 733
Qy      452 TGATAGCGCTGAGACCGCTACATTTGCGGTGGCCACCCCGTGAAGGCTTGAAGCTTCCGA 511
Db      734 CCATGAGTGTAGACCGCTACATTTGCGGTGGCCACCCCGTGAAGGCTTGAAGCTTCCGA 793
Qy      512 CACCCCTTGAAGCAAGATCATCAATATCTGCACTGGCTGTGCTGTGATCTGTTGGA 571
Db      794 CCCCCGGAATGCCAAATTTGTCAATGTCTGCACTGGAATCTCTCTTTGTCATTTGGTC 853
Qy      572 TCTTGCAATAGTCTTGGAGGACCAAAAGTCAGGGAAGACGTGATGATTAAGTGTCT 631
Db      854 TCCCGGTATGTTACATGAGCAACCAAAATACAGGAGGGGTC-----CATAGATTGA 907
Qy      632 CTTTGCAATGTTCCCAATGATGACTACTCTGCTGGGAGACCTTTTCATGAAGATCTGGCT 691
Db      908 CCTCAACGTTCTCTCAATCCCAACATGATGATGAGGAAACCTGCTC---AAAATCTGTGCT 964
Qy      692 TCATCTTTCCTTCCGATCCCTGTGCTGATCATCATGCTGCTCAACCCCTGATGATCC 751
Db      965 TCATCTTTCCTTCCGATCCGCTGATCATCATCTGTGTATGATGATGATGATGATCT 1024
Qy      752 TCCGCTCAAGACCGTCCGCTCTTTCGCTCCGAGAGAAAGATGCAACCTGCGTA 811
Db      1025 TACAGCTCAAGAGTGTCCGATGCTGTGCGGGCTCAAAAGAAAGACAGAAACCTGCGCA 1084
Qy      812 GGATCAACCAAGATGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 871
Db      1085 GGATCAACCGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1144
Qy      872 ACATATTCATCTGCTGGAGGCTCTGGGAGACCTCCACAGACAGCTGCTCTCTCA 931

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Matches 634; Conservative 0; Mismatches 299; Indels 12; Gaps 2;				
Qy	93	CGGCTGGGCCGAGCCCGACAGCAAGCGACGCGGCTCGAGAGACGCGACCTGGAGCC	152	
Db	91	CGGCTTCCAGGCGCTTCCCGACGCGGCGCGCAATGCGGGGTCCCGGAGCCCG	150	
Qy	153	CGGCGCATCTCCCGGCGCATCCGCGTCATCATGCGGCGCTACTCCGTAGTGTCT	212	
Db	151	TAGTGCTGTCTCTGCTGCTGCGCGCATCCCGCATCCGCGCTCTACTCGGCTGTGCGC	210	
Qy	213	CGTGGGCTTGTGGGCACTCGTGCTCATGTTCTGTCATTCGATACACAAAGATGA	272	
Db	211	AGTGGGGCTTCTGGGCACTGTCTCTGTCATGTTGGCATGCTCGGTACCAAAATGA	270	
Qy	273	GACAGCAACCAATTATTAATTTAACTGGCTTTGGCAAGTCTTTAGTTACTAACA	332	
Db	271	GACCGGCACCAATCTACATCTTCAATCTGGCTTTGGCTGTGAGCGCTGGCCACAGCAC	330	
Qy	333	CATGCCCTTCAAGAGTGGCTCATCTGTATGTAATTCCTGGGCTTTGGGGATGTGCTG	392	
Db	331	GCTGCCCTTCAAGAGGCGCAAGTACTGTATGTAAGTAAGTGGCGGTTGGGAGCTGTG	390	
Qy	393	CAAGATAGTAATTTCCATTTACTTACAAATGTTCAACAGCATCTTCACTTGACAT	452	
Db	391	CAAGGCTGTCTCTCATTTGACTACTACAAATGTTCACTTACATCTTCACTTCACT	450	
Qy	453	GATGAGCGGTGACCGGTATATTCGCTGTCGACCCCGTGAAGGCTTTGGATTCCGAC	512	
Db	451	GATGAGCGGTGACCGGTATATTCGCTGTCGACCCCGTGAAGGCTTTGGATTCCGAC	510	
Qy	513	ACCTTTGAAGGCAAGATCATCATATTCGATCTGGCTGTGCTGTGCTGTGGCAT	572	
Db	511	ACCAAGCAAGGCAAGCTCATATTAATGATCTGGGCTTTGGCTTCAAGTGTGGGAT	570	
Qy	573	CTTGCATATGCTCTTGAAGGCAACCAAGTCAAGGAAAGTGTGATTCATTAAGTGTG	632	
Db	571	CCCATATATGCTCATAGGCAAGTCAACCCCGGATGGTGAAGTATGATGATCTCA	630	
Qy	633	CTTGAAGTCCCAATGATGATCTCTCTGGTGGGACCTTTCAAGAAATGTGCTCTT	692	
Db	631	GTTCCCAAGTCC-----CAGCTGGTACTGGGACACTGTGACCAAGATCTGGTGT	681	
Qy	693	CATCTTTGCTTCTGTATCCCTGTCTCATCATCTGCTGCTACACCTGATGATCTT	752	
Db	682	CCTTTTGGCTTCTGTATCCCTGTCTCATCATCTGCTGCTACACCTGATGATCTT	741	
Qy	753	GCTTCTCAAGAGGCTCCGCTCTTTCTGGCTCCGAGAAAGATGCGCAACTGGTAG	812	
Db	742	GCGCTGGGCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	801	
Qy	813	GATCACAAGATGATCTGTGGTGGTGGAGCTTGTGCTGCTGCTGCTGCTGCTGCT	872	
Db	802	CATCAGCGCATGATGCTGTGGTGGTGGAGCTTGTGCTGCTGCTGCTGCTGCTG	861	
Qy	873	CATATTCATCTGTGAGGCTCTGGGG---AGCACTTCCCAACAGCAGCTGCTCTC	929	
Db	862	CATCTTCTCATCTGTGAGGCTCTGGGG---AGCACTTCCCAACAGCTGCTCTC	921	
Qy	930	CAGCTATTAATTTCTGATCTGCTTATAGGCTTATACCAAGTATGCTGAATCCATTTCT	989	
Db	922	GCACTGCACTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	981	
Qy	990	GCGCTTCTGTATGAAACTTCAAGCGGTGTTCCGGGACTTCTG 1034		
Db	982	GCGCTTCTGTATGAAACTTCAAGCGGTGTTCCGGGACTTCTG 1026		

RESULT 39
US-09-214-904-3
; Sequence 3, Application US/09214904
; Patent No. 6632977
; GENERAL INFORMATION:
; APPLICANT:

TITLE OF INVENTION: TRANSGENIC ANIMAL IN WHICH THE EXPRESSION				
TITLE OF INVENTION: OF OPIATE RECEPTORS IS MODIFIED				
NUMBER OF SEQUENCES: 6				
COMPUTER READABLE FORM:				
MEDIUM TYPE: Floppy disk				
COMPUTER: IBM PC compatible				
OPERATING SYSTEM: PC-DOS/MS-DOS				
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)				
CURRENT APPLICATION DATA:				
APPLICATION NUMBER: US/09/214,904				
FILING DATE:				
PRIOR APPLICATION DATA:				
APPLICATION NUMBER: PCT/FR97/01282				
FILING DATE:				
APPLICATION NUMBER: FR 96.08810				
FILING DATE: 15-JUL-1996				
INFORMATION FOR SEQ ID NO: 3:				
SEQUENCE CHARACTERISTICS:				
LENGTH: 2218 base pairs				
TYPE: nucleic acid				
STRANDEDNESS: double				
MOLECULE TYPE: DNA (genomic)				
FEATURE:				
NAME/KEY: CDS				
LOCATION: 58..1173				
US-09-214-904-3				
Query Match 36.6%; Score 422.6; DB 4; Length 2218;				
Best Local Similarity 67.1%; Pred. No. 6.8e-94;				
Matches 634; Conservative 0; Mismatches 299; Indels 12; Gaps 2;				
Qy	93	CGGCTGGGCCGAGCCCGACAGCAAGCGACGCGGCTCGAGAGACGCGACCTGGAGCC	152	
Db	120	CGGCTTCCAGGCGCTTCCCGACGCGGCGCAATGCGGGTCCCGGAGGCCCG	179	
Qy	153	CGGCGCATCTCCCGGCGCATCCGCGTCATCATGCGGCGTCTACTCCGATGTTGCT	212	
Db	180	TAGTGCTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	239	
Qy	213	CGTGGGCTTGTGGGCACTCGTGCTCATGTTCTGTCATTCGATCCGATACCAAGATGA	272	
Db	240	AGTGGGCTTCTGGGCAAGTGTCTGTCATGTTGGATGTCGCGTACCAAAATGAA	299	
Qy	273	GACAGCAACCAATTATTAATTTAACTGGCTTTGGCAAGTCTTTAGTTACTAACA	332	
Db	300	GACCGCACCAACATCTACATCTTCAATCTGGCTTTGGCTGTGATGCTGCGCAC	359	
Qy	333	CATGCCCTTCAAGAGTACCGGTCTACTGATGAATTCCTGGCTTTGGGATGTGCTG	392	
Db	360	GCTGCCCTTCCAGAGGCGCAAGTACTGATGAAAGTGGCGCTTTGGCGAGCTGTG	419	
Qy	393	CAAGATAGTAATTTCCATTTACTTACAAATGTTCAACAGCATCTTCACTTGACAT	452	
Db	420	CAAGGCTGTGCTCTCATTTACTTACAAATGTTCACTTCACTTGACATCTTCACT	479	
Qy	453	GATGAGGTGAGACCGCTACATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	512	
Db	480	GATGAGGTGAGACCGCTACATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	539	
Qy	513	ACCTTTGAAGGCAAGATCATCATATTCGATCTGGCTGTGCTGCTGCTGCTGCTG	572	
Db	540	ACCAAGCAAGGCAAGTGTATCATATTAATGATCTGGGCTTGTGCTTCAAGTGTG	599	
Qy	573	CTTGCATATGCTTGTGAGGCAACAAAGTCAAGGAAAGTGTGATGATGATGCTC	632	
Db	600	CCCATCATGTCATGTCAGTGAACCAACCCCGGATGTCAGTGTATGATGCTCA	659	
Qy	633	CTTGCATTTCCAGATATATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	692	
Db	660	GTTCCCAAGTCC-----CAGCTGGTATCGGAGCATGTTACCAAGATCTGCGGTT	710	
Qy	693	CATCTTGTGCTGATCCCTGTCTCATCATCATGTCGTGCTACACCTGATGATCCT	752	

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Db      711 CCTCTTGGCTTGGTGTGCGGATCTCATCAATCAAGGTGTATAGGCTCATGTACT 770
Qy      753 GGGTCTCAAGAGCGTCCGGCTCTTTTGTGGCTCCGAGAGAAAGATCGCAACTGTGTG 812
Db      771 GGGCTTGGCGACGCGTGTCTGTCTCCGGTTCCAAAGAGAAAGACCGGAGCTGTGGGG 830
Qy      813 GATCAACGACGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 872
Db      831 CATCAAGCGCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 890
Qy      873 CATATTCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 929
Db      891 CATCTTCGTCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 950
Qy      930 CAGCTATTACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 989
Db      951 CCGACTGTCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1010
Qy      990 CGCCTTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1034
Db      1011 CGCCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1055

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RESULT 40

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US-08-432-174A-1
; Sequence 1, Application US/08432174A
; Patent No. 6562587
; GENERAL INFORMATION:
; APPLICANT: KIEFER, BRIGITTE
; TITLE OF INVENTION: NOVEL POLYPEPTIDES HAVING OPIOID RECEPTOR ACTIVITY,
; FILE REFERENCE: EX92009-US
; CURRENT APPLICATION NUMBER: US/08/432,174A
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2219
; TYPE: DNA
; ORGANISM: Mus sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (59)..(1174)
US-08-432-174A-1

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Query Match      36.6%; Score 422.6; DB 4; Length 2219;
Best Local Similarity 67.1%; Pred. No. 6,8e-94;
Matches 634; Conservative 0; Mismatches 299; Indels 12; Gaps 2;

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Qy      93 CGGCTGGGCGGAGCCCGACAGCAAGCGGCGCGGCTGTGAGAGACGCGAGCTGTGAGCC 152
Db      121 CGCCTTCCCAAGCGCTTCCCAAGCGGCGCGCAATGTGTGTGTGTGTGTGTGTGT 180
Qy      153 CGCGCAATCTCCCGCGCATCCCGGTATCATCAAGGGGTCTCTCTCTGTGTGTGTGT 212
Db      181 TAGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240
Qy      213 CGTGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 272
Db      241 AGTGGGGCTTCTGGGCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 300
Qy      273 GACAGCAACCAATTTACATATTTAACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 332
Db      301 GACCGCCCAACATCTACATCTTCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
Qy      333 CATGCCCTTTCAGAGAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 392
Db      361 GCTGCCCTTTCAGAGAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
Qy      393 CAAGATAGTATTTTCATTTACTTACTACAAATGTTCACAGCATTTTCACCTTGACAT 452
Db      421 CAAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480

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Qy      453 GATGAGCGTGACCGGTACATTGGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 512
Db      481 GATGAGCGTGACCGGTACATTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 540
Qy      513 ACCCTTGAAGGCAAGATCATCAATATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 572
Db      541 ACCAGCCAAAGGCAAGCTGTATATATATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600
Qy      573 CTGTCAATATGTCTTTGAGAGCAACAAAGTCAAGGAAAGCTGTGTGTGTGTGTGTGT 632
Db      601 CCCCATCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 660
Qy      633 CTGTGAGTTCCCAATGATGATTAATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 692
Db      661 GTTCCCAAGTCC-----CAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 711
Qy      693 CATCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 752
Db      712 CCTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 771
Qy      753 GGGTCTCAAGAGCGTCCGGCTCTTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 812
Db      772 GCGCTTGGCGACGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 831
Qy      813 GATCAACGACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 872
Db      832 CATCAAGCGCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 891
Qy      873 CATATTCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 929
Db      892 CATCTTCGTCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 951
Qy      930 CAGCTATTACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 989
Db      952 CGCACTGTCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1011
Qy      990 CGCCTTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1034
Db      1012 CGCCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1056

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RESULT 41

```

US-08-147-592A-3
; Sequence 3, Application US/08147592A
; Patent No. 6096513
; GENERAL INFORMATION:
; APPLICANT: Bell, Graeme I
; APPLICANT: Reisine, Terry
; APPLICANT: Yasuda, Kazuki
; TITLE OF INVENTION: Opioid Receptor Genes,
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/147,592A
; FILING DATE: 05-NOV-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/100,694
; FILING DATE: 30-JUL-1993
; CLASSIFICATION: 435

```


FEATURE:
NAME/KEY: CDS
LOCATION: 12..1127
US-08-292-694A-3

Query Match 36.6%; Score 422.6; DB 4; Length 2272;
Best Local Similarity 67.1%; Pred. No. 6.9e-94;
Matches 634; Conservative 0; Mismatches 299; Indels 12; Gaps 2;

93 CGGCTGGGCGGAGCCGACAGACAGGAGCGCGCGCTGGAGAGCGCGACCTGAGCC 152
74 CGCCTTCCCAAGCGCTTCCAGAGCGCGGCGCCCAATGCTGGGGGTGCGCGGAGCCG 133
153 CGGCAATCTCCCGCGCATCCCGGTATCATACGGGGGTCTACTCCGTAGTGTGT 212
134 TAGTCCCTGCTCCCTGCGCTGAGCCATGCGCATACCGGCGCTTACTCGGCTGTGTCC 193
213 CGTGGGCTTGGTGGGCACTCGCTGATCTGTTGATCATCCGATACAAAGATGA 272
194 AGTGGGCTTCTGGGCAAGTGTCTGTATGTTGGCATGTCCGGTACCAAAATTGA 253
273 GACAGCAACCAATTTACATATTTAACTGCGCTTTGGCAATGCTTTAGTTACTAAC 332
254 GACCGCAACCAATCTACATCTTCAATCTGCTTTGGCTGATGCGCTGCGACAGCAC 313
333 CATGCCCTTTCAGAGTAGGCTACTTGTATGAAATTCCTGCTTTGGGGATGTGTGTG 392
314 GCTGCCCTTTCAGAGCGCGCAAGTACTGTATGAAAGTGGCGTGGGAGAGCTGTGTG 373
393 CAAGATAGTAATTTCAATGATTTACTACAAAGTTCACAGACATCTTCACTTGACAT 452
374 CAGGCTGTGCTCTCATTTACTACTACAAATGTTCACTACATCTTCACTTCACTTCA 433
453 GATGAGCGTGAACCGCTACATTTGCCGTGTGCCACCCCGTGAAGGCTTTGGAATTCG 512
434 GATGAGCGTGAACCGCTACATTTGCCGTGTGCCACCCCGTGAAGGCTTTGGAATTCG 493
513 ACCCTTGAAGGCAAGATCATATATCTGCAATCTGCGCTGTGTGTCTCTGTGGCAT 572
494 ACCAGCAAGGCAAGCTGATCATATATATGCAATCTGCGCTGTGTGTGTGTGTGTGT 553
573 CTCTCAATATGCTCTTGGAGGACCAAGATCAGGGAGAGTGTATGATGAGTGTG 632
554 CCCCATCATGTGATGAGGAGTACCCACCCCGGATGTGTGATGTGTGTGTGTGTGTGT 613
633 CTTCAGTTCACAGATGATGATCTACTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGT 692
614 GTTCCCAAGTCC-----CAGCTGTATCTGGGACATGTGACCAAGATCTGGGTGT 664
693 CATCTTTGCTTGTGTATCCGTGTCTCATATCATCTGTCTGTACACCTGTATGTCT 752
665 CTTCTTTGCTTGTGTATCCGTGTCTCATATCATCTGTGTGTGTGTGTGTGTGTGTGT 724
753 GGTCTCAAGAGGCTCCGCTCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 812
725 GGGCTTGGGAGCGGT 784
813 GATCAGCAAGTGTCTGT 872
785 CATCAGGCGCATGT 844
873 CATATTCATCTGT 929
845 CATCTTGT 904
930 CAGCTATTAATCTGT 989
905 GCGACTGACCTGT 964
990 GCGCTTTCTTGT 1034
965 GCGCTTCTGT 1009

RESULT 43
US-09-761-962A-12
; Sequence 12, Application US/09761962A
; Patent No. 6500927
; GENERAL INFORMATION:
; APPLICANT: Memorial Sloan-Kettering Cancer Center
; TITLE OF INVENTION: MULTIPLE SPLICE VARIANTS OF THE MU-OPIOID RECEPTOR GENE
; FILE REFERENCE: 830002-2000.2
; CURRENT APPLICATION NUMBER: US/09/761.962A
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/743.872
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 1346
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-761-962A-12

Query Match 35.6%; Score 411; DB 4; Length 1346;
Best Local Similarity 65.7%; Pred. No. 3.8e-91;
Matches 663; Conservative 0; Mismatches 335; Indels 11; Gaps 4;

92 CGGCTGGGCGGAGCCGACAGCAAGCGAGCGCGCTGGAGAGCGCGACCTGAGAC 151
185 CCGACCAATGGCGGTCTTAAACGACGAGGCGCTTGGGAGCCACAGACCTGTGCTCAGA 244
152 CCGGCAATATCTCCCGGCAATCCGGTATCATGACGCGGCTTACTCCGATGTTG 211
245 CCGGCAACCTTTCATATGTCATGACGATCATCATATGACCTCTTATTTATGTGTGT 304
212 TCGTGGGCTTGGTGGGCAACTCGCTGTATGTTGTGTATCATCCGATACCAAGATGA 271
305 TAGTGGGCTCTTGGAACTTCTGTGTATGTATGTATGTATGTATGTATGTATGTATGT 364
272 AGACAGCAACCAATTTACATATTTAACTGCGCTTTGGCAGATGCTTTAGTTACTACA 331
365 AGACTGCAACCAATTTACATATTTAACTGCGCTTTGGCAGATGCTTTAGCTAGCA 424
332 CCATGCGCTTTCAGATGATGATCTATGATGATGATGATGATGATGATGATGATGAT 391
425 GCGTCCCTTTCAGATGATGATCTATGATGATGATGATGATGATGATGATGATGAT 484
392 GCAAGATGATATTTCCATGATGATGATGATGATGATGATGATGATGATGATGAT 451
485 GCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 544
452 TGATGAGGTGAGCGCTTACATTTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 511
545 CCATAGATGATGAGCGCTTACATTTGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 604
512 CACCTTGAAGGCAAGATCATATTTGATGATGATGATGATGATGATGATGATGATGAT 571
605 CCCCCGAAATGCAAAATGTGATGATGATGATGATGATGATGATGATGATGATGAT 664
572 TCTGTCAATATGCTTGTGAAGGCAACCAAGTCAAGGGAAGACGTGATGATGATGAT 631
665 TGCCGTATATGCTTATGAGCAACCAAAATACAGGCAAGGATGATGATGATGATGAT 718
632 CTTGCAATTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 691
719 CCGTCAAGTCTCTATCCACATGATGATGATGATGATGATGATGATGATGATGAT 775
691 TCAATTTGCTTGTGTATCCCTGTCTCATATGATGATGATGATGATGATGATGATGAT 751
776 TCAATTTGCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 835
752 TGCGTCTCAAGAGCTCGGCTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 811
836 TAGGACTCAAGATGTCCGATGATGATGATGATGATGATGATGATGATGATGATGAT 895


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/ Patent No. 6562587
/ GENERAL INFORMATION:
/ APPLICANT: BRIGITTE
/ TITLE OF INVENTION: NOVEL POLYPEPTIDES HAVING OPIOID RECEPTOR ACTIVITY,
/ TITLE OF INVENTION: NOVEL POLYPEPTIDES HAVING OPIOID RECEPTOR ACTIVITY,
/ FILE REFERENCE: EX92009-US
/ CURRENT APPLICATION NUMBER: US/08/432,174A
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 3
/ LENGTH: 998
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)..(996)
/ NAME/KEY: modified_base
/ LOCATION: (922)
/ OTHER INFORMATION: a, t, c, g, other or unknown
/ NAME/KEY: modified_base
/ LOCATION: (927)
/ OTHER INFORMATION: a, t, c, g, other or unknown
/ NAME/KEY: modified_base
/ LOCATION: (931)..(932)
/ OTHER INFORMATION: a, t, c, g, other or unknown
US-08-432-174A-3

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Query Match      34.6%; Score 399; DB 4; Length 998;
Best Local Similarity 67.8%; Pred. No. 2,9e-88;
Matches 593; Conservative 0; Mismatches 270; Indels 12; Gaps 2;

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QY 163 TCCCGGCGCATCCCGGTATCATCAGGGGGTCTACTCCGTAGTGTCTCGTGGGCTTG 222
DB 13 TCCCTCGCCCTGGCATCCGCATCCGCGCTCTACTCGCGGTGCGCGCTGGGGCTG 72
QY 223 GTGGGCACTCGTGTGATGTTGCGATCATCCGATACCAAGAATGAAGCAGCAACC 282
DB 73 CTGGGCACTGTGTCTATGTTCCGATCTGCGGTACCTAGATGAAGACACACC 132
QY 283 AACATTATCATTTTAACCTGCTTGGAGATGCTTTAGTAACTAACCAATGCCCTTT 342
DB 133 AAGATCTACATCTTCAACCTGGGCTTACGCCGATGGCGTGGCCACGACGCTGCTTC 192
QY 343 CAGAGTACGCTCTACTGATGAATTCCTGCGCTTTGGGAGATGCTGTGCAAGATGTA 402
DB 193 CAGAGTCCAGATCCTGATGAGAGCTGCGCTTGGCGAGCTGCTGCAAGGCTGTG 252
QY 403 ATTTCCATGATTAATCAACAATGTTACACAGCATCTTCACTGACATGATGAGCGTG 462
DB 253 CTCTCATGCTACTACATATGTTACACAGCATCTTCACTGACATGATGAGTGT 312
QY 463 GACCGCTACATTCGCTGTCACACCCGCTGAAGGCTTTGAGCTTCGCAACCCCTTGAAG 522
DB 313 GACCGCTACATTCGCTGTCACACCCGCTGAAGGCTTTGAGCTTCGCAACCCCTTGAAG 372
QY 523 GCAAGATATCAATATCTGCAATCTGCGTGTCTGCTATCTGTTGCAATCTCTGCAATA 582
DB 373 GCAAGCTGATCAACATCTGATCTGCGCTTGGCGCTTGGCGCTGCTGCTGCTGCTG 432
QY 583 GTCTTGAAGGACCAAGATCAAGGAGAGCTGATGATGAGTGTCTTGTGAGTTTC 642
DB 433 GTCTTGAAGGACCAAGATCAAGGAGAGCTGATGATGAGTGTCTTGTGAGTTTC 492
QY 643 CCAGATGATGATCTCTGATGAGGACCTCTTCAATGAGATGCTGCTTCAATCTTGGCC 702
DB 493 CC-----CAGCTGATGATGAGGACGAGTGAACCAATCTGCTGCTTCCCTTCCGCG 543
QY 703 TTCTGATCCCTGTCTCTATCATCTGCTGTCTACACCTGATGATCTCTGCTGCAAG 762
DB 544 TTCTGATCCCTGTCTCTATCATCTGCTGTCTACACCTGATGATCTCTGCTGCTGCTG 603
QY 763 AGCGTCCGCTCTTCTGCTGCTCCGAGAGAAAGATCGCACTGCTGATGATCAACGAGA 822

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DB 604 AGTGTCCGCTCTGTCTGCGGCTTCAAGAGAGACCGGCTGCGGGCATACAGCCC 663
QY 823 CTGTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 882
DB 664 ATGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 723
QY 883 CTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 939
DB 724 ATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 783
QY 940 TTCTGATCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 999
DB 784 CTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 843
QY 1000 GATGAATACTTCAAGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1034
DB 844 GACGAGAACTTCAAGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 878

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RESULT 46
US-08-405-271A-18
/ Sequence 18, Application US/08405271A
/ Patent No. 6432652
/ GENERAL INFORMATION:
/ APPLICANT: EVANS, CHRISTOPHER J.
/ TITLE OF INVENTION: OPIOID RECEPTOR GENES
/ NUMBER OF SEQUENCES: 25
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: MORRISON & FOERSTER
/ STREET: 2000 PENNSYLVANIA AVENUE, NW, Suite 5500
/ CITY: WASHINGTON
/ STATE: DC
/ COUNTRY: USA
/ ZIP: 20006-1888
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: IBM PC compatible
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ FILING DATE: 14-MAR-1995
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: MURASHIGE, KATE H.
/ REGISTRATION NUMBER: 29,959
/ REFERENCE/DOCKET NUMBER: 22000-20526.22
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202) 887-1500
/ TELEFAX: (202) 887-0763
/ TELEX: 90-4030 MRSNFOERSWSH
/ INFORMATION FOR SEQ ID NO: 18:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1805 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 10..1119
US-08-405-271A-18

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Query Match      34.1%; Score 393.4; DB 4; Length 1805;
Best Local Similarity 65.1%; Pred. No. 8.6e-87;
Matches 615; Conservative 0; Mismatches 321; Indels 9; Gaps 2;

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QY 153 GCGGCAATCTTCCCGGCACTCCGCTCATCATCAGCGGCTCTACTCCGATGTTGCT 212
DB 138 GCGCTTCTCTGCGCCCTCGGGCTCAAGGTCAACATCTGTGGGGCTCTACCTGGCGGTGT 197
QY 213 CGTGGGCTTGTGTGGCACTCGCTGTGATGTTCTGTATCATCCGATACCAAAAGATGA 272

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Db	198	CGAGGGGCTCCGTGGGGAAGTGGCTTGTATGTACGTCATCTCCAGGACACCAAAATGAA	257
Qy	273	GACAGCAACCAACATTTACATATTTAAACCTGGCTTTGGCAGATGCTTTAGTACTAACAC	332
Db	258	GACAGCCACCAATATTTACATCTTTAAACCTGGCCCTGGCCGACACTCTGGTCCGTGCAC	317
Qy	333	CATGGCCCTTCAAGATACGGTCTACTGTAGTGAATTCCTGGCCCTTTTGGGGAGTGTGTGG	392
Db	318	GCTGGCCCTTCAAGGACAGGACATCCTCTGGGCTTCTGGCCGTTTGGGAATGCGGTGG	377
Qy	393	CAAGATAGTAATTTCCATTTGATTACTACAAACATGTTTACACAGCATCTTCAACCTTGACAT	452
Db	378	CAAGACATGTCATTTGCACTTGACTACTACAAACATGTTTACACAGCATCTTCAACCTTAC	437
Qy	453	GATGAGCGTGAGCCGCTACATTTGCCGTGTGCCACCCCGTGAAGCCTTTGAACTTCCGAC	512
Db	438	CATGAGTGTGATCCGCTATGTAGCATCTGCACCCCATCCGTCGCCCTGACGTCCGCAC	497
Qy	513	AACCTTGAAGGAAAGATCATCATATTTCTGCATCTTGGCTCTGTGTGTATCTGTTGGCAT	572
Db	498	GTCCAGCAAAAGCCCAAGGCTGTCAATGTGGCCATCTGGGCCCTCTGTTGTGGTGT	557
Qy	573	CTTGTGCATATGCTCTTGGAGGCAACCAAGTCAAGGAGACGTCGATGTCAATGAGTGTCT	632
Db	558	TCCGCTTGGCATCATAGGCTCGGACAGGTCTC-----GAGATGAAAGATGAGTGGCT	611
Qy	633	CTTGCAGTTCCCAAGATGATGACTACTCTCTGTGGGACCTTTTCATGAAGATCTGGCTTT	692
Db	612	GGTGAGATCCCTTACCCCTCAGAGATTAC---TGGGGCCCGGAGTTTGCCATCTGCATCTT	668
Qy	693	CATCTTGGCTTCGATGCCCTGTGCTCTATATCATATGCTGTGCTTACACCTGTATATCCT	752
Db	669	CCTCTCTTCTTCATCTGTCCTCCGTCGTGTACTCTGTCTGTCTACAGCTCATATATCCG	728
Qy	753	GCGTCTCAAGAGCGTCCGCGCTCTTTCTGGCTTCCGAGAGAAAGATCCGACCTCGTAG	812
Db	729	GCGGCTCCGTGGAATCCGCTGCTCTCGGGCTTCCGAGAGAGAACCGGAACCTTCCGGG	788
Qy	813	GATCACCAAGCTGTCTGTGTGTGTGTGTGACATCTTTCGTGCTGTGTGACTTCCATTCA	872
Db	789	CATCACTCGGCTGT	848
Qy	873	CATATTTACTCTGT	932
Db	849	GGTCTTGT	908
Qy	933	CTATTTACTTGTGCATCGCTTAGCTTATACCAACAGTAGCTGAATCCATCTTCAAGC	992
Db	909	TCTGGCTTCTGTGCAGGCGCTTGGCTTAGCGTCAACAGCTGTCTCAACCCCATCTTACGC	968
Qy	993	CTTTCCTTGTATGAAAACCTTCAAGCGGTGTTCCTGGGACCTTGTCTTTCACATGAAGTAG	1057
Db	969	CTTCTCGATGAGAACTTCAAGGCTGTGCTTCGGCAAGTTCTGTGTGATCTGCCTGG	1028
Qy	1053	GATGAGCGGAGAGACCTAGAGAGTCCGAAATACATGTCAGA	1097
Db	1029	CCGGAGCGTGAAGTCTGAACCGGTGTGAGCAATGTCCAAAGGA	1073

RESULT 47
US-09-016-434-1391
Sequence 1391, Application US/09016434
Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Sellhammer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE

```

1 CITY: PALO ALTO
2 STATE: CALIFORNIA
3 COUNTRY: USA
4 ZIP: 94304
5 COMPUTER READABLE FORM:
6 MEDIUM TYPE: floppy disk
7 COMPUTER: IBM PC compatible
8 OPERATING SYSTEM: PC-DOS/MS-DOS
9 SOFTWARE: word perfect 6.1 for windows/MS-DOS 6.2
10 CURRENT APPLICATION DATA:
11 APPLICATION NUMBER: US/09/016.434
12 FILING DATE: HERewith
13 CLASSIFICATION:
14 PRIOR APPLICATION DATA:
15 APPLICATION NUMBER:
16 FILING DATE:
17 CLASSIFICATION:
18 ATTORNEY/AGENT INFORMATION:
19 NAME: Zeller, Karen J.
20 REGISTRATION NUMBER: 37,071
21 REFERENCE/DOCKET NUMBER: PA-0002 US
22 TELECOMMUNICATION INFORMATION:
23 TELEFAX: (650) 845-4166
24 INFORMATION FOR SEQ ID NO: 1391:
25 SEQUENCE CHARACTERISTICS:
26 LENGTH: 1973 base pairs
27 TYPE: nucleic acid
28 STRANDEDNESS: single
29 TOPOLOGY: linear
30 IMMEDIATE SOURCE:
31 LIBRARY: GENBANK
32 CLONE: g9471316
33 US-09-016-434-1391

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Query Match	34.1%;	Score 393.4;	DB 4;	Length 1973;
Best Local Similarity	65.1%;	Pred. No. 8.9e-87;		
Matches 615;	Conservative 0;	Mismatches 321;	Indels 9;	Gaps 2;

Oy	153	CGGCGACATCTCCCCGGGACATCCGGGTCATCATCAGCGGGCTTCACTCCGATGGTTCGT	212
Db	306	CGCCTTCTGCGCCCTCGGGGCTCAAGGTCAACATGTTGGGGCTTCACTCGGCGGTGTGCT	365
Oy	213	CGTGGGCTTGGTGGGCAACTCGCTGTGATGTTGATATCATCCGATACCAAAAGATGA	272
Db	366	CGAGGGCTCTGGGGAACTGCTTGTTCATGTATCGTATCTTCAGGCGACACCAAAATGAA	425
Oy	273	GACAGCAACCAACTTACATATTTAAACCTGGCTTTGGCAATGCTTATGTACTACAC	332
Db	426	GACGCGCAACAAATTTTAACTTTTAACTGGCCCTGGCCGACACTGTGTCCTGCTGAC	485
Oy	333	CATGCCCCCTTCAGAGTACGGGTCTACTGATGAATTCCTGGGCGCTTTGGGGATGTCGTG	392
Db	486	GCTGCCCCCTTCAGGGGACGAGACATCTCTGAGGCTTCTGGCCGTTTGGGAATGCGCTGTG	545
Oy	393	CAAGATAGTAAATTTCCATTGATTACTACCAACATGTTACCGACATCTTACCTTGACCAT	452
Db	546	CAAGACAGTATTTGCCATTGTACTACTAACATGTTACCGACACCTTCAACCTTAACATGC	605
Oy	453	GATAGCGTGGACCGCTACATTTGCCGTGTGCACCCCGTGAAGCTTTGACCTTCCGAC	512
Db	606	CATAGAGTGGATGCTATGTAGGCAATCTGCAACCCATCGTGCCTCTGACAGTCCGAC	665
Oy	513	ACCCCTTAAGGCAAAAGATCAATCAATCTGATCTGGCGTGTGTGTCATCTGTTGGCAT	572
Db	666	GTCACGAAAGCCCGAGGCTGTCAATGTGGCCATCTGGGCCCTTGGCTCTGTGTTGCGGTGT	725
Oy	573	CTTGTCAATAGTCTCTTGAGAGGCAACCAAGTCAGAGGAAGACGTGCATGTCAATGAAGTCTC	632
Db	726	TCCCGTTGCCATATAGGGCTTCGACAGGTC-----GAGGATGAAGAGATCGAGTGCCCT	779
Oy	633	CTTGCAGTTCCAGATGATGATCTACTCTGTGGGACCTCTTCAATGAAGATCTGCTCTT	692

Db 780 GGTGAGATCCCTACCCCTCAGAGATTAC---TGGGGCGCGGTGTGGCATCTGCATCTT 836
Qy 693 CATCTTGGCTTCGGATCCCTGTCTCTCATCATCTCTCTACACCTGATATCTT 752
Db 837 CCTCTTCTCTCATCTGCTCCGCTGTCTGTCTCTCTCTCTCTCTCTCTCTCTCT 896
Qy 753 GCGTCTCAAGAGCGTCCGCTCTCTTCTGGCTCCGAGAGAAAGATCGCAACTGCGTAG 812
Db 897 GCGGCTCCGCTGAGTCCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 956
Qy 813 GATCACAGACTGTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 872
Db 957 CATCACTCGGCTGT 1016
Qy 873 CATATTCACTCTGT 932
Db 1017 GGTCTCTGT 1076
Qy 933 CATATTCACTCTGT 992
Db 1077 TCTGGCTCTCTCAAGGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1136
Qy 993 CTCTCTGT 1052
Db 1137 CTCTCTGT 1196
Qy 1053 GATGAGCGGCGAGACCTAGACAGAGTCCGAAATACAGTTCCAGGA 1097
Db 1197 CCGGAGCGTGCAGGT 1241

RESULT 48
US-09-023-655-1417
; Sequence 1417, Application US/09023655

; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; FILING DATE: US/09/023,655
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1417:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1973 base pairs
; TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: 9471316
US-09-023-655-1417

Query Match 34.1%; Score 393.4; DB 4; Length 1973;
Best Local Similarity 65.1%; Pred. No. 8,9e-87;
Matches 615; Conservative 0; Mismatches 321; Indels 9; Gaps 2;

Qy 153 GCGGACATCTCCCGGCGATCCCGATCATCAAGCGGCTCTACTCCGATGTTCT 212
Db 306 CGCTTCTCGCCCTCGGCTCAAGTACCATCGTGGGCTCTACCTGCGCTGTCT 365
Qy 213 GGTGGGCTGTGGGCACTCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 272
Db 366 GCGAGGGCTCTGGGGAACCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 425
Qy 273 GACAGCAACCAATTTTCAATTTTAACTGGCTTTGGAGATGCTTTAGTTACAG 332
Db 426 GACAGCCACCAATTTTCAATTTTAACTGGCTTTGGAGATGCTTTAGTTACAG 485
Qy 333 CATGCCCTTCAAGATACGCTCTAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 392
Db 486 GCTGCCCTTCAAGGCAAGGCAATCTCTGTGGCTTTGGGCTTTGGGAAATGCGTGT 545
Qy 393 CAAGATAGTAAATTTCAATTTTCAATTTTCAATTTTCAATTTTCAATTTTCAAT 452
Db 546 CAAGACAGTAAATTTCAATTTTCAATTTTCAATTTTCAATTTTCAATTTTCAAT 605
Qy 453 GATGAGCGTGCAGGCTCATTTGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 512
Db 606 CATGAGT 665
Qy 513 ACCCTTGAAGCAAGATCATATATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 572
Db 666 GTCCAGCAAGGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 725
Qy 573 CTCTCAATAGTCTTGTGAAGGCAAGATGTCAAGGAGAGATGTATGTAGTGTCT 632
Db 726 TCCCGTTCATCATGAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 779
Qy 633 CTGTGAGTTCCTCAAGTATGACTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGT 692
Db 780 GGTGAGATCCCTACCCCTCAGAGATTAC---TGGGGCGCGGTGTGGCATCTGCATCT 836
Qy 693 CATCTTGGCTTCGGATCCCTGTCTCTCATCATCTCTCTACACCTGATATCTT 752
Db 837 CCTCTTCTCTCATCTGCTCCGCTGTCTGTCTCTCTCTCTCTCTCTCTCTCTCT 896
Qy 753 GCGTCTCAAGAGCGTCCGCTCTCTTCTGGCTCCGAGAGAAAGATCGCAACTGCGTAG 812
Db 897 GCGGCTCCGCTGAGTCCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 956
Qy 813 GATCACAGACTGTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 872
Db 957 CATCACTCGGCTGT 1016
Qy 873 CATATTCACTCTGT 932
Db 1017 GGTCTCTGT 1076
Qy 933 CATATTCACTCTGT 992
Db 1077 TCTGGCTCTCTCAAGGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1136
Qy 993 CTCTCTGT 1052
Db 1137 CTCTCTGT 1196
Qy 1053 GATGAGCGGCGAGACCTAGACAGAGTCCGAAATACAGTTCCAGGA 1097

Db 1197 CCGGACGTGACGTGTCTGACCGCGTGGCAGCATTTGCCAAGA 1241

RESULT 49
US-09-976-594-171
Sequence 171, Application US/09976594
Patent No. 6673549
GENERAL INFORMATION:
APPLICANT: Furness, Michael
APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REFERENCE: PA-0041 US
CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/240,409
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
SOFTWARE: PERL Program
SEQ ID NO 171
LENGTH: 3205
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6673549 222181.1
US-09-976-594-171

Query Match 34.1%; Score 393.4; DB 4; Length 3205;
Best Local Similarity 65.1%; Pred. No. 1.le-86;
Matches 615; Conservative 0; Mismatches 321; Indels 9; Gaps 2;

QY 153 CGCGACATCTCCCGGCATCCGGTCAATCATACAGCGGTCTCTCGTATGTTGCT 212
DB 380 CCGCTTCTGCTCCGCGCTAAGGTACCATGCGGCTCTTACCTGCGCGTGTGT 439
QY 213 CGTGGCTGTGGGCACTCGGTGATGTTGCTGATCATCCGATACACAAAGTAA 272
DB 440 CGAAGGCTCGTGGGAAGTGTGTGATGATGATGATGATGATGATGATGATGAT 499
QY 273 GACGACAAACAAATTTACATTTTAACTGGCTTTGGCAGATGCTTTACTTACAC 332
DB 500 GACGACCAACATATTTACATCTTTTAACTGGCTTTGGCAGATGCTTTACTTACAC 559
QY 333 CATGCCCTTTCAGATGAGGTCTACTGTATGATTCCTGGCCCTTTGGGAAATGTCGTG 392
DB 560 GCTGCCCTTTCAGGACGAGATCTCTGGGCTTTGGCCCTTTGGGAAATGTCGTG 619
QY 393 CAAGATGATTAATTTGATGATTTACTTACAAATGTTTCAACAGCATTTTACCTTGACCAT 452
DB 620 CAAGACATGATTTGATGATTTACTTACAAATGTTTCAACAGCATTTTACCTTGACCAT 679
QY 453 GATGAGCTTGACCGCTTACATTTGCGGTGTCACCCCGTGAAGGCTTTGGACTTCGAC 512
DB 680 CATGATGTGATGCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 739
QY 513 ACCCTTGAAGCAAGATCATCAATATCATGATGATGATGATGATGATGATGATGATGAT 572
DB 740 GTCCAGCAAGCCCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 799
QY 573 CTTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 632
DB 800 TCCCGTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 853
QY 633 CTTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 692
DB 854 GAT 910
QY 693 CATCTTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 752
DB 911 CTTCTTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 970
QY 753 GCGTCTCAAGAGCTCGGCTCTTTTGGCTCCGAGAAAGATGCAACCTGCGTAG 812

DB 971 GCGGCTCGGTGAGTCCGCTCTGCTGCGGCTCCCGAGAGAACCGGAACCTCGGCG 1030
QY 813 GATCACGAGTGTCTGT 872
DB 1031 CATCATCTGCTGT 1090
QY 873 CATATTCATCTGT 932
DB 1091 GGTCTTGT 1150
QY 933 CTATTACTTGTGATGCTGT 992
DB 1151 TGTGGCTTGTGACGGGCTGT 1210
QY 993 CTTTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1052
DB 1211 CTTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1270
QY 1053 GATGAGCGGACGACGATGACGATGACGATGACGATGACGATGACGATGACGATGACG 1097
DB 1271 CCGGACGTGACGT 1315

RESULT 50
US-09-761-962A-2
Sequence 2, Application US/09761962A
Patent No. 650927
GENERAL INFORMATION:
APPLICANT: Memorial Sloan-Kettering Cancer Center
TITLE OF INVENTION: MULTIPLE SPLICER VARIANTS OF THE MU-OPIOD RECEPTOR GENE
FILE REFERENCE: 830002-2000.2
CURRENT APPLICATION NUMBER: US/09/761,962A
CURRENT FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/743,872
PRIOR FILING DATE: 1999-07-15
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 1238
TYPE: DNA
ORGANISM: Mus musculus
US-09-761-962A-2

Query Match 33.6%; Score 387.6; DB 4; Length 1238;
Best Local Similarity 67.8%; Pred. No. 2e-85;
Matches 575; Conservative 0; Mismatches 264; Indels 9; Gaps 2;

QY 252 CATCCGATTAACAAGATGAAGACAGCAACCAATTAATTAATTAATTAATTAATTAATTAAT 311
DB 179 CTTGATATTAACAAGATGAAGACAGCAACCAATTAATTAATTAATTAATTAATTAATTAAT 238
QY 312 AGATGCTTTAGTTACTTAAACAATGATGATGATGATGATGATGATGATGATGATGATGAT 371
DB 239 AGATGCTTTAGTTACTTAAACAATGATGATGATGATGATGATGATGATGATGATGATGAT 298
QY 372 GCTTTTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 431
DB 299 GCTTTTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 358
QY 432 CAGCATCTTCACTTGAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 491
DB 359 CAGCATCTTCACTTGAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 418
QY 492 GAAGCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 551
DB 419 CAAGGCTTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 478
QY 552 GCTGTGCTCATGTTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 611
DB 479 CTTCTTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 535
QY 612 CTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 671

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Db      536  ---GGGTCATAGATTGCAACCTCAGCTTCTCATCCACATGAGTATGGGAACCT 592
Qy      672  CTTGATGAAGATCTGGCTTTTATCTTTGCGTTCGATCCCTGCTCATCATCTGT 731
Db      593  GCTC---AAATCTGTCTTCATCTTCCCTTCATCATGCGGTCCTCATCATCTGT 649
Qy      722  CTGCTACACCCCTGATGATCTGCGTCTCAAGAGCGGCTCTTTCTGGCTCCGAGA 791
Db      650  GTGTTATGAGACTGATGATCTTACGACTCAAGAGTGTCCGATGCTGTGGGCTCCAAAGA 709
Qy      792  GAAGATGCAACCTGCGTAGATACACAGACTGTCGTGTCGTGTCGTGTCGTGTCGT 851
Db      720  AAAGACAGAAACCTGCGAGATACCCGAGATGTCGTGTCGTGTCGTGTCGTGTCGT 769
Qy      852  CGTCTGCTGAGATCCCATTCACATATTCATCTGTCGTGAGGCTCTGGGAGACCTCCA 911
Db      770  TGTCTGTGAGACCCCATTCACATATGTCATCATCAAGACATGATCAGATTCAGAG 829
Qy      912  CAGCAGAGTGTCTCTCCAGCTATTTACTTCGACATCCGCTTAGGCTATACCAAGTAG 971
Db      830  AACCATTTCCAGACTGTTTCTGGGACTTCTGCAATGCTTGGGTTACACAAAGCTG 889
Qy      972  CCTGATCCCATTTCTACGCTTTCTTGATGAAAACTTCAAGCGGTGTTCCGGGACTT 1031
Db      890  CCTGAACCAAGTCTTTATGCGTCTCTGATGAAAACTTCAACGATGTTTATGAGAGTT 949
Qy      1032  CTGCTTTCCACTGAAGATGAGATGAGCGGAGAGCACTAGCAGAGTCCGAATATACGT 1091
Db      950  CTGCATCCCACTTCTCTCCACATGGAACAGCAAAACTGCTGCAATCCGTCAAACAC 1009
Qy      1092  TCAGATC 1099
Db      1010  TAGGAAC 1017

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RESULT 51
US-09-761-962A--5
; Sequence 5, Application US/09761962A
; Patent No. 6500927
; GENERAL INFORMATION:
; APPLICANT: Memorial Sloan-Kettering Cancer Center
; TITLE OF INVENTION: MULTIPLE SPLICED VARIANTS OF THE MU-OPIOD RECEPTOR GENE
; FILE REFERENCE: 830002-2000 2
; CURRENT APPLICATION NUMBER: US/09/761,962A
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/743,872
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-761-962A-5

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Query Match      33.6%; Score 387.6; DB 4; Length 1257;
Best Local Similarity 67.8%; Pred. No. 2e-85;
Matches 575; Conservative 0; Mismatches 264; Indels 9; Gaps 2;

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Qy      252  CATCGATACCAAGATGAAGAGCAACCAATTTACATTTAACTTGGCTTGGC 311
Db      179  CTTGATATATACCAAAATGAAGACGCGCAACATTTACATTTCACTTGGCTTGGC 238
Qy      312  AGATGCTTAGTACTACAAACCATGCTTTCAGAGTACGCTCTGATGAATTCGCG 371
Db      239  AGATGCTTAGTACTACAAACCATGCTTTCAGAGTACGCTCTGATGAATTCGCG 298
Qy      372  GCTTTTGGGAGTGTGCTGTGCAAGATGAATTTTCCATGATTACTACACATGTTAC 431
Db      299  GCTTTTGGGAGTGTGCTGTGCAAGATGAATTTTCCATGATTACTACACATGTTAC 358

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Qy      432  CAGCATCTTCACTTGAACCATGATGAGCGTGGACCGCTACATTCGCTGTCACCCCGT 491
Db      359  CAGTATCTTCAACCTCTGACCATATGATGTAGACCGCTACATTCGCTGTCACCCCGT 418
Qy      492  GAAGCTTTGAGCTTTCGCAACCCCTTGAAGGCAAGATCATCAATATCTGATCTGCT 551
Db      419  CAAGCCCTGAGATTTCCGTACCCCGCAAAATGCCAAATTTGTCATGTCGCACTGAT 478
Qy      552  GCTGTCTCATCTGTGGGATCTCTGCAATAGTCTTGGAGGACCAAAAGTACAGGAGA 611
Db      479  CTTCTTTCTGCAATGATGTGCGCCGTATGTCATGTCACCAAAATATACAGGA--- 535
Qy      612  CGTCATGATCATGATGATCTCTTTCAGATTCGCAATGATGATGATGATGATGATGAT 671
Db      536  ---GGGTCATAGATTGCAACCTCAGCTTCTCATTCACATAGTATGGGAACCT 592
Qy      672  CTTGATGAAGATCTGCGTCTTCATCTTTCGCTTGTGATCCCTGTCCTCATCATCTGT 731
Db      593  GCTC---AAATCTGTCTTCATCTTTCGCTTTCATCATGCGGTCCTCATCATCTGT 649
Qy      732  CTGCTACACCTGATGATCTGCGTCTCAAGAGCTCCGGCTCTTCTGCTCCGAGA 791
Db      650  GTGTTATGAGACTGATGATCTTACGACTCAAGAGTGTCCGATGTCGTGGGCTCCAAAGA 709
Qy      792  GAAGATGCAACCTGCGTAGATACACAGACTGTCGTGTCGTGTCGTGTCGTGTCGT 851
Db      710  AAAGACAGAAACCTGCGAGATACCCGAGATGTCGTGTCGTGTCGTGTCGTGTCGT 769
Qy      852  CGTCTGCTGAGATCCCATTCACATATTCATCTCTGTGAGAGGCTCTGGGAGACCTCCA 911
Db      770  TGTCTGTGAGACCCCATTCACATATGTCATCATCAAGACATGATCAGATTCAGAG 829
Qy      912  CAGCAGAGTGTCTCTCCAGCTATTTACTTTCGATCCGCTTAGGCTATACCAAGTAG 971
Db      830  AACCATTTCCAGACTGTTTCTGGGACTTCTGCAATGCTTGGGTTACACAAAGCTG 889
Qy      972  CCTGATCCCATTTCTACGCTTTCTTGATGAAAACTTCAAGCGGTGTTCCGGGACTT 1031
Db      890  CCTGAACCAAGTCTTTATGCGTCTCTGATGAAAACTTCAACGATGTTTATGAGAGTT 949
Qy      1032  CTGCTTTCCACTGAAGATGAGATGAGCGGAGAGCACTAGCAGAGTCCGAATATACGT 1091
Db      950  CTGCATCCCACTTCTCTCCACATGGAACAGCAAAACTGCTGCAATCCGTCAAACAC 1009
Qy      1092  TCAGATC 1099
Db      1010  TAGGAAC 1017

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RESULT 52
US-08-889-108-16
; Sequence 16, Application US/08889108
; Patent No. 6103492
; GENERAL INFORMATION:
; APPLICANT: Yu, Lei
; TITLE OF INVENTION: Mu Opioid Receptors: Compositions and Methods
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/889,108
; FILING DATE:
; CLASSIFICATION:

```

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/305,518
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: INDA005\WIM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1567 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 173..1273
US-08-889-108-16

Query Match 32.7%; Score 377.6; DB 3; Length 1567;
Best Local Similarity 63.9%; Pred. No. 6e-83;
Matches 607; Conservative 0; Mismatches 334; Indels 9; Gaps 2;

QY 153 CGCGACATCTCCCGGCGCATCCCGTCATCTACGGCGGTCTCTCCGTAGTGTCTGT 212
DB 292 CGCTTCTCCGCGCTTGACCTCAAGCTACCATCGTGGGCTCTACCTTGGCTGTGCTAT 351
QY 213 CGTGGGCTTGTGGGCAACTCGCTGTCATGTTCTGTATCATCCATACACAAAGATGAA 272
DB 352 CGGGGGGCTCTCGGGGAAGTGCCTGTATGTATCTCTCAGGACACCAAGATGAA 411
QY 273 GACAGCAACCAATTATCAATTTTAACTTGGCAATGCTTTAGTTACTACAC 332
DB 412 GACAGCTACCAATTATCAATTTTAACTTGGCAATGCTTTAGTTACTACAC 471
QY 333 CATGCCCTTTCAGATAGCTGTATGTATGAATTCCTGGCTTTTGGGAGATGTCTGTG 392
DB 472 ACTGCCCTTTCAGAGGACAGACATCTCTAGGCTTTCGGCCATTTGGGAATGCACTGTG 531
QY 393 CAAGATAGTAAATTTTCATTGATTACTACAACATGTTACACAGCATCTTCACTTGACAT 452
DB 532 CAAGCTGTCTATGTCTATGCACTACTACAACATGTTTACAGCACTTTTACTTGACCCG 591
QY 453 GATGAGCGTGAACCGCTACATTTGCGGTGCCACCCCGTGAAGGCTTTGAATTCCGAC 512
DB 592 CATGAGCGTGAACCGCTATGTGCTATCTGCCACCCCTATCGGTGCCCTTGAATGTTCCGAC 651
QY 513 ACCCTGAAGGCAAAAGATCATCAATATCTGCATCTGCTGTCTGTATCTGTTGGCAT 572
DB 652 ATCCAGCAAAAGCCAGGCTGTAAATGTGCAATATGAGCCCTGAGTTGAGTGTG 711
QY 573 CTCTGCATATGCTCTTGGAGGACACCAAGTCAAGGAAAGCTGCATGTCATTGAGTGTG 632
DB 712 TCCTGTGTCATCATGAGGTTGACACAGT-----GGAATGAAAGATCGAGTGTCT 765
QY 633 CTTCGAGTTCCCAATGATGACTACTCTGTGTGGGACCTCTTCAATGAAGATCTGCTGT 692
DB 766 GGTGAGATCCCTGCGCCCTCAGACATATTTGGGG---CCCTGATATTCGCATCTGATCTT 822
QY 693 CATCTTGGCTTTCGATCCCTGCTCTCATATCATCTCTGCTATCAACCTGATGATCTCT 752
DB 823 CTTTTCCTTTCATCATCTCTGCTGTATCATCTCTGCTATCAACCTCCTCATGATTTG 882
QY 753 GCGTCTCAAGAGCGTCCGCTCTCTTCTGCTCCGAGAGAAAGTCACTGCGTAG 812
DB 883 ACGACTCTGTGTCTCTCTGCTTTCAGGCTCCCGGAGAAAGACCAAACTCTGCGCG 942
QY 813 GATCAACAGACTGTCTGTGTGTGTGTGGAAGTCTTCTGCTGTCTGAGACTCCCATTTCA 872
DB 943 TATCACTGACCTGGGT 1002

QY 873 CATATTCCTCTGTGAGGCTTGGGAGACCTCCACAGCAGCTGCTCTCCAG 932
DB 1003 GGTGTGTCTCTGTGTAAGGACTGGGTCTTACCCAGAGTGTGAGATGAGTGTGCCAT 1062
QY 933 CTATTACTTCTGCAATCGCTTAGGCTATACCAAGTAGTAGCTGATCCCATTTCTACGC 992
DB 1063 CTGCGCTTCTGCAACGCGCTGGGCTATGTCAACAGTGTCTCAATCCCATTTCTATGC 1122
QY 993 CTTTCTGTATGAAAATTCAAGCGGTGTTCCGGGACTTCTGCTTTCACATGAAGTAG 1052
DB 1123 TTTCTGTATGAAAGACTTCAAGCGCTGCTTGAAGAGTGTCTGTGCTATCCCTGCA 1182
QY 1053 GATGAGCGGAGAGCACTAGACAGTCCGAAATACATTTAGATCTGT 1102
DB 1183 CGGAGATGCAAGGTTTCTGTATGTGTGGGAGCATTTGCCAAGATGTGTG 1232

RESULT 53
PCT-US94-10358-16
Sequence 16, Application PC/TUS9410358
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10358
FILING DATE: Concurrently herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/120,601
FILING DATE: 13 SEPTEMBER 1993
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARK B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: INDA005P--
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1567 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 173..1273
PCT-US94-10358-16

Query Match 32.7%; Score 377.6; DB 5; Length 1567;
Best Local Similarity 63.9%; Pred. No. 6e-83;
Matches 607; Conservative 0; Mismatches 334; Indels 9; Gaps 2;

QY 153 CGCGACATCTCCCGGCGCATCCCGTCATCTACGGCGGTCTCTCCGTAGTGTCTGT 212
DB 292 CGCTTCTCCGCGCTTGACCTCAAGCTACCATCGTGGGCTCTACCTTGGCTGTGCTAT 351
QY 213 CGTGGGCTTGTGGGCAACTCGCTGTCATGTTCTGTATCATCCATACACAAAGATGAA 272

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Db      352 CGGGGGGCTCCCTGGGAACTGCTGTATGATCATCTCCAGGACACCAAGATGAA 411
Qy      273 GACAGCAACCAACATTTACATTTTAACCTGGCTTGGCAGATGCTTTAGTTACTACAAC 332
Db      412 GACACCTACCAACATTTATATTTAATCTGGCAGCTGGCTGATACCTGGCTTCTTAAC 471
Qy      333 CATGCCCTTTGAGATAGGCTACTGTATGAAATTCCTGGCCTTTTGGGGAATGCTGTG 392
Db      472 ACTGCCCTTCCAGGACACAGACATCTACTGGGCTTCTGGCCATTTGGGAATGACCTCG 531
Qy      333 CAAGATAGTAAATTTCCATTTACTATTACAAAGTTCACACAGATCTTCACTTACACAT 452
Db      532 CAAGACTGTGATGTATGACTACTACAAAGTTCACACAGATCTTCACTTACACACG 591
Qy      453 GATGACGCTGACCCGCTACATTTGCGGTGTGCAACCCCGTGAAGGCTTTGGAATTCGAC 512
Db      592 CATGACGCTGACCCCTATGTGGCTATCTGCCACCTTATCCGCTGCTTGAATGTTCCGAC 651
Qy      513 ACCCTTGAAGGCAAGATCATATATCTGCATCTGGCTGTGTGATCTGTGGCAT 572
Db      652 ATCCAGCAAAAGCCAGGCTGTAAATGTGGCATATGGCCCTTGGCTTCACTGTGGTGT 711
Qy      573 CTCTGCAATAGTCTTGGAGGACCAAGTCAAGGAAGACGTGATGATTAAGTGTCTC 632
Db      712 TCCTTTGGCATCATAGGCTTACAGCAAGT-----GGAAGATGAAGATGAGATGCTT 765
Qy      633 CTTCGAGTTCCGAGATGATGACTACTCTGTGTGGGACCTCTTCAATGAAGATCTGCTCTT 692
Db      766 GGTGAGATATCCCTGCCCCCTCAGGACTATGGGG---CCCTGATTCGCGCATCTGCATCTT 822
Qy      693 CATCTTGGCTTCGATGCCCTGTCTCTCATCATCTGCTCTCAACCTTATATATCT 752
Db      823 CTTTTCCTTCATCATATCCCTGTGCTGATCATCTCTGTCTCAAGCTTCAATATCTG 882
Qy      753 GCGTCTCAAGACGCTCCGCTCTCTTCTGCTCCGAGAGAAAGATTCGCACTGCTAG 812
Db      883 AGGATCTGTGTGTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 942
Qy      813 GATCAACCAAGTGTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 872
Db      943 TATCACTGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1002
Qy      873 CATATTCATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 932
Db      1003 GGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1062
Qy      933 CTATTAATCTTGTGATCTGCTTGTAGGCTATACCAAGTGTGTGTGTGTGTGTGTGTGT 992
Db      1063 CTGTGGCTTCTGCAACAGCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1122
Qy      993 CTTTCTGTATGAAAATCTTCAAGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1052
Db      1123 TTTCTGTATGAGACTTCAAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1182
Qy      1053 GATGAGCGGCGAGACACTAGAGAGTCCGAATATACAGTTCAGATCTCG 1102
Db      1183 CCGGAGATGACGGTTTCTGATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1232

```

RESULT 54
US-08-454-549-1

Sequence 1, Application US/08454549
Patent No. 5863324
GENERAL INFORMATION:
APPLICANT: EPLER, C. Mark
APPLICANT: OZEMBERGER, Bradley A.
APPLICANT: HILMES, Jeffrey D.
TITLE OF INVENTION: CDNA'S ENCODING PROTEINS CLOSELY RELATED
TITLE OF INVENTION: TO OPIOID RECEPTORS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESS: Darby & Darby, P.C.

```

; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/454,549
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Robinson, Joseph R.
; REGISTRATION NUMBER: 33,448
; REFERENCE/DOCKET NUMBER: 0646/1A818-US5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 527-7700
; TELEFAX: (212) 753-6237
;
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2706 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; TISSUE TYPE: Rat brain
;
; US-08-454-549-1
;
; Query Match 32.7%; Score 377.6; DB 2; Length 2706;
; Best Local Similarity 63.9%; Pred. No. 7.4e-83;
; Matches 607; Conservative 0; Mismatches 334; Indels 9; Gaps 2;

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Qy      133 CGGGCAATCTCCCCGGGCAATCCCGGTGATATCAAGCGGCTTATCCGTATGTTGCT 212
Db      226 GCGCTTCTGCCCCCTTGAGCTCAAGGTACCATCTGTGGGCTTACTTGGCTGTGTGCT 285
Qy      213 CGTGGCTTGTGGGCACTCGCTGTATGTTCTGTATCATCCGATACCAAGATGAA 272
Db      286 CGGGGGGCTCCTGGGGAATGCTGCTGTATGATATATCTTCAAGGACACCAAGATGAA 345
Qy      273 GACAGCAACCAACATTTATATTTTAACCTTGGCAAGTGTCTTATCTACAAC 332
Db      346 GACACCTACCAACATTTATATTTAATCTGGCACTGGCTGATACCTGTCTTCTTAAC 405
Qy      333 CATGCCCTTCAAGATAGGCTTACTGTATGAAATTCCTGGCCTTTTGGGGAATGCTGTG 392
Db      406 ACTGCCCTTCCAGGACACAGACATCTTACTGGGCTTCTGGCCATTTGGGAATGACCTGTG 465
Qy      393 CAAGATAGTAAATTTCCATTTGATTTACTACAACATGTTCAACAGATCTTCACTTACACAT 452
Db      466 CAAGACTGTGATGTATGACTACTACAAGTTCACAGATCTTCACTTACTCTACCCG 525
Qy      453 GATGACGCTGACCGCTTCAATTTGCGGTGTGCAACCCCGTGAAGGCTTTGGAATTCGAC 512
Db      526 CATGAGCGTAGACGCTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 585
Qy      513 ACCCTTGAAGGCAAGATCATATATCTGCATCTGGCTGTGTGTGTGTGTGTGTGTGTGTGT 572
Db      586 ATCCAGCAAAAGCCAGGCTGTAAATGTGACCATATATGGCCCTTGGCTTCAAGTGTGTGT 645
Qy      573 CTCTGCAATAGTCTTGGAGGACCAAGTCAAGGAAGACGTGATGATTAAGTGTCTC 632
Db      646 TCCTTTGGCATCATAGGCTTACAGCAAGT-----GGAAGATGAAGATGAGATGCTT 699
Qy      633 CTTCGAGTTCCGAGATGATGACTACTCTGTGTGGACCTCTTCAATGAAGATCTGCTCTT 692
Db      700 GGTGAGATATCCCTGCCCCCTCAGGACTATTTGGGG---CCCTGATTCGCGCATCTGCATCTT 756

```



```
; Sequence 1, Application US/08676351C
; Patent No. 6046026
; GENERAL INFORMATION:
; APPLICANT: EPPLE, CECIL
; APPLICANT: OZENERGER, BRADLEY
; APPLICANT: HULMES, JEFFREY
; TITLE OF INVENTION: CDNAS ENCODING PROTEINS CLOSELY RELATED
; TITLE OF INVENTION: TO OPIOID RECEPTORS
; FILE REFERENCE: 0646/1A81BUS1
; CURRENT APPLICATION NUMBER: US/08/676,351C
; CURRENT FILING DATE: 1996-09-12
; EARLIER APPLICATION NUMBER: PCT/US95/00939
; EARLIER FILING DATE: 1995-01-20
; EARLIER APPLICATION NUMBER: US 08/185,360
; EARLIER FILING DATE: 1994-01-21
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2706
; TYPE: DNA
; ORGANISM: Rat
; US-08-676-351-1

Query Match      32.3%; Score 372.8; DB 3; Length 2706;
Best Local Similarity 63.6%; Pred. No. 1.1e-81;
Matches 604; Conservative 0; Mismatches 337; Indels 9; Gaps 2;

QY 153 CGCGACATCTCCCGGCCATCCGGTATCATCAACGCGGATCTACCTCGTAGTGTCTG 212
DB 226 CGCCTTCCGCGCCCTTGAGACTCAAGGTCAACATCGGGGCTCTACTTGCTGTGTGAT 285
QY 213 CCGTGGCTTGGTGGCACTCGCTGTATCTTCTGTATCTCCATACAAAGATGAA 272
DB 286 CGGGGGGCTCCGCGGAACTGCTGTATGTATGTATGATCTCCAGCAACCAAGATGAA 345
QY 273 GACAGCAACCAATTATACATTTAACTTGGCTTTGGAGATGCTTTAGTACTAACA 332
DB 346 GACAGCTACCAATTTATATTTATTTATGTGACATCGCTGTATACCTGTCTTGTAC 405
QY 333 CATGCCCTTTAGAGTACGCTTACTTGTATGATTTCTGGCTTTGGGAGATGTCTGT 392
DB 406 ACTGCCCTTCCAGGACACAGACATCTACTGCGGCTTTGGCCATTTGGGAATGACTCTG 465
QY 393 CAAGATAGTAATTTCCATTTGATTACTTACAACTTTTACACACACTTTTACCTGAC 452
DB 466 CAAGCTGTATGTCTATCTGACTACTACAACTTTTACACACACTTTTACCTGACGCG 525
QY 453 GATGAGCGTGACCGCTACATTTGCGGTGCGCACCCCGTGAAGGCTTTGGACTTCCGAC 512
DB 526 CATGACGCTAGACCGCTATGTGGCTATCTGCAACCTTACCTGCTGATGTTGAGAC 585
QY 513 ACCCTTGAAGGCAAGATCATATATCTGATCTGCGCTGTGTCTGTATCTTGGGCA 572
DB 586 ATCCAGCAAAAGCCCGCTGTATATGTGGCCATATGGCCCTGTGAGTGTGTGTGT 645
QY 573 CTCTGCATATGTCTTGGAGGCAACAAAGTCAAGGAAAGCGTATGTATGATGCTGC 632
DB 646 TCCTGTGGCATCATAGGTTTCAAGCAAGT-----GGAAGATGAAGATGAGTGTGCT 699
QY 633 CTTCGAGTTCCAGATGATGACTACTCCTGTTGGGACCTCTTCAAGAAATCTGGTCTT 692
DB 700 GGTGAGATCTCTGCGCCCTCAGAGACTATTGGGG---CCTGTATTTGCCATCTGATCTT 756
QY 693 CATCTTTGCTTGTGATCTCTGTCTCTATCATCTGTCTGCTACACCTGTATGATCTCT 752
DB 757 CTTTTTTTCTTCAATCATCTCTGTGTGTATCTGTCTGTCTATCAGCTCATGATTTG 816
QY 753 GGGTCTCAAGAGCGTCCGGCTCTTTCTGCTCCGAGAGAAAGATCGAACCTGTGCTAG 812
DB 817 ACGACTCTGTGTGTCTCTCTCTTCAAGCTCCCGGAGAAAGACCGAAACCTGTGCGGG 876
QY 813 GATCACAAGACTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 872
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DB 877 TATCAGCTGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGCA 936
QY 873 CATATTATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGCG 932
DB 937 GGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 996
QY 933 CTATTACTTTGTCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 992
DB 997 CTGTGCTTTGTGCAACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1056
QY 993 CTTTCTTATGATAAACTTCAAGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1052
DB 1057 TTTCTGTATGAGACTTCAAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1116
QY 1053 GATGAGCGGCGAGACACTTACGAGTCCGAATACAGTTACGATCTGCTG 1102
DB 1117 CGGGAGATGAGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1166

RESULT 57
US-08-149-093A-3
; Sequence 3, Application US/08149093A
; Patent No. 5658783
; GENERAL INFORMATION:
; APPLICANT: Bunzow, James R
; APPLICANT: Grandy, David K
; TITLE OF INVENTION: A No. 5658783el Mammalian Methadone-Specific
; TITLE OF INVENTION: Opioid Receptor Gene and Uses
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Banner & Allegretti, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/149,093A
; FILING DATE: 06-NOV-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5658783nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 93,311
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1452 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..181
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 182..1282
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 1283..1452
; US-08-149-093A-3

Query Match      31.9%; Score 368; DB 1; Length 1452;
Best Local Similarity 63.3%; Pred. No. 1.3e-80;
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QY 453 GATGAGCGGTGACCGCTATACATTCGCGTGTGGCCACCCCGTGAAGGCTTTGGACCTTCGGAC 512
DB 601 CATGAGCGGTGACCGCTATACATTCGCGTGTGGCCACCCCGTGAAGGCTTTGGACCTTCGGAC 660
QY 513 ACCCTTGAAGGCAAGATCATCATATATCTGACATCTGGCTGTCTGTCTATCTGTGGCAT 572
DB 661 ATCCAGCAAAAGCCCAAGGCTGTATATGTGGCATTATAGGCGCTGGCTTCAAGTGTGGTGT 720
QY 573 CTCTGCAATATGCTCTTGGAGGACCAAAATCATGAGGAAAGCTGTATGTATGATGCTTC 632
DB 721 TCCTGTGGCATCATAGGCTTCAAGCAAGT-----GGAAGATGAAGATGAGAGGCTT 774
QY 633 CTTCGAGTTCACGATGATGATCACTCCGTGTGGAGCCTCTTCAAGATCTGGGCTT 692
DB 775 GGTGAGATCTCTGCGCTCAGAGACTATTGGG---CCCTGATTCGCCATCTGACATCTT 831
QY 693 CATCTTTGCTTGTGTATCTCTGCTCTCATCATCATCTGTCTACACCCGTATGATCTCT 752
DB 832 CTTTTCCTTTCATCATCTCTGTGTATCATCTGTCTGTCTGTCTGTACAGCTCATGATTCG 891
QY 753 GGTCTCAAGAGCGCTCCGCTCTTCTGTGGCTCCGAGAGAAAGATCGCACTGTGGTATG 812
DB 892 ACGACTTCGTGTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 951
QY 813 GATCAGCAGACTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 872
DB 952 TATCAGCTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1011
QY 873 CATATTCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 932
DB 1012 GGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1071
QY 933 CTATATCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 992
DB 1072 CTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1131
QY 993 CTTCGTATGAAACTTCAAGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1052
DB 1132 TTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1191
QY 1053 GATGAGCGGTGACCGCTATACATTCGCGTGTGGCCACCCCGTGAAGGCTTTGGACCTTC 1102
DB 1192 CCGGAGATGACGAGTTCGATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1241

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RESULT 59
US-08-553-058C-3
Sequence 3, Application US/08553058C
Patent No. 5821219

GENERAL INFORMATION:
APPLICANT: Grisel, Judith E.
APPLICANT: Grandy, David K.
APPLICANT: Mogil, Jeffrey S.
TITLE OF INVENTION: Opioid Antagonists and Methods of Their Use
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klarquist Sparkman Campbell Leigh & Whinston LLP
STREET: 121 S.W. Salmon, Suite 1600
CITY: Portland
STATE: Oregon
COUNTRY: USA
ZIP: 97204
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Version MP6, ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,058C
FILING DATE: 11/3/95
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:

```

; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: William D. No. 5821219nan, M.D.
; REGISTRATION NUMBER: 30,878
; REFERENCE/DOCKET NUMBER: 899-40006/WDN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 226-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1452 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; DESCRIPTION: GDNA
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..181
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 182..1282
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 1283..1452
; US-08-553-058C-3

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Query Match 31.9%; Score 368; DB 1; Length 1452;
Best Local Similarity 63.3%; Pred. No. 1.3e-80;
Matches 601; Conservative 0; Mismatches 340; Indels 9; Gaps 2;

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QY 153 CCGGCAATCTTCCCGGCGCATCCGCTCATCTACAGCGGCTTACTCGTATGTTCCT 212
DB 301 CGCCTTCTGCGCCCTTGTGACATCAAGTCAACATGTGGGGCTCATCTGGCTGTGTGAT 360
QY 213 CGTGGGCTTGTGGGCACTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 272
DB 361 CCGGGGGCTCTGGGGAAGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
QY 273 GACAGCAACCAATTATATTTAATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 332
DB 421 GACAGCTACCAATTTATATTTATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480
QY 333 CATGCCCTTTCAGAGTACGCTTACTTATGTAATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGT 392
DB 481 ACTGCCCTTTCAGAGGACAGACATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 540
QY 393 CAAGATGATTAATTTTCAATGATTTACTTACCAACATGTTTACACGATCTTACCTTGACAT 452
DB 541 CAAGATGATTTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600
QY 453 GATGAGCGGTGACCGCTATACATTCGCGTGTGGCCACCCCGTGAAGGCTTTGGACCTTCGGAC 512
DB 601 CATGAGCGGTGACCGCTATACATTCGCGTGTGGCCACCCCGTGAAGGCTTTGGACCTTCGGAC 660
QY 513 ACCCTTGAAGGCAAGATCATCATATATCTGACATCTGGCTGTCTGTCTATCTGTGGCAT 572
DB 661 ATCCAGCAAAAGCCCAAGGCTGTATATGTGGCATTATAGGCGCTGGCTTCAAGTGTGGTGT 720
QY 573 CTCTGCAATATGCTCTTGGAGGACCAAAATCATGAGGAAAGCTGTATGTATGATGCTTC 632
DB 721 TCCTGTGGCATCATAGGCTTCAAGCAAGT-----GGAAGATGAAGATGAGAGGCTT 774
QY 633 CTTCGAGTTCACGATGATGATCACTCCGTGTGGAGCCTCTTCAAGATCTGGGCTT 692
DB 775 GGTGAGATCTCTGCGCTCAGAGACTATTGGG---CCCTGATTCGCCATCTGACATCTT 831
QY 693 CATCTTTGCTTGTGTATCTCTGCTCTCATCATCATCTGTCTACACCCGTATGATCTCT 752
DB 832 CTTTTCCTTTCATCATCTCTGTGTATCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 891
QY 753 GGTCTCAAGAGCGCTCCGCTCTTCTGTGGCTCCGAGAGAAAGATCGCACTGTGGTATG 812

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QY 1053 GATGAGGGGCGAGACACTAGACAGAGTCCGAATAACATTGACAGATCTCG 1102
Db 1192 CCGGAGATGACGAGTTTCTGATCGTGTGCGAGCATGCGCAAGAGATGTTG 1241

RESULT 61

US-09-170-331-3
; Sequence 3, Application US/09170331C
; Patent No. 6028175
; GENERAL INFORMATION:
; APPLICANT: Bunzow, James R
; APPLICANT: Grandy, David K.
; TITLE OF INVENTION: A No. 6028175el Mammalian Methadone-Specific Opioid Receptor
; FILE REFERENCE: 93-311-C
; CURRENT APPLICATION NUMBER: US/09/170,331C
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1452
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (182)..(1282)
US-09-170-331-3

Query Match 31.9%; Score 368; DB 3; Length 1452;
Best Local Similarity 63.3%; Pred. No. 1,3e-80;

Matches 601; Conservative 0; Mismatches 340; Indels 9; Gaps 2;

QY 153 CGCGACATCTCCCGGCCATCCGGTCATCATCAGCGGCGTCTACTCCGATGTTGCT 212
Db 301 CGCCTTCCGCGCCCTTGAGCTCAAGTCAACATCGGGGCTCATCTTGCTGTGCAT 360
QY 213 CGTGGGCTTGGTGGGCACTCGCTGTCTATGTTCTGATCATCCGATACAAAGTAA 272
Db 361 CGGGGGGCTCTGGGGAATGCTCGTCATGATGTCATCTTCAGAGACCCCAAGATGA 420
QY 273 GACAGCAACCAACATTTATATTTAACTGCGTTTGGAGATGCTTATGTTACTACAAC 332
Db 421 GACAGCTACCAACATTTATATTTATTTATGTCATCTGCTGTATCCCTGTCTGTAAC 480
QY 333 CATGCCCTTTCAGAGTACGCTGCTACTGATGAATTCCTGGCCCTTTGGGAGTGTCTGTG 392
Db 481 ACTGCCCTTTCAGAGGACAGACATCTACTGAGGCTTCTGGCCATTTGGGAAGACCTCTG 540
QY 393 CAAGATAGTAAATTTGATGATTTACTACAAAGTTCACAGACATCTTCACTTGACCAT 452
Db 541 CAAGACTGTATGCTATGCTACTACTACAAAGTTCATGACACATTTTAACTCTACACGC 600
QY 453 GATGAGCGGAGCGCTACATTCGCGTGTGCGACCCCGGAAGGCTTGGACTTCCGAC 512
Db 601 CATGAGCGTACCGCTATGTGCTATCTGCCACCCCTATCCGTGCCCTTGATGTTCCGAC 660
QY 513 ACCCTTGAAGGCAAGATCATCATATATCTGATCTGGCTGTCTGTCTCTGTTGGCAT 572
Db 661 ATTCAGCAAAAGCCAGGCTGTATATGTGGCCATATGGGCGCTTGGCTGATGTTGGTGT 720
QY 573 CTCTGCAATAGTCTCTTGAAGGCAACCAAGTCAAGGGAAGCTGATGTCATTTGATGCTC 632
Db 721 TCCTGTTCGATCATGAGGTTTCAACCAAGT-----GGAAGATGAAGATGAGTGTCT 774
QY 633 CTTCGAGTTCCAGATGATGATCTACTCCGATGGGAGCCCTTCATGAAGATCTGCGCTT 692
Db 775 GGTGAGATCTCTGCGCCCTCAGAGCTATTTGGG---CCCTGATTCGCCATCTGCATCTT 831
QY 693 CATCTTGGCTTCTGATGCTCTGTCTCTCATCATCTGCTGCTCAACCCCTGATGATCT 752
Db 832 CTTTTCCTTCTCATCATCTCTGTGTGCTGATCATCTCTGCTCAAGCCTCATGATTCG 891

QY 753 GCGTCTCAAGACCGTCCGGGCTCTTTCTGCTCCCGAGAGAAAGATCCGAACCTGCTAG 812
Db 892 ACGACTTGTGTGTGTCCTGCTCTCTTCAAGGCTCCCGGAGAGAGACCGAACTCTGCGG 951
QY 813 GATCACCACTGTGCTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 872
Db 952 TATCACTCGACTGT 1011
QY 873 CATATTCATCTGT 932
Db 1012 GGTGTTTCTCTGT 1071
QY 933 CTATTAATCTGATGAGCTTATAGGCTATACCAAGTACGCTGAATCCATCTCTACGC 992
Db 1072 CTGCGCTTCTGCAACGCCCTGAGCTATGTCAACAGTTGTCTCAATCCATCTCTATGC 1131
QY 993 CTTTCTGATGAAAACTTCAAGCGGTGTTTCGCGGACTTGTCTTCACTGAGATGAG 1052
Db 1132 TTTCTGATGAGAACTTCAAGGCGCTGCTTATGAAAGTTCTGTGTGTGTGTGTGTGT 1191
QY 1053 GATGAGGGGCGAGACACTAGACAGAGTCCGAATAACATTGACAGATCTCG 1102
Db 1192 CCGGAGATGACGAGTTTCTGATCGTGTGCGAGCATGCGCAAGAGATGTTG 1241

RESULT 62

US-09-510-473-3
; Sequence 3, Application US/09510473
; Patent No. 6280973

GENERAL INFORMATION:

APPLICANT: Bunzow, James R
APPLICANT: Grandy, David K

TITLE OF INVENTION: A No. 6280973el Mammalian Methadone-Specific
TITLE OF INVENTION: Opioid Receptor Gene and Uses

NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:

ADDRESSEE: Banner & Allgeiretti, Ltd.
STREET: 10 South Wacker Drive, Suite 3000

CITY: Chicago
STATE: Illinois

COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/510,473
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/149,093
FILING DATE: 06-NOV-1993

ATTORNEY/AGENT INFORMATION:
NAME: No. 6280973nan, Kevin E

REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 93,311

TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000

TELEFAX: 312-715-1234
TELEX: 910-221-5317

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:

LENGTH: 1452 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: cDNA
FEATURE:

NAME/KEY: 5'UTR
LOCATION: 1..181

FEATURE:

NAME/KEY: CDS
LOCATION: 182..1282
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 1283..1452
US-09-510-473-3

Query Match 31.9%; Score 368; DB 3; Length 1452;
Best Local Similarity 63.3%; Pred. No. 1.3e-80;
Matches 601; Conservative 0; Mismatches 340; Indels 9; Gaps 2;

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155 |||||
301 CCGCTTCCCGGCTTGGATCAAGGTCAACATCGGGGCTCATCTGGCTGTGCT 360
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303 |||||
213 CGTGGCTTGGTGGGCACTCGCTGCTCATGTTGCTGATCATCCATACAAAGATGA 272
214 |||||
215 |||||
361 CCGGGGGCTCTGGGGACCTGGCTGCTCATGTATGTCTCATGACCAAGATGA 420
362 |||||
363 |||||
273 GACAGCAACCAATTATATATATTAACCTGGCTTGGGAGATGCTTAACTAAC 332
274 |||||
275 |||||
421 GACAGCTACCAATTATATATATTAATCTGGACCTGGCTGATACCTGCTTGAAC 480
422 |||||
423 |||||
333 CATGCCCTTTCAGAGTACGCTTACTGATGAATTCCTGGCCCTTTGGGGATGCTG 392
334 |||||
335 |||||
481 ACTGCCCTTCCAGGCAAGACATCTACTGGGCTTGGCCATTTGGAAAGCACTCTG 540
482 |||||
483 |||||
393 CAAGATAGTAAATTTCCATTTGATTTACTACAAATGTTACACAGACTCTTACCTGACCAT 452
394 |||||
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541 CAAGCTGTATGCTATGCTACTACTACAAATGTTTACAGCACTTTTACTGACCGC 600
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453 GATGAGCGGACCGCTCATTTGCGGTGGCCACCCCGTGAAGGCTTGGATTCGGAC 512
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601 CATGAGCTGACCCCTATGTTGCTATCTGCCACCTTACCTGCTTGAATGTTGAC 660
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513 ACCCTTGAAGGCAAGATCATATATCTGATCTGGCTGCTGATCTGTTGGCAT 572
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661 ATCCAGAAAGCCAGGCGTTAATGTGGCCATATGGGCCCTGGCTTAAAGTGTGCT 720
662 |||||
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573 CTCTCAATATGCTCTTGGAGGACCAAGTCAAGGAAAGCTGATGTCATGATGCTC 632
574 |||||
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721 TCTGTTGCCATCATGAGGTTGACCAAGT-----GGAAGATGAAGATCGAGTCC 774
722 |||||
723 |||||
633 CTTCAGTTCCAGATGATGACTACTCCGTTGGGACCTCTTCAAGATCTGCTGCT 692
634 |||||
635 |||||
775 GGTGAGATCTCTGCTCCCTCAGACTATTTGGG---CCCTGATTCGCGCATCTGATCT 831
776 |||||
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693 CATCTTGCCTTGCATCTCTGCTCTGCTCATCATCTGCTGCTTACACCTGATGATCT 752
694 |||||
695 |||||
832 CTTTCTTCTTCAATCATCCCTGCTGATCATCTGCTGCTGCTGCTGCTGCTGCTG 891
833 |||||
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753 GCGTCTCAAGAGCGTCCGCTCTCTTCTGCTGCTCCGAGAAAGATGCGAACCTGCTG 812
754 |||||
755 |||||
892 ACGACTTGGTGGTCCCTGCTGCTTCAAGGCTCCCGGAGAAAGACCCAAACCTGCGCG 951
893 |||||
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813 GATCAACAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 872
814 |||||
815 |||||
952 TATCACTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1011
953 |||||
954 |||||
873 CATATTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 932
874 |||||
875 |||||
1012 GGTGTTGCTCTGCTGCTTCAAGAGCTGGGTTGCTCAGCAGAGTAGTAGACTGAGTTG 1071
1013 |||||
1014 |||||
933 CTATATCTTTCGATCTGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCT 992
934 |||||
935 |||||
1072 CTGCGCTTTCGCAAGCCCTGCTGCTTTCGCAAGGTTGCTCAATCCCATCTCTTATG 1131
1073 |||||
1074 |||||
993 CTTCCTTTCGATGAAATCTTCAAGCGGCTGCTTTCGCGGACTTTCGCTTTCGCTTTCG 1052
994 |||||
995 |||||
1132 TTTCTGATGAGAACTTCAAGGCTGCTTTCGAAAGTTCTGCTGCTTTCATCTCTGCA 1191
1133 |||||
1134 |||||
1053 GATGAGCGGCAAGCACTGAGAGTCCGAATTCAGATCTGCTGCTGCTGCTGCTGCT 1102
1054 |||||
1055 |||||
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Db 1192 CCGGAGATGAGATTCTGATCTGTGCGGAGCAATTCGAAGATGTTG 1241

RESULT 63
US-09-916B-3
Sequence 3, Application US/09048916B
Patent No. 6406866
GENERAL INFORMATION:
APPLICANT: Grandy et al.
TITLE OF INVENTION: Method of screening a compound for binding to MSOR
FILE REFERENCE: 49888
CURRENT APPLICATION NUMBER: US/09/048,916B
PRIOR APPLICATION NUMBER: 08/514,451
PRIOR FILING DATE: 1995-08-11
PRIOR APPLICATION NUMBER: 08/149,093
PRIOR FILING DATE: 1993-11-08
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 1452
TYPE: DNA
ORGANISM: Rattus sp.
FEATURE:
NAME/KEY: 5'UTR
LOCATION: (1)..(181)
NAME/KEY: CDS
LOCATION: (182)..(1282)
NAME/KEY: 3'UTR
LOCATION: (1283)..(1452)
US-09-916B-3

Query Match 31.9%; Score 368; DB 4; Length 1452;
Best Local Similarity 63.3%; Pred. No. 1.3e-80;
Matches 601; Conservative 0; Mismatches 340; Indels 9; Gaps 2;

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153 CGGCAATCTCCCGGACATCCCGGATCATCAAGGGGCTACTCCGATGTTGCT 212
154 |||||
155 |||||
301 CCGCTTCCCGGCTTGGATCAAGGTCAACATCGGGGCTCATCTGGCTGTGCT 360
302 |||||
303 |||||
213 CGTGGCTTGGTGGGCACTCGCTGCTCATGTTGCTGATCATCCATACAAAGATGA 272
214 |||||
215 |||||
361 CCGGGGGCTCTGGGAACTGGCTGCTCATGTATGTCTCATGACCAAGATGA 420
362 |||||
363 |||||
273 GACAGCAACCAATTATATATATTAACCTGGCTTGGGAGATGCTTAACTAAC 332
274 |||||
275 |||||
421 GACAGCTACCAATTATATATATTAATCTGGACCTGGCTGATACCTGCTTGAAC 480
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423 |||||
333 CATGCCCTTTCAGAGTACGCTTACTGATGAATTCCTGGCCCTTTGGGGATGCTG 392
334 |||||
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481 ACTGCCCTTCCAGGCAAGACATCTACTGGGCTTGGCCATTTGGAAAGCACTCTG 540
482 |||||
483 |||||
393 CAAGATAGTAAATTTCCATTTGATTTACTACAAATGTTTACACAGACTCTTACCTGACCAT 452
394 |||||
395 |||||
541 CAAGCTGTATGCTATGCTACTACTACAAATGTTTACAGCACTTTTACTGACCGC 600
542 |||||
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453 GATGAGCGGACCGCTCATTTGCGGTGGCCACCCCGTGAAGGCTTGGACTTCGGAC 512
454 |||||
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601 CATGAGCTGAGACCGCTATGCTGCTATCTGCCACCTTATCCGCTGCTGCTGCTG 660
602 |||||
603 |||||
513 ACCCTTGAAGGCAAGATCATATATCTGATCTGGCTGCTGCTGCTGCTGCTGCTG 572
514 |||||
515 |||||
661 ATCCAGAAAGCCAGGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCT 720
662 |||||
663 |||||
573 CTTCGATGATCTTTCGATGATGATGATGATGATGATGATGATGATGATGATGATG 632
574 |||||
575 |||||
721 TCTGTTGCCATCATGAGGTTTCAAGCAAGT-----GGAAGATGAAGATGAGTGGCT 774
722 |||||
723 |||||
633 CTTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 692
634 |||||
635 |||||
775 GGTGAGATCTCTGCTCCCTCAGACTATTTGGG---CCCTGATTCGCGCATCTGATCT 831
776 |||||
777 |||||
693 CATCTTGCCTTGCATCTCTGCTCTGCTCATCATCTGCTGCTTACACCTGATGATCT 752
694 |||||
695 |||||
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[illegible]

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RESULT 64
US-09-743-871B-14
; Sequence 14, Application US/09743871B
; Patent No. 6627734
; GENERAL INFORMATION:
; APPLICANT: Memorial Sloan-Kettering Cancer Center
; TITLE OF INVENTION: IDENTIFICATION AND EXPRESSION OF MULTIPLE SPLICED VARIANTS OF MOUSE
; FILE REFERENCE: 830002-2001.1
; CURRENT APPLICATION NUMBER: US/09/743, 871B
; CURRENT FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: PCT/US99/15977
; PRIOR FILING DATE: 1997-07-15
; PRIOR APPLICATION NUMBER: 60/093, 002
; PRIOR FILING DATE: 1996-07-16
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 14
; LENGTH: 1134
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-743-871B-14

Query Match      31.9%; Score 367.8; DB 4; Length 1134;
Best Local Similarity 62.1%; Pred. No. 1.3e-80;
Matches 617; Conservative 0; Mismatches 367; Indels 9; Gaps 2;

Qy      105 GCCGACAGCAACGGCAGCGCGCGCTCGGAGAGACGGAGCTGGAGCCCGGCACATCTC 164
Db      81 GTCCCTCTTGAGCCCCCAACAGCTGCTGCCCCCCGCATCTGCTCAATGCCAGCCA 140

Qy      165 CCCGGCCATCCCGGTCAATCAGCGCGGTCTACTCCGTAGTGTTCGTGGCTTGGT 224
Db      141 CGGGCGCTTCTCGGCCCTCGGGGCTCAAGGTCAACATGTGGGGCTTACCTCGGCCGTGTG 200

Qy      225 GGGCACTCGCTGGTCATGTTCTGTGATCATCCGATACCAAAAGATGAAGACGACACCA 284
Db      201 TGTGGAGAGGCTCTCGGGGAATGCTTGTATGACACCAAAATGAAGACAGCACCAA 260

Qy      285 CATTACATATTAACTGGCTTGGCAGATGCTTACTTACTCAACACCATGCCCTTTCA 344
Db      261 TATTACATCTTTAACTCGGCCCTCGGCCGACACACTGTGCTCGTGAAGCGCTTCCCA 320

Qy      345 GAGTACGGTCACTTGATGAATTCCTGGCTTTTGGGGATGTGCTGTCAGATAGTAT 404
Db      321 GAGTACGGTCACTTGATGAATTCCTGGCTTTTGGGGATGTGCTGTCAGATAGTAT 404

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Db	321	GGGACGGACATCCTCTGGGGCTTTGGCCGTTTGGGAATGCGCTGTGCAAGACATCAT	380
Qy	405	TTCCATTGATTACTACAACATGTTCCACGACATCTTCACTTGACCATGATGAGCGTGA	464
Db	381	TGCCATTGACTTACTACAACTGTTTACACGAGCACTTCAACCTTAATGCGCATGAGTGTGA	440
Qy	465	CCGCTACATTGCGGTGTGCGCACCCCGTGAAGCTTTGGACTTTCGCGACACCTTGAAGC	524
Db	441	TGCGTATGTAGCCATCTGCGACCCCATCCGTGCTCCACGCTCCACAGTCCAGCAAAAC	500
Qy	525	AAAGTATCAATATCTGACATCTGGCTGTGCGTCAATCTGTGTGGCATCTCTGCAATAGT	584
Db	501	CGAGCTCTCAATGTGCGCATCTGGAGCCCTGTGCTCTGTGTGTGCTTCCCTGTTCAT	560
Qy	585	CCTTGAAGGACCAAAAGTCAGGGAAGACGTGATGATCAATTGAGTCTCTCTGCAATTCC	644
Db	561	CATGGGCTCGGACACAGTCTGAAGATGAAG-----ATCGAGTCCGTGTGGAGATCCC	614
Qy	645	AGATGATGACTACTCTGTGTGGGACCTTCTTCAATGAAGATCTGCGTCTTCACTTTGGCCTT	704
Db	615	TACCCCTCAGAGATTAC--TGGGGGCCCGATGTTTTCATCTGCAATCTTCTTCTCTT	671
Qy	705	CGTATCCCTTCCCTCATCATCATCTGTGTGCTACACCCGTAGATCTCGCGTCTGAAG	764
Db	672	CATGCTCCCGGTGCTCGTCACTCTGTGTGCTACAGCTCATGATCTCGAGGCTCGTGG	731
Qy	765	CGTCCGAGCTCTTCTTGTGACTCCCGAGAAAGATGCAACCTGCTAGATATACAGACT	824
Db	732	AGTCCGCTGCTCTCGGGCTCCCGAGAAAGAACCGAACTCGGGCGCATATCTGGCT	791
Qy	825	GGTCCGTGTGTGTGGGAGTCTTGTGCTGTGTACTCCCATTCACATATTCATCT	884
Db	792	GGT	851
Qy	885	GGTGAAGCTTTGGGGAGCACTCCCAAGACACAGTGTCTCTACAGTATTAATCTTG	944
Db	852	GGCCCAAGGGGTGGGGGTTTCAGCCGAGAGGAGATCTCCCGTGCATTTCTGCGCTTCTG	911
Qy	945	CATGAGCTTAGGCTATACCAACAGTAGGCTTAATCCATTCTTACGCGCTTTCTGTATGA	1004
Db	912	CAGGCGCTTGGGCTACGTCAACAGTGTCTCAACCCCATCTCTACGCTTCTTGGATGA	971
Qy	1005	AAACTTCAAGGGGTGTTCGCGGACCTTGTGCTTTCACACTGAAGATGAGATGAGACGGCA	1064
Db	972	GAACTTCAAGGCTGTCTCCGCAAGTTCTGTGTGTGTCATCTGCGCTCGGCCGGGACGTGA	1033
Qy	1065	GAGCATTAGCAGATGCTCGAAATATACATTTACAGA	1097
Db	1032	GGTGTGTGATCCGCGTGGCGACATTTGCCAAGA	1064

```

? RESULT 65
? US-08-147-592A-5
? Sequence 5, Application US/08147592A
? Patent No. 6096513
? GENERAL INFORMATION:
? APPLICANT: Bell, Graeme I
? APPLICANT: Reisine, Terry
? APPLICANT: Yasuda, Kazuki
? TITLE OF INVENTION: Opioid Receptor Genes,
? TITLE OF INVENTION: Compositions and Methods
? NUMBER OF SEQUENCES: 43
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Arnold, White & Durkee
? STREET: P.O. Box 4433
? CITY: Houston
? STATE: Texas
? COUNTRY: United States of America
? ZIP: 72210
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
?

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TELEFAX: (713) 789-2679
 TELEX: 79-0924
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1330 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 FEATURE:
 MOLECULE TYPE: cDNA
 NAME/KEY: CDS
 LOCATION: 161..1261
 US-08-292-694A-5

Query Match 31.9%; Score 367.8; DB 4; Length 1330;
 Best Local Similarity 63.4%; Pred. No. 1.4e-80;
 Matches 599; Conservative 0; Mismatches 337; Indels 9; Gaps 2;

154 GGGCAATCTCCCGGCAATCCCGGTCATCATCAGCGCGGTCTACTCCGTAGTGTTCGTC 213
 DB 281 GCGTTCCTGCGCCCTTGAGACTCAAGGTACCATCGTGGGCTTACTTGGCTGTGTCATC 340
 QY 214 GTGGCTTGTGGGCACTCGGTGTCATGTTCTGATCATCCGATACCAAGAATGAA 273
 DB 341 GGGGGGCTCCTGGGAAGCTCGTCATGATGATCATCTCAGGACACCAAGATGAAG 400
 QY 274 ACAGCAACCAATTATTAATTTAACTGCTTTGGCAGATGCTTAACTTAACTAACACC 333
 DB 401 ACTGCTACCAACATTATTAATTTAATCTGGCACTGGCATGATTAACCTGCTTGGCTGACA 460
 QY 334 ATGCCCTTCAAGATACGGTCTACTGATGAATTCCTGGCCCTTTGGGGATGTCGTGTC 393
 DB 461 CTGCGCTTCCAGGACACAGATCTCTTCTGGGCTTCTGGCAATTTGGGATGCATGTC 520
 QY 394 AAGATAGTAATTTCCATTGATTACTACACATGTTTACCAGAGATCTTCACTTGAACATG 453
 DB 521 AAGACGGTCATGTCATGATGACTACTACACATGTTTACCAGAGATCTTGAATGTC 580
 QY 454 ATGACCGTGAACCGCTCACTTCCGTGTCACACCCCGTGAAGCTTTGGACTTCCGACA 513
 DB 581 ATGATGTAGACCGTTATGTATGATCTATCTGCACCTTATCCGCTTGTATGTTGGACA 640
 QY 514 CCTTGAAGGCAAGATCATCAATATCTGCATCTGGCTGTCGTCATCTGTGGACATC 573
 DB 641 TCCAGTAAAGCCCAAGCCCTTAAATGTGGCATATGGCCCTTGGCTTGGTGTGTT 700
 QY 574 TCTGCAATAGTCTTGAAGGCAACCAAGTCAAGGAAAGCTGATGTCAATTAAGTCTCC 633
 DB 701 CCTGTGGCATCATGGGCTCAGCACAGT-----GAGGATGAAAGATGAGTGGCTG 754
 QY 634 TTGCATTTCCAGATGATGACTACTCTCTGTGGGAACTCTTTCATGAAGATCTGCGTTTC 693
 DB 755 GTGGAGATCCCGCCCTCAGAGA---CTATTGGGGCCCTGTATTGGCATCTGCATCTTC 811
 QY 694 ATCTTGGCTTGTATCCCTGCTGCTCATCATCATCTGCTGTACACCTGATGATCTCG 753
 DB 812 CTTTTCCTTATATCCCGGTTCGATCATCTCTGTCTACAGCTTCATGATGATGGA 871
 QY 754 GGTCTCAAGAGCGTCCGGCTCTTCTGAGCTCCGAGAGAAAGATCGCAACTCGGTAGG 813
 DB 872 CGACTTCGTGTGTCCGGCTGCTTTCAAGGCTCCGAGAGAAAGACCGAACTCGGAGCGC 931
 QY 814 ATCAACCAAGTGTCTGT 873
 DB 932 ATCAACAGCGGT 991
 QY 874 ATATTCATCTGT 933
 DB 992 GTCTTTGTCTGT 1051
 QY 934 TATTAATTTCTGATCGCTTGTAGCTTAAACCAACAGTATGCTGATATCCATTTCTTACGCC 993
 DB 1052 CTGGCTTCTGTGACAGCCCTGGGCTATGTCAACAGTGTGTCTCAATCCATTTCTTATGCT 1111

QY 994 TTTCTGTATGAAGAACTTCAAGGGGTGTTCCGGGACTTCTGTCTTCCACTGAAGATGAG 1053
 DB 1112 TTCTGTGATGAGAACTTCAAGGGCTGTGCTTTTAAAGTTGTGTGTGTGTGTGTGTGTGT 1171
 QY 1054 ATGAGCGGACAGACCTAGACAGAGTCCGAAATTAACAGTTACAGAT 1098
 DB 1172 CGGAGATGACAGGTTTCTGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1216

RESULT 67
 US-08-986-209A-1
 Sequence 1, Application US/08986209A
 Patent No. 6660496
 GENERAL INFORMATION:
 APPLICANT: Sloan-Kettering Institute for Cancer Research
 APPLICANT: Pasteur, Gavril W
 APPLICANT: Pan, Ying-Xian
 TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING KAPPA OPIOID RECEPTORS, RECEPTOR
 FILE REFERENCE: 830002-2004
 CURRENT APPLICATION NUMBER: US/08/986,209A
 CURRENT FILING DATE: 1997-12-05
 NUMBER OF SEQ ID NOS: 5
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 1
 LENGTH: 2600
 TYPE: DNA
 ORGANISM: Mus musculus
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (299)..(1402)
 OTHER INFORMATION:
 US-08-986-209A-1

Query Match 31.9%; Score 367.8; DB 4; Length 2600;
 Best Local Similarity 63.4%; Pred. No. 1.8e-80;
 Matches 599; Conservative 0; Mismatches 337; Indels 9; Gaps 2;

154 GGGCAATCTCCCGGCAATCCCGGTCATCATCAGCGCGGTCTACTCCGTAGTGTTCGTC 213
 DB 419 GCGTTCCTGCGCCCTTGAGACTCAAGGTACCATCGTGGGCTTACTTGGCTGTGTCATC 478
 QY 214 GTGGCTTGTGGGCACTCGGTGTCATGTTCTGATCATCTCGATACCAAGAATGAA 273
 DB 479 GGGGGGCTCCTGGGAAGCTCGTCATGATGATCATCTCAGGACACCAAGATGAAG 538
 QY 274 ACAGCAACCAATTATTAATTTAACTGCTTTGGCAGATGCTTAACTTAACTAACACC 333
 DB 539 ACTGCTACCAACATTATTAATTTAATCTGGCACTGGCATGATTAACCTGCTTGGCTGACA 598
 QY 334 ATGCCCTTCAAGATACGGTCTACTGATGAATTCCTGGCCCTTTTGGGATGTCGTGTC 393
 DB 599 CTGCGCTTCCAGGACACAGATCTCTTCTGGGCTTCTGGCAATTTGGGATGACATGTC 658
 QY 394 AAGATAGTAATTTCCATTGATTACTACACATGTTTACCAGAGATCTTCACTTGAACATG 453
 DB 659 AAGACGGTCATGTCATGATGACTACTACACATGTTTACCAGAGATCTTCACTTGAACATG 718
 QY 454 ATGACCGTGAACCGGCTACATTTGGCGGCAACCCCGTGAAGGCTTTGGACTTCCGACA 513
 DB 719 ATGATGTAGACCGTTATGTATGATCTATCTGCCACCTTATCCGTCCTGTGATGTTGGACA 778
 QY 514 CCTTGAAGGCAAGATCATCAATATCTGCAATCTGAGCTGTGTGTGTGTGTGTGTGTGTGT 573
 DB 779 TCCAGTAAAGCCCAAGCGCTTAAATGTGGCATATGAGGCTTGGCTTGGTGTGTGTGTGT 838
 QY 574 TCTGCAATAGTCTTGTGAAGGCAACCAAGTCAAGGAAAGCTGATGTCAATTAAGTCTTC 633
 DB 839 CCTGTTCATCATGAGGCTCAGCACAGT-----GAGGATGAAAGATGAGTGAAGTGTG 892
 QY 634 TTGCATTTCCAGATGATGACTACTCTGTGTGGGACTCTTTCATGAAGATCTGCGTTTC 693

Db 893 GTGAGATCCCGCCCTCAGGA---CTATTGGGGCCCTGATTATTGGCATCTGCATCTTC 949
 Qy 694 ATCTTGGCTTGTGTATCCCTGTCTCATCATCATCTGTCTGTACACCTGTATGATCTG 753
 Db 950 CTTTTCCTTTCATCATCCCGGCTTCGATCATCTGTCTGTACAGCCTCATGATTGCA 1009
 Qy 754 CCGTCAAGAGCGTCCGGCTCTTCTGTGCTCCCGAGAGAAAGATGGCAACCGGGTAG 813
 Db 1010 CGACTTCGGGTGTCCGGCTGTCTTCAGGCTCCGAGAGAGAGACCGGAACCTGGAGCC 1069
 Qy 814 ATACCAAGCTGTCTGT 873
 Db 1070 ATACCAAGCTGT 1129
 Qy 874 ATATTCATCTGT 933
 Db 1130 GTCTTGTCTGT 1189
 Qy 934 TATTCTTGT 993
 Db 1190 CTGGCTTGT 1249
 Qy 994 TTTCTGT 1053
 Db 1250 TTTCTGT 1309
 Qy 1054 ATGAGCGGAT 1098
 Db 1310 CGGAT 1354

RESULT 68
 US-09-743-871B-13
 ; Sequence 13, Application US/09743871B
 ; Patent No. 6627724
 ; GENERAL INFORMATION:
 ; APPLICANT: Memorial Sloan-Kettering Cancer Center
 ; TITLE OF INVENTION: IDENTIFICATION AND EXPRESSION OF MULTIPLE SPLICE VARIANTS OF MOUS
 ; FILE REFERENCE: 830002-2001.1
 ; CURRENT APPLICATION NUMBER: US/09/743,871B
 ; CURRENT FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: PCT/US99/15977
 ; PRIOR FILING DATE: 1997-07-15
 ; PRIOR APPLICATION NUMBER: 60/093,002
 ; PRIOR FILING DATE: 1996-07-16
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: Patencin version 3.0
 ; SEQ ID NO 13
 ; LENGTH: 1177
 ; TYPE: DNA
 ; ORGANISM: homo sapiens
 US-09-743-871B-13

Query Match 30.9%; Score 357; DB 4; Length 1177;
 Best Local Similarity 63.3%; Pred. No. 5,8e-78;
 Matches 616; Conservative 0; Mismatches 320; Indels 37; Gaps 3;
 Qy 153 CGCGGACATCTCCCGGCGCATCCCGGTGATCATACCGCGGCTTACCTCCGATGTTGCT 212
 Db 144 CGCTTCTCTGCGCCCTCGGCGCTCAAGGTACATCGTGGGCTCTTACCTGGCGGTGTGT 203
 Qy 213 CGTGGGCTTGT 259
 Db 204 CGAGAGGCTCTGTGGGAAGTCCCTTGTGATGTAGTATCTCTCAGTAGAGGTGGGCCCA 263
 Qy 260 -----ACCAAGATGAAGACAGACAGACCAATTATTAATTTAACTGG 304
 Db 264 AGGTTCCTGTCTGTGACACCAAAATGAAGACAGACCAAAATTTAATTTAACTGG 323
 Qy 305 CTTTGGAGATGCTTTTGTATTACTACAAACCATGCGCTTTCAAGTACAGTGTGTGTGTGT 364
 Db 324 CCTGGCGGACATCTGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 383

Qy 365 ATCTTGGCTTGT 424
 Db 384 GCTTCTGTGCGGTGTGGGATCGCTGTGCAAGAGATGATGATGATGATGATGATGATGAT 443
 Qy 425 TGTTCACAGCATCTTCACTTGAACATGATGATGATGATGATGATGATGATGATGATGAT 484
 Db 444 TGTTCACAGCATCTTCACTTGAACATGATGATGATGATGATGATGATGATGATGATGAT 503
 Qy 485 ACCCGTGAAGCTTTGACCTTTCGACACCCCTTGAAGGCAAGATCATTAATTTACGA 544
 Db 504 ACCCATCGAGCCCTGACGTCGACGACGTCAGAGAAAGCCAGGCTGTCAATGTGGCA 563
 Qy 545 TGTGCTGT 604
 Db 564 TGTGCGCCCTGT 622
 Qy 605 GGAAGAGCTGATGTCTTGT 664
 Db 623 -----GAGATGAAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 674
 Qy 665 GGAACCTTTCATGAAGATCTGAGTCTTTCATCTTGTGTGTGTGTGTGTGTGTGTGTGT 724
 Db 675 GGGGCGCGGT 734
 Qy 725 TCATGT 784
 Db 735 TCTGT 794
 Qy 785 CCCGAGAGAAAGATGCAACCTGCGTAGATACCAAGATGATGATGATGATGATGATGATG 844
 Db 795 CCCGAGAGAAAGATGCAACCTGCGTAGATACCAAGATGATGATGATGATGATGATGATG 854
 Qy 845 TCTTGT 904
 Db 855 TGT 914
 Qy 905 CCGTCCAGAGACAGCTGT 964
 Db 915 AGCGAGAGAGAGATGCGGTGCGCATTTCTGCGCTTCTGTGAGCGCCTGGCTACGCTCA 974
 Qy 965 ACAATGACCTGAATCCATCTCTACCGCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGT 1024
 Db 975 ACAGCTGCTTCAACCCCATCTGTAGCGCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGT 1034
 Qy 1025 GGAAGCTTGT 1084
 Db 1035 GCAAGT 1094
 Qy 1085 ATACAGTTCAAGA 1097
 Db 1095 GCATTGCCAAGGA 1107

RESULT 69
 US-08-147-949A-1
 ; Sequence 1, Application US/08147949A
 ; Patent No. 5747279
 ; GENERAL INFORMATION:
 ; APPLICANT: Pasteur, Gavril W.
 ; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING
 ; TITLE OF INVENTION: KAPPA3 OPIOID RECEPTORS, RECEPTORS
 ; TITLE OF INVENTION: ENCODED THEREBY, AND USES THEREOF
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Cooper & Dunham
 ; STREET: 1185 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036
 ; COMPUTER READABLE FORM:

Query Match	Similarity	29.9%	Score 34.48	DB 1	Length 2600
Best Local	Similarity	29.9% <td>Score 34.48 <td>DB 1 <td>Length 2600</td> </td></td>	Score 34.48 <td>DB 1 <td>Length 2600</td> </td>	DB 1 <td>Length 2600</td>	Length 2600
Matchee	Conservative	0	Mismatches 337	Indels 11	Gaps 4
QY	154	GCGCAGATCTCCCGGCGCATCCGGTCATCACGCGCGTCTACTCCGTAAGTTCGTC	213		
Db	419	GCTTCTCGCCCTTGAGACTCAAGGTACACATCGGGGCTTACTTGGCTGTGTCATC	478		
QY	214	GTGGGCTTGGGGGGAATTCGCTGTGTCATGTTCTGTGATATTCGGATACCAAGATGAAG	273		
Db	479	GGGGGGCTTCGGGGGAATCGCTCGATCATGTAATGTCATCTTAAGGACACCAAGATGAAG	538		
QY	274	ACAGCAACCAACATTTACATATTTTAACCTGCGCTTTGGGAGATGCTTAAGTACTCAAC	333		
Db	539	ACTGTACCAACATTTACATATTTTAATCTGAGCATGTCGATATACCTGGTCTTGGTCGACA	598		
QY	334	ATGCCCTTTCAGAGTAGCGGTCTACTGTATGAATTCCTGGCCCTTTTGGGAGTGCCTGTC	393		
Db	599	CTGCCCTTTCAGGGGACAGACATCTTCTGGGCTTCTGGCCATTGGGAATGACATGTGC	658		
QY	394	AAGATAGTAATTTCCATGATGATTACTACAAACATGTTCAACAGATCTTCACTTTGACATG	453		
Db	659	AAGACGGATATGTCATGACACTACTACAAACATGTTTACAGACATTTCACTTTGACTGCC	718		
QY	454	ATGAGCGTGAACCGGCTACATGCGCGCTGTGACCAACCCCGTGAAGGCTTTGGACTTCGACA	513		
Db	719	ATGAGTGAAGCCGTTATGATGATCTGTGCAACCCCTATCCGTCCTTGATGTTGGACA	778		
QY	514	CCCTTGAAGGCAGAAAGATCATCAATATCTGCACTGTGGCTGCTGTCATCTGTGGCATC	573		
Db	779	TCCAGTAAAGCCACAGCCGTTATATGTGGCAATATG - GCTGGCTGTGGTGTGGTGT	837		
QY	574	TCTGCAATAGTCCCTTGAAGGACCAAAAGTCAAGGAAGAAGTGAATGTCAATTAAGTCTCC	633		
Db	838	CTGTGTCCATCATGAGGCTCAGACAAAGT - - - - - GAAAGATGAAGAGATCGAGTCCCTG	891		
QY	634	TTGCAAGTCCAGATGATGACTACTCTGTGTGGGACCTTTTCATGAAGATCTGCGTCTTC	693		
Db	892	GTGAGGATCCCGGCCCTCAGAGCATATG - - - - - GGGCCCTGTAATTTGGCATCTGCATCTTC	948		
QY	694	ATCTTGGCTTGTGATTCCTG - TCTCATATCATGCTGTCTACACCTGTATGATCT	752		
Db	949	CTTTTTCCTTCATATCCCGGTAACTGATATCTGTGTGCTACAGGCTCATATATCG	1006		

```

: GENERAL INFORMATION:
: APPLICANT: Memorial Sloan-Kettering Cancer Center
: TITLE OF INVENTION: IDENTIFICATION AND EXPRESSION OF MULTIPLE SPLICE VARIANT
: TITLE OF INVENTION: KAPPA3-RELATED OPIOID RECEPTOR (KOR-3) GENE
: FILE REFERENCE: 830002-2001.1
: CURRENT APPLICATION NUMBER: US/09/743,871B
: PRIOR FILING DATE: 2001-01-16
: PRIOR APPLICATION NUMBER: PCT/US99/159377
: PRIOR FILING DATE: 1997-07-15
: PRIOR APPLICATION NUMBER: 60/093,002
: PRIOR FILING DATE: 1996-07-16
: NUMBER OF SEQ ID NOS: 26
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 11
: LENGTH: 1223
: TYPE: DNA
: ORGANISM: mus musculus
US-09-743-871B-11

Query Match      29.1%; Score 336.2; DB 4; Length 1223;
Best Local Similarity 63.9%; Pred. No. 7.2e-73;
Matches 544; Conservative 0; Mismatches 286; Indels 9; Gaps 2;

Oy      252 CATCGATTACACAAGAATGGAAGACAGCAACCAACATTTAATATTAACTGGCTTGGC 311
Db      281 CAGCAGGCACACCAAGATGGAAGACAGCTACCAACATTTAATATTAACTGGCAGCGC 340

Oy      312 AGATGCTTTAGTACTCAACACCATGCGCTTTCAGAGTACGGTCTACTTGATGAATTCTGT 371
Db      341 TGAATACCTCGTCTTGCTAACACTGCGCTTCCAGGGCAGACACATCTTACTGGGCTTGT 400

Oy      372 GCCTTTTGGGAGATGTGCTGTGCAGAAATGATAATTTCATTGATTACTACAAACATGTTAC 431
Db      401 GCCATTTGGGAATGCATCTGTGCAGAACTGTTCATTGTCTATGACATCAACAAATGTTAC 460

Oy      432 CAGCATTTCACTTGAACCATGATGAGCGTGGACCGCTACATTTGCGTGTGCCACCCGT 491
Db      461 CAGCATTTTAATCTGTGACCCGCCCATGAGCGTAAACCGCTAATGTGGCTATCTGCCACCTAT 520

Oy      492 GAAGGCTTTGGAATTCGGCACAACCCCTTGAAGGCAAAATCATCAATATCTGCAATCGGCT 551
Db      521 CCGTGCCCTTGATGTTGGACATTCACGAACCAAGCCCAAGGCTGTTAATGTGGCCATATGGGC 580

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; SEQ ID NO 8
; LENGTH: 2634
; TYPE: DNA
; ORGANISM: mus musculus
US-09-743-871B-8

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Query Match	28.4%;	Score 327.4;	DB 4;	Length 2634;
Best Local Similarity	63.4%;	Pred. No. 1.4e-70;		
Matches 537; Conservative	0;	Mismatches 301;	Indels 9;	Gaps 2

Qy	252	CATCCGATACACAAAGATGAGACAGCAACAACTTACATATTTAACTCTGGCTTGGC	311
Db	551	CAGACGGACACCAAGATGAGAACCTGCTACCAACATTTACATATTTAACTCTGGC	610
Qy	312	AGATGCTTTAGTTACTACACCATGACCTCTTCAGAGTACGGTCTACTTGATGAATTCCTG	371
Db	611	TGATATCCCTGGCTCTTGACACTGACCTCCCTTCAGGGGACAGACATCTCTTGGGCTTCTG	670
Qy	372	GCCCTTTTGGGAGTGTGCTGTGTAAGATATAGTAAATTCATATGATTTTACTAACATATGTCAC	431
Db	671	GCCATTTTGGGAATGACCTGTGMAAACGGTCAATGCTATCGACTACATACATATGTTTAC	730
Qy	432	CAGCATCTTCAACCTTGACCATGATGAGCGGTGACCGCTACATTTGCGTGTGACCCCGT	491
Db	731	CAGCATCTTCACTTGTACTGATCTGCATATGATGTAAACGCTTATATGATATCTGCAACCTTAT	790
Qy	492	GAAAGCTTTGACATTCCGACACCCCTTGAAAGGCAAAAGATCATCAATATCTGCATCTGGCT	551
Db	791	CCGTGCCCTTGATGTTTGGAGATCTCAGTAAAGCCAGGCGGTTAATGTGGCATATGGGC	850
Qy	552	GCTGTCTGTATCTGTTGGCATCTCTGCATATAGTCTTGGAGGACCAAAAGTCAGGAGAGA	611
Db	851	CCTGGCTTCTGGGTGTGGGTGTTCTCTGTGCCATCATAGGCTTCAGACAAAGT-----GGA	904
Qy	612	CGTGATGTCAATGATGTGCTCCTTGACAGTTCACAGATGATGACTCTCCCTGGTGGGAGCT	671
Db	905	GGATGAAAGATCAGATGTCTGTGTGAGATCCCCGCCCTTCAGAA---CTATTTGGGGCCC	961
Qy	672	CTTCATGAAGATCTGCGTCTTCATCTTTGCTTGATCCCTGTCTTCATCATATCGT	731
Db	962	TGTATTTGCCATCTGACATCTTCTTTTTCTTCATCATACCGGTTTGTATCTGTCTGT	1022
Qy	732	CTGTACACCTGATGATCTGTGCTCAAGAGCGTCCGGCTCTTTCTGTGCTCCCGAGA	791
Db	1022	CTGTACACGCTCATGATTCGACGACTTGTGTGTCGGCTGCTTTCAGGCTCCCGAGA	1082
Qy	792	GAAAGATGGCAACCTGGATGAGATACACAGACTGTGCTCGTGTGTGTGTGTGGCAGTCTTGT	851
Db	1082	GAAAGATCGGAACCTGGACGATACACGCTGTGTATCTGTATGTGTGTGTGTGTGT	1144
Qy	852	CGTCTGTGAGCTCCCATTTCAATATTCCTGTGTGAGGCTCTGGGAGACACTGCCCA	911
Db	1142	GGGCTGTGTGACACTGTGTGAGGTCTTGTCTGTGTCAAGGATGTGGGTTCAGCCAGG	1202
Qy	912	CAGCAGAGCTGTCTCTCCAGCTATTACTTGTGATGTGCTTAGGCTATACCAACAGTAG	971
Db	1202	TAGTGAAGTCAAGAGCCATCTGCGCTTTCGACAGGCCCTGGGCTATGTCAACAGTTG	1262
Qy	972	CCTGAATCCCATCTCTTAAGCTTTCTTGTATGATAAACTTCAAGCGGTGTTCCGGGACTT	1032
Db	1262	TCTCATATCCCATCTCTTAAGCTTTCTTGTATGATAAACTTCAAGCGCTGTGTTTAAAGTT	1322
Qy	1032	CTGCTTTCCACTGAAGATGAGGATGAGCGGCGAGAGACTAGACAGAGTCCGAATATACAGT	1092
Db	1322	CTGCTGTGCTTCTGCTCCTGTGACCGGGAAGTGAAGGTTTCTATCTGTGTGCGAGCATTGC	1382
Qy	1092	TCAGGAT	1098
Db	1382	CAGGAT	1388

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: Sequence 9, Application US/09743871B
: Patent No. 6627734
:
: GENERAL INFORMATION:
: APPLICANT: Memorial Sloan-Kettering Cancer Center
: TITLE OF INVENTION: IDENTIFICATION AND EXPRESSION OF MULTIPLE SPLICED VARIANTS OF MOUSE KAPPA3-RELATED OPIOID RECEPTOR (KOR-3) GENE
: FILE OF INVENTION: KAPPA3-RELATED OPIOID RECEPTOR (KOR-3) GENE
: FILE REFERENCE: 830002-2001.1
:
: CURRENT APPLICATION NUMBER: US/09/743, 871B
: CURRENT FILING DATE: 2001-01-16
:
: PRIOR APPLICATION NUMBER: PCT/US99/15977
: PRIOR FILING DATE: 1997-07-15
:
: PRIOR APPLICATION NUMBER: 60/093, 002
: PRIOR FILING DATE: 1996-07-16
:
: NUMBER OF SEQ ID NOS: 26
:
: SOFTWARE: PatentIn version 3.0
:
: SEQ ID NO 9
:
: LENGTH: 1256
:
: TYPE: DNA
:
: ORGANISM: mus musculus
:
: US-09-743-871B-9

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Query Match	28.3%;	Score 327;	DB 4;	Length 1256;
Best Local Similarity	63.4%;	Pred. No. 1.3e-70;		
Matches 536; Conservative	0;	Mismatches 300;	Indels 9;	Gaps 2;

[illegible]

TELEX: 90-4030 MRSNFOERSWSH
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 830 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-405-271A-13

Query Match 27.7%; Score 319.6; DB 4; Length 830;
Best Local Similarity 60.8%; Pred. No. 7.1e-69;
Matches 502; Conservative 0; Mismatches 312; Indels 11; Gaps 4;

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QY 257 GATACCAAGAATGAGAGACAGACCAACATTTACTTAACTGGGCTTGGGAGATG 316
DB 16 GATACCAAGAATGAGAGACAGACCAACATTTACTTAACTGGGCTTGGGAGATG 74
QY 317 CTTTAACTTAACTGGGCTTGGGAGATG 376
DB 75 CTTTAACTTAACTGGGCTTGGGAGATG 134
QY 377 TTGGGAGATGCTGGGAGATGATTTCAATTTCAATTTCAATTTCAATTTCAATTT 436
DB 135 TTGGGAGATGCTGGGAGATGATTTCAATTTCAATTTCAATTTCAATTTCAATTT 194
QY 437 TCTTCACTTGAACATGATGAGGAGACCGCTACATTTGGGAGACCGGCTGGAAG 496
DB 195 TATTAACCTTGGACCATGATGATGATGATGATGATGATGATGATGATGATGATG 254
QY 497 CTTTGAAGCTTGGACCATGATGATGATGATGATGATGATGATGATGATGATG 556
DB 255 CTTTGAAGCTTGGACCATGATGATGATGATGATGATGATGATGATGATGATG 308
QY 557 CGTCACTGCTGGGAGATGCTGCAATGCTTGGAGGACCAAGTCAGGAGACGTCG 616
DB 309 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 368
QY 617 ATGTGATGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 676
DB 369 GTTCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 425
QY 677 TGAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 736
DB 426 TGAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 485
QY 737 ACACCTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 796
DB 486 ATGACTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 545
QY 797 ATTCGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 856
DB 546 ACAGGAATCTTGAAGAGATCACAGAGATGCTGCTGCTGCTGCTGCTGCTGCTG 605
QY 857 GCTGACTCCCATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCA 916
DB 606 GCTGACTCCCATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCA 665
QY 917 CAGCTGCTCTCACTTAACTTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 976
DB 666 CGTTCAGACTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 725
QY 977 ATCCGATCTCTAGGCTTCTTCTGATGAAATTTGAAGGCTTCTGCTGCTGCTG 1036
DB 726 ACCGAGCTCTTATCATTTTCTGATGAAATTTCTCA-CGATGCTTCAAGAGGTTCTG 784
QY 1037 TTCCACTGAAGATGAGATGAGCGGAGAGACTGAGAGATGAGAGATGAGAG 1081
DB 785 TCCCAAGCTCTTCAACATGAGCAAACTCACTGCAATTC 829
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RESULT 76
US-08-387-707-12
; Sequence 12, Application US/08387707

Patent No. 626563
; GENERAL INFORMATION:
; APPLICANT: EVANS, CHRISTOPHER J.
; APPLICANT: KEITH, DUANE E.
; TITLE OF INVENTION: OPIOID RECEPTOR GENES
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, N.W. Suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/387,707
; FILING DATE: 10-SEP-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; TELEPHONE: (202) 887-1500
; TELECOMMUNICATION INFORMATION:
; REFERENCE/DOCKET NUMBER: 22000-20526.20
; TELEFAX: (202) 887-0763
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2447 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-387-707-12

Query Match 21.1%; Score 243; DB 3; Length 2447;
Best Local Similarity 100.0%; Pred. No. 5.7e-50;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 368 CTTGCTTTGGGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 427
DB 1 CTTGCTTTGGGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60
QY 428 TCACGATCTTCACTTGAACATGATGAGCGTGAACCGCTACATTTGCGGTG 487
DB 61 TCACGATCTTCACTTGAACATGATGAGCGTGAACCGCTACATTTGCGGTG 120
QY 488 CCGTGAAGCTTTGACCTTCCGACACACCTTGAAGGCAAAATCATATCTGCA 547
DB 121 CCGTGAAGCTTTGACCTTCCGACACACCTTGAAGGCAAAATCATATCTGCA 180
QY 548 GAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 607
DB 181 GAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
QY 608 AAG 610
DB 241 AAG 243
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RESULT 77
US-08-405-271A-12
; Sequence 12, Application US/08405271A
; Patent No. 6432652
; GENERAL INFORMATION:
; APPLICANT: EVANS, CHRISTOPHER J.
; APPLICANT: KEITH, DUANE E.
; TITLE OF INVENTION: OPIOID RECEPTOR GENES
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER

```

/ STREET: 2000 PENNSYLVANIA AVENUE, NW, Suite 5500
/ CITY: WASHINGTON
/ STATE: DC
/ COUNTRY: USA
/ ZIP: 20006-1888
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: IBM PC compatible
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/405,271A
/ FILING DATE: 14-MAR-1995
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: MORASHIGE, KATIE H.
/ REGISTRATION NUMBER: 29,959
/ REFERENCE/DOCKET NUMBER: 22000-20526.22
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202) 887-1500
/ TELEFAX: (202) 887-0763
/ TELEEX: 90-4030 MRSNFORMSH
/ INFORMATION FOR SEQ ID NO: 12:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 2447 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/
/ US-08-405-271A-12

```

```

Query Match      21.1%; Score 243; DB 4; Length 2447;
Best Local Similarity 100.0%; Pred. No. 5.7e-50;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 368 CCTGACCTTTGGGAGATGCTGTGCAAGATGTATTTCCATTGATTAACAACATGT 427
DB 1 CTTGGCCTTTGGGAGATGCTGTGCAAGATGTATTTCCATTGATTAACAACATGT 60
QY 428 TCACGAGATCTTCACTTACCATGATGAGCGGTGACCGGTACATTGCGGTGCGCAC 487
DB 61 TCACGAGATCTTCACTTACCATGATGAGCGGTGACCGGTACATTGCGGTGCGCAC 120
QY 488 CCGTGAAGCTTTGGAGCTTCCGACACCCCTTGAAGGCAAGATCATCAATATCTGCATCT 547
DB 121 CCGTGAAGCTTTGGAGCTTCCGACACCCCTTGAAGGCAAGATCATCAATATCTGCATCT 180
QY 548 GCGTGTCTGTGCTATCTGTGTCATCTGCAATATGCTTGGAGGACCAAGTCAAGG 607
DB 181 GCGTGTCTGTGCTATCTGTGTCATCTGCAATATGCTTGGAGGACCAAGTCAAGG 240
QY 608 AAG 610
DB 241 AAG 243

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RESULT 78
US-09-016-434-1446
/ Sequence 1446, Application US/09016434
/ Patent No. 6500938
/ GENERAL INFORMATION:
/ APPLICANT: Janice Au-Young
/ APPLICANT: Jeffrey J. Sellhamer
/ TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
/ TITLE OF INVENTION: PATHWAY GENE EXPRESSION
/ NUMBER OF SEQUENCES: 1490
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
/ STREET: 3174 PORTER DRIVE
/ CITY: PALO ALTO
/ STATE: CALIFORNIA
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:

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/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/016,434
/ FILING DATE: HEREMITH
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Zeller, Karen J.
/ REGISTRATION NUMBER: 37,071
/ REFERENCE/DOCKET NUMBER: PA-0002 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (650) 855-0555
/ TELEFAX: (650) 845-4166
/ INFORMATION FOR SEQ ID NO: 1446:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1317 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: GENBANK
/ CLONE: 9693907
/
/ US-09-016-434-1446

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Query Match      21.0%; Score 242.6; DB 4; Length 1317;
Best Local Similarity 55.0%; Pred. No. 5.6e-50;
Matches 523; Conservative 0; Mismatches 419; Indels 9; Gaps 2;

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QY 96 CTGGGCGGAGCCGACGACGACGACGCGCGCTCGAGAGCGCGAGTGGACCCGC 155
DB 110 CTGTCAGCAAGATGCGAGTACGCGCTCGGCGAGGCGGAGAGCGGAGTGGCGGCGG 169
QY 156 GCACATCTCCCGGCGCATCCCGGTATCATCAGCGGTATCTCCGTATGTTCCGT 215
DB 170 GGAAGCGCGGCGCGCGGCGATGCTATCAGTGCATCTAAGCGGTGTCGCTGCT 229
QY 216 GGGCTTGTGGGGAACCTCGTGTGATGTTGATGATCATCCGATTAACAAGATGAAGAC 275
DB 230 GGGCTGTGTGGGGAACCCCTGATCATCTTCGATGATCTTCGTCAGCCAGATGAAGAC 289
QY 276 AGCAACCAATTTACATATTTAACTGCTTGGAGATGCTTTAGTTAATAAACAT 335
DB 290 GGTACCAACATTTACTGCTCAACCTGGCCGTAAGCCGAGAGCTCTTCACTGAGCGT 349
QY 336 GCCCTTCAAGATGAGGTCTACTTGATGAAATTCGTGCGCTTTGGGAGATGCTGTCGA 395
DB 350 GCCCTTGTGCTGCTGTGCGCGCGCTGCGCACTGCGCTTGTGCTGCTGTCGCG 409
QY 396 GATGTAATTTCCATTGATTACTTAACAAGTTCACACGATCTTCACTTGAACATGAT 455
DB 410 CGGGTGTGCTGAGGTGAGCGCTCAACATGTTTCAACAAGTCTTGTGTCACCGTGT 469
QY 456 GAGCGTGAACCGCTTAATTCGCTGTGCAACCCCGTGAAGGCTTTGAACTTCCGACAC 515
DB 470 CACCGTGAACCGCTTAATTCGCTGTGCAACCCCGTGAAGGCTTTGAACTTCCGACAC 529
QY 516 CTTGAAGGCAAGATCATCAATATTCGATGCTGCTGTGTCATCTGTTGGCATCTC 575
DB 530 CAGCGTGGCAAGCTATCACTGAGCGGTGTGCTGCACTCTTGTGTCATCTTCCC 589
QY 576 TGAATATGCTTGTGAAGGACCAAGTCAAGGAGAGCGTGAATGATGATGATGCTCTT 635
DB 590 CATGCAATCTTGTGAGACACAGACCGGCTGCGGCGGCGAGGCGGCTGCAACT 649
QY 636 GCAATTCAGATGATGATCTCTGCTGTGGAACCTCTTCAATGAAGATCTGGCTTCAAT 695
DB 650 GCAATGCGCA-----CACCGGCTGTGCTGAGCTTTCGT---GTTCTAATCTTCTT 700

```


GENERAL INFORMATION:
APPLICANT: Bell, Graeme I.
APPLICANT: Yamada, Yuichiro
APPLICANT: Seino, Susumu
TITLE OF INVENTION: SOMATOSTATIN RECEPTORS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: PO Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/816,283
FILING DATE: 19911231
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McDaniel, C. Steven
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-787-1400
TELEFAX: 713-789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1634 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-07-816-283-1

Query Match 19.9%; Score 229.6; DB 1; Length 1634;
Best Local Similarity 55.1%; Pred. No. 9,2e-47;
Matches 523; Conservative 0; Mismatches 409; Indels 18; Gaps 3;

QY 75 CAGCAGCCCTGCTGCTCCGCGCTGGCGGAGCCGACAGCAAGCGCGCGCTCCGA 134
DB 171 CGGCGGCGAGCGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAA 230
QY 135 GAGCGCGGAGCTGAGCGCGCGCGCGCATCTCCCGCGCATCCCGGTCATCAGCGCGCT 194
DB 231 TCGCGTCCGAGAACGGGACCTTGAGGAGGAGGCGCGCGCGCGCATCTCTTCAT 290
QY 195 CTACTCCGTAAGTGTGCTGCTGGGCTTGTTGGGCAACTCGCTGCTGCTGCTGCTGCT 254
DB 291 CTACTCCGTAAGTGTGCTGCTGGGCTTGTTGGGCAACTCTGCTGCTGCTGCTGCTGCT 350
QY 255 CGATACACAAAGATGAGAGAGAGCAACCAATTATTAATTATTAATTATTAATTATTA 314
DB 351 GCGGTATGCAAGATGAGAGAGAGAGCAACCAATTATTAATTATTAATTATTAATTATTA 410
QY 315 TGCCTTACTTACTACAAACATGCGCTTTCAGAGTACGCTTACTTATGAAATCTTGCC 374
DB 411 TGAAGTGTCTACTGCTCAGCGTGCCTTCTTACTGCTCCTCAAGTGTGCGCGCATGCGC 470
QY 375 TTTTGGGATGCTGCTGCAAGATGTAATTTCATTGATTAATTATTAATTATTAATTATTA 434
DB 471 CTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 530
QY 435 CATCTTCACTTGAACATGATGAGCGTGAACCGCTACATTCGCTGCTGCTGCTGCTGCTG 494
DB 531 CATCTTCACTTGAACATGATGAGCGTGAACCGCTACATTCGCTGCTGCTGCTGCTGCTG 590
QY 495 GCGCTTGAAGCTTCCGACACCTCTTGAAGCAAAAGATCAATATCTGATCTGGCTGCT 554
DB 591 GCGCGCCCGCTAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGCTGCT 650

QY 555 GTCGTCATCTGTGGCATCTGCAATGATCTTGAAGCAACCAAGTCAGAGAAAGCT 614
DB 651 ATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 710
QY 615 CGATGCTATGAGTGTCTCTTGCAGTTCAGATGATGATGATGATGATGATGATGATGATGAT 674
DB 711 CACGG---TGCTTGAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 767
QY 675 CATGAAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 734
DB 768 GGT---GTGTGACATTTCTCATGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 824
QY 735 CTACACCTGATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 794
DB 825 CTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 884
QY 795 AGATGCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 854
DB 885 CAGGCGCTCGGAGGCAAGATCACTTAATGATGATGATGATGATGATGATGATGATGATGAT 944
QY 855 CTGCTGATCTCCATTCATATTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 914
DB 945 CTGCTGATGCTCTTCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1004
QY 915 CACAGCTGCTCTCCAGCTATTTACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 974
DB 1005 CACGCTGATC-----AGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1052
QY 975 GAATCCCATCTCTACGCTTCTTGAAGAACTTCAAGCGGTGTTCC 1024
DB 1053 CAACCCATCTCTATGCTTCTCTCAAGCACTTCAAGGCTCTTCC 1102

RESULT 81
US-08-417-103-1
Sequence 1, Application US/08417103
Patent No. 5723299
GENERAL INFORMATION:
APPLICANT: Bell, Graeme I.
APPLICANT: Yamada, Yuichiro
APPLICANT: Seino, Susumu
TITLE OF INVENTION: SOMATOSTATIN RECEPTORS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,103
FILING DATE: 05-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/816,283
FILING DATE: 01-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: ARCD:144
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1634 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
 TOPOLOGY: linear
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 100..1272
 US-08-417-103-1

Query Match 19.9%; Score 229.6; DB 1; Length 1634;
 Best Local Similarity 55.1%; Pred. No. 9.2e-47;
 Matches 523; Conservative 0; Mismatches 409; Indels 18; Gaps 3;

QY 75 CAGCAGCCGCTGGTTCCTCCGCTGGGCGGAGCCCGACAGCAAGCGAGCGCGGCTCGGA 134
 DB 171 CGGCGGCGAGCGAGGCGCGCGGCGCGCTCGGACGCGACAGAGAGAGCGAGGCGGAA 230
 QY 135 GAGCGCGAGCTGAGAGCGCGGCGACATCTCCCGGCGATCCGCTCATCAGCGCGGT 194
 DB 231 TCGCTGCCAGAACGGGACCTTGAGCGAGGCGGAGCGCGCGCATCTGATCTCTTTCAT 290
 QY 195 CTACTCCGAGTGTTCGCTGGGCTGGTGGGCAATCGCGGTGATGATCAT 254
 DB 291 CTACTCCGAGTGTTCGCTGGGCTGGTGGGCAATCTGATGATCATCTTACGATCTCT 350
 QY 255 CCGATACACAAAGATGAGAGACAGCAACCAATTTACATATTTAACTGGCTTGGCAGA 314
 DB 351 GCGCTATGCCAAGATGAGAGACGCGCACCAATCTACATCTTAACTGGCCATGCTGA 410
 QY 315 TGCCTTAGTACTACAAACCATGCGCTTTCAGAGTACGGTCTAATTGATGAATTCCTGGC 374
 DB 411 TGAGCTGCTCATGCTCAGCGGTGCGCTTCTAGTCACTCAGCTGATGTTGCGCACGTGCG 470
 QY 375 TTTTGGGAGTGTCTGTGCAAGATGATTTTCCATGATTTACTACATGATTTACCGG 434
 DB 471 CTTCGCTGCTGCTCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 530
 QY 435 CATCTTCACTTGCATGATGAGCGGTGAGCGGTACATTTGCGGTGCGACCGCGTGA 494
 DB 531 CATCTATCTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 590
 QY 495 GCGCTTGAATTCGCGCACACCGCTTGAAGGCAAGATCATCAATTCATCTGCTGCTGCT 554
 DB 591 GCGCGCGCGCTACCG 650
 QY 555 GTCTGCTATCTGTGGCATCTCTGCAATGATCTCTTGAAGGCAAGATGATGAGGAGAGCT 614
 DB 651 ATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 710
 QY 615 CGATGCTATGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 674
 DB 711 CACGG---TGCTTGCACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 767
 QY 675 CATGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 734
 DB 768 GGT---GTTGTAACATTTCTCATGAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 824
 QY 735 CTACACCTGATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 794
 DB 825 CTACCTGCTCATCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 884
 QY 795 AGATGCAACCTGCGGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 854
 DB 885 CAGGCGCTGCGAGCGGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 944
 QY 855 CTGCTGAGCTTCCATTTACATATTTACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 914
 DB 945 CTGCTGAGTGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1004
 QY 915 CACAGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 974
 DB 1005 CACGCTGAGTCT-----AGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1052
 QY 975 GAATCCCATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1024

DB 1053 CAACCCCATCTCTATGCTTCTCTCAGACAACTTCAAGCGCTCTTCC 1102

RESULT 82

US-09-016-434-1302
 / Sequence 1302, Application US/09016434
 / Patent No. 6500938

GENERAL INFORMATION:

APPLICANT: Janice Au-Young

APPLICANT: Jeffrey J. Seilhamer

TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING

TITLE OF INVENTION: PATHWAY GENE EXPRESSION

NUMBER OF SEQUENCES: 1490

CORRESPONDENCE ADDRESS:

ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

STREET: 3174 PORTER DRIVE

CITY: PALO ALTO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/016,434

FILING DATE: HEREWITH

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Zeller, Karen J.

REGISTRATION NUMBER: 37,071

REFERENCE/DOCKET NUMBER: PA-0002 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 855-0555

TELEFAX: (650) 845-4166

INFORMATION FOR SEQ ID NO: 1302:

SEQUENCE CHARACTERISTICS:

LENGTH: 1634 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: GENBANK

CLONE: 9307433

US-09-016-434-1302

Query Match 19.9%; Score 229.6; DB 4; Length 1634;

Best Local Similarity 55.1%; Pred. No. 9.2e-47;

Matches 523; Conservative 0; Mismatches 409; Indels 18; Gaps 3;

QY 75 CAGCAGCCGCTGGTTCCTCCGCTGGGCGGAGCCCGACAGCAAGCGAGCGCGGCTCGGA 134
 DB 171 CGGCGGCGAGCGAGGCGCGCGGCGCGCTGCGGACGCGACAGAGAGCGAGGCGGAA 230
 QY 135 GAGCGCGAGCTGAGAGCGCGGCGACATCTCCCGGCGATCCGCTCATCAGCGCGGT 194
 DB 231 TCGCTGCCAGAACGGGACCTTGAGCGAGGCGGAGCGCGCATCTGATCTCTTTCAT 290
 QY 195 CTACTCCGAGTGTTCGCTGGGCTGGTGGGCAATCGCTGATGATGATCAT 254
 DB 291 CTACTCCGAGTGTTCGCTGGGCTGGTGGGCAATCTGATGATCATCTTACGATCTCT 350
 QY 255 CCGATACACAAAGATGAGAGACAGCAACCAATTTACATATTTAACTGGCTTGGCAGA 314
 DB 351 GCGCTATGCCAAGATGAGAGACGCGCACCAATCTACATCTTAACTGGCCATGCTGA 410
 QY 315 TGCCTTAGTACTACAAACCATGCGCTTTCAGAGTACGGTCTAATTGATGAATTCCTGGC 374

Db 936 CTGATGCTCTTCTACGTGTACAGCTGTGCAAGTGTTCGCCGAGCAAGACGCCAC 995
Qy 918 AGCTCTCTCTCAGCTATTAATTCGTGATCGCCTTAGGCTATACCAAGTACCTGA 977
Db 996 CGTGAGCC-----AGTGTCTGTCACTCCGGGCTATGCGCAAGCTGTGCCA 1043
Qy 978 TCCCATTTCTACGCGCTTTCTTGATGAAATTCGAAGCGGTGTTCCGGGACTTC 1032
Db 1044 CCCCATCTCTACGCGCTTCTCTCGGACACTTCAAGCGCTTTCCAGCGCATC 1098

RESULT 84
US-08-417-103-3
; Sequence 3, Application US/08417103
; Patent No. 5723299
; GENERAL INFORMATION:
; APPLICANT: Bell, Graeme I.
; APPLICANT: Yamada, Yulchiro
; APPLICANT: Seino, Susumu
; TITLE OF INVENTION: SOMATOSTATIN RECEPTORS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/417,103
; FILING DATE: 05-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/816,283
; FILING DATE: 01-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: ARCD:144
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1265 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 88..1260
; US-08-417-103-3

Query Match 19.6%; Score 226.6; DB 1; Length 1265;
Best Local Similarity 54.8%; Pred. No. 4.5e-46;
Matches 523; Conservative 0; Mismatches 414; Indels 18; Gaps 3;

Qy 258 ATACAAAGATGAAGACAGCAACCAATTTACATATTAACTGTGCTTTGGAGATGC 317
Db 342 CTACGCCAAGATGAAGACCGCTACCAACATCTACATTTTAACTGGCTATTCGTGATGA 401
Qy 318 TTTAGTTTCTACAAACATGCGCTTTTCAGATGAGCTCTACTTGTATGAAATTCCTGCGCTTT 377
Db 402 GCTGCTCATGCTCAGCGTGGCCCTTTCTGTGTACTTCCAGCGTGTGGCCCACTGGCGCTT 461
Qy 378 TGGGATGTGCTGTGCAAGATAGTAAATTTCCATTGATTACTAACACATGTTCAACAGCAT 437
Db 462 CGGCGGCTACTTTGCGCCCTGTGTCTCAGCGTGTGATCGGTCAACATGTTCAACAGCAT 521
Qy 438 CTTCACCTTGAACCATGATGAGCGGTGACCGGTACATGTCGGTGTGCAACCGGTGAAGGC 497
Db 522 CTACTGTCTGACTGTGCTTAAAGTGTGACCGCTATGTGTGTGTGTGTGTGTGTGTGTGTGT 581
Qy 498 TTTGGAATTCGCGCACACCTTTGMAAGCAAGATCATATATCTGCATCTGCTGTCTC 557
Db 582 AGCGGCTACGCTGTGGCCCACTGTGGCCAAAGTATGAACCTGGGCGTGTGGGTCTGTCTC 641
Qy 558 GTCATCTGTGGCATCTCTGCATATGCTCTTGAGGCAACAAATGAGGAAGAGCTGCA 617
Db 642 ATTACTGTGTTATCTTGCCCATGTGTGTCTTCTCAGCACCGGACCAACAGCATGTGCAC 701
Qy 618 TGTCAATGAGTCTCTTGCAGTTCCCAATGATGATGATCTCTGTGTGAGCTCTTCTAT 677
Db 702 GG---TAGCTTGAACATGCTCATATGCGAGCGCCGACGCGCTGTGTGTGTGTGTGTGTGTGT 758
Qy 678 GAAGATCTGCGTCTTCTCATCTTTGCTGTGATGCTGTCTCTCTCATCATCATCTGTGCTA 737
Db 759 ---CTTATACATTTCTCATATGAGGCTTCTGTGTCTCTGTGTGTGTGTGTGTGTGTGTGT 815
Qy 738 CACCTGTATGATCTGCGCTCTCAAGAGGCTCGGCTCTTCTGTGCTCTCCGAGAGAAAGA 797
Db 816 TGTGCTCATATGTCGAAGATGCGCATGTGTGCTCTCAAGGCTGTGCTGTGACAGACGCA 875
Qy 798 TCGCAACCTGCTGATGATCAACAGCTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 857
Db 876 GCGCTCAAGCGCAAGATCATCTATATGTATGTATGTATGTATGTATGTATGTATGTATGT 935
Qy 858 CTGACATCCCATTTCAATATTCATCTGTGTGAGGCTCTGAGGACACCTCCCAAGACAC 917
Db 936 CTGATGCTCTTCTCATATGCTGTACAGTGTCTCAAGTGTCTCCGAGCAAGACGAGCCAC 995
Qy 918 AGCTGCTCTCTCAGCTATTAATCTGTGATGCGCTTGAAGCTATACCAACGTAAGCTTGA 977
Db 996 CGTGAGCC-----AGTGTCTGTCACTCTGGGCTATGCGCAACAGCTGTGCCA 1043
Qy 978 TCCCATTTCTACGCGCTTTCTTGATGAAATTCGAAGCGGTGTTCCGGGACTTC 1032
Db 1044 CCCCATCTCTACGCGCTTCTCTCGGACACTTCAAGCGCTTTCCAGCGCATC 1098

RESULT 85
US-07-816-283-7
; Sequence 7, Application US/07816283
; Patent No. 5436155
; GENERAL INFORMATION:
; APPLICANT: Bell, Graeme I.
; APPLICANT: Yamada, Yulchiro
; APPLICANT: Seino, Susumu
; TITLE OF INVENTION: SOMATOSTATIN RECEPTORS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: PO Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk


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QY 218 GCTTGGGGCAACTCGCTGTCATGTTGTCATCATCCGATACCAAGATGAAGACAG 277
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Db 193 GCGTGGGGCAACCGCTGTCATTTATGTCATCTCCGTCATGCAAGATGAAGACCA 252
QY 278 CAACCAATTTACATTTAACTGCTTTGGCAGATGCTTTAGTACTACCAACATGC 337
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 253 TCACCAATCATCATCTTAACTGGCCATTCAGATGAATCTTCAATGCAAGGCTTC 312
QY 338 CTTTCAGATGAGCTTACTGATGAATCTGCGCTTTTGGGAGTGTCTGCAAGA 397
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 313 CTTCTTGGCCATGAGGTGGCGCTAGTCCACTGGCTTTTGGCAAGGCATCTGCGGG 372
QY 398 TAGTAATTTCAATGATTACTACCAATGTTACACAGATCTTCACTTGAACATGTA 457
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 373 TGGTATATATCTGTAGATGGCATCAATCAGTTACACAGATCTTCTGTGCTGAGCTCA 432
QY 458 GCGTGGACCGCTACATTTGCGTGTGCACCCCGTGAAGGCTTTGGACTTCCGACACCT 517
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 433 GCATGACCGCTACCTGGCGGTGGTGCACCCCATTAAGTCAACCAATGGAGCGACCC 492
QY 518 TGAAGGCAAGATCATCAATATCTGCACTGCTGCTGTCTGTCATCTGTGGCATCTG 577
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 493 GGACAGCCCAAGATGATCAATGAGCTGTGTGTGTG-----TCTGCTGCTCATTT 546
QY 578 CAATAGCTCTGGAGGACCAAGTCAAGGAGAGAGTGGATGTCATGATGCTCTTGC 637
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 547 TGCCCATCATGATATACCGCGGCTCCGAGCAACAGTGGGAGAGAGACATGTACCA 606
QY 638 AGTTCCCAAGATGATGATCTCTGCTGGGACCTCTTCAATGAAGATCTGCTCATCT 697
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 607 TCAACTGGCCAGCGAATCCGGGGGTGTACACAGTTTCAATTAATCAAGCTTCAATCC 666
QY 698 TTGCTTGTGATCCCTGTCTCATCATCATGCTGTCTACACCTGATGATCTGCTGC 757
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 667 TGGGGTCTCTGGTACCCCTTACATCATTTGCTCTGCTACCTGTTCAATCATCAAG 726
QY 758 TCAAGAGGTCCGGCTCTTCTGTGCTCCGAGAGAAAGATGGCAACCTGCGTAAATCA 817
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 727 TGAATCTCTGGAATCCGAGTGGATCATCCAAAGAGAAAGTCAAGAAAGGTGA 786
QY 818 CCAGATGCTCTGCTGTGAGTGGAGATCTTGTGCTGTGCTGACATCCCATTCACATAT 877
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 787 CCGCATGATGTCATCATGATGCTGTCTTCAATCTTCTGCTGCTCCCTTCTCAATCT 846
QY 878 TCATCTGTGAGGCTCTGCTGAGACATCTCCACAGACAGAGTGTCTCTTCACATAT 937
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 847 TCAAGCTCTCTCCGTGTCTGTGCTCATCATGCCACCCCATGAAAGGCATGTTG 906
QY 938 ACTTCTGATGCGCTTAAGCTTATACCAAGTAAAGCTGAATCCCATTTCTTACGCTTTC 997
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 907 ACTTGTGTGTATCTCTACATATGCAACAGCTGCGCAACCCCATCTGTAGGCTTCT 966
QY 998 TTGATGAATCTTCAAGCGGTGTTTCCGGGACTTGTGCTTTCACATGAAGATGAATG 1057
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 967 TGTCTGCAACTTCAAGAAAGCTTCCAGAAATGTTCTTGTGCTTCAAGGATGATGTA 1026
QY 1058 AGCGGACAGACCTAGCAGAGTCCGAAA 1085
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1027 CGAGAGATGGGAGAGAGACGACAGTAA 1054
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RESULT 87
US-09-743-871B-10
; Sequence 10, Application US/09743871B
; Patent No. 662734
; GENERAL INFORMATION:
; APPLICANT: Memorial Sloan-Kettering Cancer Center
; TITLE OF INVENTION: IDENTIFICATION AND EXPRESSION OF MULTIPLE SPLICE VARIANTS OF MDS
; FILE REFERENCE: KAPPA3-RELATED OPIOID RECEPTOR (KOR-3) GENE
; CURRENT APPLICATION NUMBER: US/09/743,871B
; CURRENT FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: PCT/US99/15977

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; PRIOR FILING DATE: 1997-07-15
; PRIOR APPLICATION NUMBER: 60/093,002
; PRIOR FILING DATE: 1996-07-16
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 2518
; TYPE: DNA
; ORGANISM: mus musculus
US-09-743-871B-10

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Query Match      19.0%; Score 219.4; DB 4; Length 2518;
Best Local Similarity 58.0%; Pred. No. 3.4e-44;
Matches 490; Conservative 0; Mismatches 286; Indels 69; Gaps 3;

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QY 254 TCCGATACCAAGATGAAGACAGCAACCAACATTTACATATTTAACTGCTTGGCAG 313
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 380 TCAGGCAACCAAGATGAAGACTGCTACCAACATTTACATATTTAATCTGGCAGCTGG 439
QY 314 ATGCTTATGTTACTACCAACATGCTTTTCAAGATGAGCTCTACTTGAATTTCTGGC 373
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 440 ATACCTGTGTCTTGTGACACTGCTTCCAGGGACAGACATCTCTGGGCTTCTGCG 499
QY 374 CTTTGGGAGTGTGCTGCAAGATGTAATTTCCATGATTTACTACAAACATGTTACCA 433
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 500 CATTTGGAAATGACTGTGCAAGAGGCTCATTTGCTATGAC----- 540
QY 434 GCATCTTCACCTTGACATGATGAGCGTGACCGCTACATTTCCGCTGTGCCACCCGTGA 493
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 541 -----GCTATCTGCCACCTTATCC 559
QY 494 AGCTTTGAGACTTCGACACCTTTGAAGGCAAGATCATCAATATCTGCACTGCGTGC 553
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 560 GTGCCCTTGATGTTTCGACATCCAGTAAAGCCAGCGCTTAATGTGCCATATGAGGCC 619
QY 554 TGTGTCATCTGTTGGCATCTCTGCAATATGCTTGAAGGACCAAGATGAGGAAGAG 613
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 620 TGGCTTGGGTGTGTGTCTCTGTGCTCATCATGAGCTCAGACACAAAGTGAAGAT---- 675
QY 614 TCGATGATTTAGTGTCTCTTGCATGTTCCAGATGATGATCTCTCTGTGGAGCTCT 673
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 676 --GAAGATGAGAGTCTGTGTGAGATCCCGGCCCTCAGAGATAT--TGGGCCCTG 730
QY 674 TCATGAATATGCGCTCTTCAATCTTGTCTGTGATCTCTGTCTCTCATCATCATCTCT 733
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 731 TATTGCCATCTGCAATCTTCTTTTCTTTCATCATCTCCGCTTGTGATCATCTGTCT 790
QY 734 GCTAACCCGTATGATCTCTGCTCAAGAGGATCGGCTCTCTTCTGAGCTCCGAGAGA 793
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 791 GCTACAGCTTATGATTTGACAGATCTTGTGTGTCTGCTCTTTCAGGCTTCCAGAGA 850
QY 794 AAGATCGCAACCTGCTGATGATACACAGATGCTGCTGTGTGTGTGAGTCAATCTTCTG 853
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 851 AGGACCGGAACCTGGAAGCATACACAGCTGTGTATCTGTGTGTGTGTGTGTGTGTG 910
QY 854 TCTGCTGATCTCCATTTCAATATTCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 913
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 911 GCTGTGACACACTGTGTGAGGCTTGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 970
QY 914 GCACAGCTGCTCTCCAGCTATTTACTCTGTGATGAGCTTGTGTGTGTGTGTGTGTGTGT 973
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 971 GTGAGATGCAATGAGCCATTTCTGCGCTTCTGTGACAGCCCTGTGTGTGTGTGTGTGT 1030
QY 974 TGAATCCCATTTCTACGCTTTTCTTGTATGAATACTTCAAGCGGTGTTCCGGGACTTCT 1033
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1031 TCAATCCCATTTCTATGCTTTCTTGTATGAATACTTCAAGCGCTTGTGAAGTGTCT 1090
QY 1034 GCTTTCACATAAGATGAGATGAGCGGAGAGACCTAGACAGATCCGAATATACAGTTC 1093
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1091 GCTGTGCTTCTGCGCTGACCGGAGATGAGGTTTGTGATGTGTGTGTGTGTGTGTGTGCA 1150
QY 1094 AGGAT 1098
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TELEX: 79-0924
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1351 base pairs
 TYPE: NUCLEIC ACID
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-07-816-283-5

Query Match 18.6%; Score 214.8; DB 1; Length 1351;
 Best Local Similarity 54.0%; Pred. No. 3.5e-43;
 Matches 485; Conservative 0; Mismatches 407; Indels 6; Gaps 2;

```

QY 155 CGCAGATCTCCCGGCGATCCGGGTATCATCAGCGGGTCTAATCCGAGTGGTGTG 214
DB 189 CGTACTATGACCTGACAAAGCAATGACAGTCTCATCTATTTTGGGCTGCATCA 248
QY 215 TGGGCTTGGGGAACCTGCTGATGTTGATGATCCGATACAAAGATGAAGA 274
DB 249 TTGGGTTGTGTGGCAACACATTTGATTTATGTCATCTCCGCTATGCGAAGATGAAGA 308
QY 275 CAGCAACCAATTTAATATTTAACTTGGCTTGGCAGATCTTATGTTACTAACAACA 334
DB 309 CCATCACCACATTTAATCATCTCAACCTGGCATGCAATGAGCTCTTATGCTGGGTC 368
QY 335 TGCCCTTTCAGAGTACGGTCTACTGATGAATTCCTGGCTTTTGGGGATGTGCTGCA 394
DB 369 TGCCCTTTCAGAGTACGGTCTACTGATGAATTCCTGGCTTTTGGGGATGTGCTGCA 428
QY 395 AGATAGTAATTTCCATTGATTACTAACAATGTTACAGCAATCTTACCTTGACCATGA 454
DB 429 GGGTGTCTATGATCTGTGATGATGATCAATCAAGTCAACGACATCTTCTGCTGAAGTCA 488
QY 455 TGAGCGTGAGCCGCTACATTTGCGTGTGCCACCCCGTGAAGGCTTTGACCTCCGACAC 514
DB 489 TGAGCATGAGCCGATACCTGGCTGTGGTGCACCCCATCAAGTCCGCAAGTGAAGAGAC 548
QY 515 CCTTGAAGGCAAGATCATCATATCTGATCTGGCTGTGCTGCTGCTGCTGCTGCTGCT 574
DB 549 CCCGAGCGCCAAATGATCACCATGCTGTGTGGGAGT---CTCTGCTGCTGCTGCTGCT 605
QY 575 CTGCAATAGTCTTGGAGGACCAAGTGAAGAGAGTGCATGATGATGATGCTGCTGCT 634
DB 606 TGCCCATCTATGATATATGCTGGGCTCCGAGCAACAGTGGGAGAGAACACCTGACCA 665
QY 635 TGCACTTCCAGATGATGATGATCTCTGCTGGAGACCTCTTCAATGAAGTCTGCTGCTTCA 694
DB 666 TCACTGGCGCAGTGAATCTGGGGCTGGTACAGAGGTTTATCA---TCTACACTTTCA 722
QY 695 TCTTGGCTTGGTATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 754
DB 723 TCTTGGGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 782
QY 755 GTCTGAAGAGCTCCGGCTCTTTCTGGTCCCGAGAGAAAGATGCAACCTGCGATGAAGA 814
DB 783 AGGTAAAGCTCTGGAATCCAGATGGGCTCTCTTAAGAGAAAGTCTGAAGAAAGAG 842
QY 815 TCACAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 874
DB 843 TCACCGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 902
QY 875 TATTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 934
DB 903 TATTCAAGCTTTCTTCCGCTCCATGAGCCATCAGCCCAACCCCAAGCTTAAAGCAATGT 962
QY 935 ATTACTTTCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 994
DB 963 TTGACTTTTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1022
QY 995 TTTCTTGAAGAAATTCAGAGCGTGTTCCTGGGAGATCTTCTTTCACCTGAAGATGAG 1052
DB 1023 TCTTGTCTGACAACTTCAAGAGAGCTTCCAAATGTCTCTGCTTGGTCAAGGTGAG 1080
  
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RESULT 90

US-08-417-103-5

; Sequence 5, Application US/08417103
 ; Patent No. 573229

GENERAL INFORMATION:

; APPLICANT: Bell, Graeme I.
 ; APPLICANT: Yamada, Yuchiro

; TITLE OF INVENTION: SOMATOSTATIN RECEPTORS
 ; NUMBER OF SEQUENCES: 16

; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Arnold, White & Durkee

; STREET: P.O. Box 4433
 ; CITY: Houston

; STATE: Texas
 ; COUNTRY: United States of America

; ZIP: 77210

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/417,103
 ; FILING DATE: 05-APR-1995

; CLASSIFICATION: 435
 ; PRIOR APPLICATION NUMBER:

; APPLICATION NUMBER: US 07/816,283
 ; FILING DATE: 01-DEC-1991

; ATTORNEY/AGENT INFORMATION:
 ; NAME: Wilson, Mark B.

; REGISTRATION NUMBER: 37,259
 ; REFERENCE/DOCKET NUMBER: ARCD:144

; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (512) 418-3000

; TELEFAX: (512) 474-7577
 ; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1351 base pairs

; TYPE: nucleic acid
 ; STRANDEDNESS: single

; TOPOLOGY: linear
 ; FEATURE:

; NAME/KEY: CDS
 ; LOCATION: 83..1189

US-08-417-103-5

Query Match 18.6%; Score 214.8; DB 1; Length 1351;
 Best Local Similarity 54.0%; Pred. No. 3.5e-43;

Matches 485; Conservative 0; Mismatches 407; Indels 6; Gaps 2;

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QY 155 CGCAGATCTCCCGGCGATCCGGGTATCATCAGCGGGTCTAATCCGAGTGGTGTG 214
DB 189 CGTACTATGACCTGACAAAGCAATGACAGTCTCATCTATTTTGGGCTGCATCA 248
QY 215 TGGGCTTGGGGAACCTGCTGATGTTGATGATCCGATACAAAGATGAAGA 274
DB 249 TTGGGTTGTGTGGCAACACATTTGATTTATGTCATCTCCGCTATGCGAAGATGAAGA 308
QY 275 CAGCAACCAATTTAATATTTAACTTGGCTTGGCAGATCTTATGTTACTAACAACA 334
DB 309 CCATCACCACATTTAATCATCTCAACCTGGCATGCAATGAGCTCTTATGCTGGGTC 368
QY 335 TGCCCTTTCAGAGTACGGTCTACTGATGAATTCCTGGCTTTTGGGGATGTGCTGCA 394
DB 369 TGCCCTTTCAGAGTACGGTCTACTGATGAATTCCTGGCTTTTGGGGATGTGCTGCA 428
QY 395 AGATAGTAATTTCCATTGATTACTAACAATGTTACAGCAATCTTACCTTGACCATGA 454
DB 429 GGGTGTCTATGATCTGTGATGATGATCAATCAAGTTCACCAAGATCTTCTGCTGAAGTCA 488
  
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OY	455	TCAGGCTGACCGGCTACATTTGCCGTGTGGCACCCCGGTGAAGGCTTTGACTTCCGACAC	514
Db	468	TGAGCATGCACCGAATACCTGGCTGTGTGTCACCCCATCAAGTGGCCAAGTGAGGAGAC	548
OY	515	CCTTGAAGGCAAAAGATCATCAATATCTGCATCTGGCTGTGTGTCATCTGTGTGACATCT	574
Db	549	CCCGGACGGCCAAAGATGATTCACCATGGCTGTGTGGGAGT---CTCTGTGTGTGTATCT	605
OY	575	CTGCAATTAAGTCTTGGAGGACCAACCAAGTCAGGGAGAACGTCCATGTATCTTGAAGTCTCT	634
Db	606	TGCCCATATGATATATATGTGTGGGCTCCGAGACAACGATGGGGAGAACGCTGACCA	665
OY	635	TGCAGTTCCAGATGATGACTACTCTGTGTGGGACCTCTTCATGAAGATCTGGCTCTTCA	694
Db	666	TCAACTGGCAGGTGATCTGGGGGCTTGGTATCACAGGGTTATCA---TCTACACTTTCA	722
OY	685	TCTTTGCTTGGTATCCCTGTCTCTCATATCATGCTGTCTGTCACCTGTGATGATCTGC	754
Db	723	TTCTGGGGTCTCTGTGATCCCTTCACCATCATCTGTCTTGTGTAACCTGTTCATTATCATCA	782
OY	755	GTCTCAAGAGCGTCCGGGCTCTCTTCTGGCTCCGAGAGAAAGTGCACCTGGCGTAGGA	814
Db	783	AGGTAAAGTCTCTGGAATCCAGATGGGCTCTCTTAAGAGAGAAAGTCTGAGAGAG	842
OY	815	TCACCAGACTGTCTCTGTGTGTGTGGACAGTCTTGTCTGTCTGTGACTGCCATTTACA	874
Db	843	TCACCCGATGGTGTTCATCTGTGTGGCTGTCTTCACTTCTGTGTGGCTTCCCTTCTACA	902
OY	875	TATTCATCTGTGTGAGGCTCTGTGGGAGACCTCCACAGCACAGTGTCTCTCCAGCT	934
Db	903	TATTCAGGTTTCTTCCGCTTCCATGACCATAGACCCCAAGCCCTTAAGAGCATGT	962
OY	935	ATTACTCTGCATCGCCTTAGGCTATACCAAGAGTACCTGATCCATCTCTAGCGCT	994
Db	963	TTGACTTTGTGTGTGCTTCACTATGTCTAACAGCTGTGCCAACCTATCTAATAGCT	1022
OY	995	TTCTTGATGAATACTTCAAGCGGTGTTCGCGGACCTTCTGCTTTCACCTGAAGATGAG	1052
Db	1023	TCCTGTGCACACTTCAAGAAAGACCTTCCAGATGTCTCTGTGTGTCAGAGTGAG	1080
RESULT 91			
US-09-016-434-1303			
Sequence 1303, Application US/09016434			
Patent No. 6500938			
GENERAL INFORMATION:			
APPLICANT: Janice Au-Young			
APPLICANT: Jeffrey J. Seilhamer			
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING			
TITLE OF INVENTION: PATHWAY GENE EXPRESSION			
NUMBER OF SEQUENCES: 1490			
CORRESPONDENCE ADDRESS:			
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.			
STREET: 3174 PORTER DRIVE			
CITY: PALO ALTO			
STATE: CALIFORNIA			
COUNTRY: USA			
ZIP: 94304			
COMPUTER READABLE FORM:			
MEDIUM TYPE: Floppy disk			
COMPUTER: IBM PC compatible			
OPERATING SYSTEM: PC-DOS/MS-DOS			
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: US/09/016,434			
FILING DATE: HERewith			
CLASSIFICATION:			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER:			
FILING DATE:			
CLASSIFICATION:			
ATTORNEY/AGENT INFORMATION:			
NAME: Zeller, Karen J.			

/	REGISTRATION NUMBER:	37,071
/	REFERENCE/DOCKET NUMBER:	PA-0002 US
/	TELECOMMUNICATION INFORMATION:	
/	TELEPHONE:	(650) 855-0555
/	TELEFAX:	(650) 845-4166
/	INFORMATION FOR SEO ID NO:	1303:
/	SEQUENCE CHARACTERISTICS:	
/	LENGTH:	1351 base pairs
/	TYPE:	nucleic acid
/	STRANDEDNESS:	single
/	TOPOLOGY:	linear
/	IMMEDIATE SOURCE:	
/	LIBRARY:	GENBANK
/	CLONE:	G307435
/	US-09-016-434-1303	

Query Match	18.6%;	Score 214.8;	DB 4;	Length 1351;
Best Local Similarity	54.0%;	Pred. No. 3.5e-43;		
Matches 485; Conservative	0;	Mismatches 407;	Indels 6;	Gaps 2;

Oy	155	CGCAGATCTCCCGGCCATCCCCGGTCATCATCACGCGCGTCTACCTCCGTAGTTCCGTC	214
Dd	189	CGATCTATGACTTGACAAGCAATGAGTCCCTCACATTTCATCTATTTGTGTCTGCATCA	248
Oy	215	TGGGCTTGGTGGGAACCTCGCTGTGATGTTGTGTGATCATCCGATACCAAGAATGAAGA	274
Dd	249	TTGGGTTGTGGCAACACCTTGTCATTTATGTTCATCTCCGGTATGCCAAGATGAAGA	308
Oy	275	CAGCAACCAATTTTACATATTTAACTGGCTTTGGCAGATGCTTTAGTTACTACACCA	334
Dd	309	CCATCACCAATTATTAATCTCTCAACCCTGGCCATCGAAGTAGACTCTTTCATGCTGGCTC	368
Oy	335	TGCCCTTTCAGAGTAGACGGTCTACTTGATGAAATTCCTGGCTTTTGGGAGTGTGCTGSCA	394
Dd	369	TGCTTTTCTTGGCTATGAGAGTGGCTCTGTCCACTGGCCCTTTGGCAAGCCATTGGC	428
Oy	395	AGATGTAATTTCCATTGATTAATTAACAAATGTTTCCAGCATCTTCACTTTAACCATGA	454
Dd	429	GGGTGTGTCATACCTGTGGATGGATCAATCAGTTTACAGAGATCTTTCGCTGCACATGA	488
Oy	455	TGAGCGTGGACCGGTACATTGGCGTGGGCCACCCCGTGAAGGCTTTGGACTTCCGCACAC	514
Dd	489	TGAGCATGACCGATACTGTGGCTGTGTGCCAACCCTCATCAAGTCCGCAAGTGGAGAGAC	548
Oy	515	CTTTGAAGGCAAGATCATCATATATCTGCATCTGGCTGTGTCTGTATCTGTGGCACT	574
Dd	549	CCCGAGCGGCAAGATGATCACTATGGCTGTGTGGGAGT---CTCTGTGCTGTGTATCT	605
Oy	575	CTGCATATGTCCTTGGAGGACCAAAGTCAGGGAGAAAGTCGATGTCAATTGAGTGTCTCT	634
Dd	606	TGCCATCATGATATATGTGTGGGCTCCGGAGCAACAGTGGGGAGAAAGCAGCTGCACCA	665
Oy	635	TGCAGTTCCCGATGATGATCACTACTCTGTGGGAGCACTTTTCATGAMAATCTGCCTCTTCA	694
Dd	666	TCACTGGCCAGGTGATCTGTGGGCTTTGTATCAAGAGGTTTCATCA---TCTACACTTTCA	722
Oy	695	TCTTGTGCTTGTGATCCCTGTCTCTCATCATCATGCTGTCTGTACACCTGTGATCTCTGC	754
Dd	723	TTCTGGGGTTCCTGTGATACCCCTCACATCATCTGTCTTGTCTACCTGTTCATTTATCTCA	782
Oy	755	GTCTCAAGAGGATCGGAGCTCCTTTCTGGGTCCTCCAGAGAAAGATCGCAACCTGTGGTGA	814
Dd	783	AGGTGAAGTCTCTGTGAATCCGAGTGGGCTTCTTAAAGAGAAAGTCTGAGAAAGG	842
Oy	815	TCACCAAGATGTCCTGTGTGTGGTGGCAATCTTTCGTCTGTCTGTGCACTCCATTCACA	874
Dd	843	TCACCCGAATGATGTCATGATGTGTGTGTCTTTCATCTTCTGTGTCTTCCCTTTCACA	902
Oy	875	TATTCATCTGTGTGAGAGGCTCTGGGAGGACATCCCAACAGACAGTGTCTCTCCAGCT	934
Dd	903	TATTCACAGTTTTCTTCGTCTCATGTGCATCAAGCCCACCCAGCCCTTAAAGGCATGT	962
Oy	935	ATTACTTCTGCATGCGCTTAGGCTATATCCAACAGTAGCTGAATCCCATTTCTCTACGCT	994

Db 963 TTGACTTGTGGTGTCTCTCAACCTATGCTAAACAGCTGTGCGCAACCTATCTATATGCTT 1022
Qy 995 TTCTTGATGAAGAACTTTCAAGCGGTGTTTCCGGACCTTCTGCTTTCCACTGAAGATGAG 1052
Db 1023 TCTGTGTGACAACTTCAAGAGAGCTTCCAGAAATGCTCTGCTTGTGTGCAAGGTGAG 1080

RESULT 92

US-09-170-496D-15
; Sequence 15, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496D
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: Patent version 3.1
; SEQ ID NO 15
; LENGTH: 1002
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-170-496D-15

Query Match 18.2%; Score 210.4; DB 4; Length 1002;
Best Local Similarity 55.2%; Pred. No. 3.8e-42;
Matches 478; Conservative 0; Mismatches 376; Indels 12; Gaps 3;

Qy 166 CCGGCATCCCGGTATATATACAGCGGCTTACTCCGATGTTGTTGTTGGGCTTGTG 225
Db 124 CCGTTCCTTATATGCTCTCTGCGCCCGGTGACTCCGGGATCTGTGCTGGGGCTGACT 183
Qy 226 GGCAACGCTGCTGATGTTGTGATCATCCGATACAAAGATGAAGACGACCAAC 285
Db 184 GGCAACGCTGCTGATGTTGTGATCATCCGATACAAAGATGAAGACGCTGACCAAC 243
Qy 286 ATTACATATTTTAACTGCTTGTGAGATGCTTATGTTACTACAAACATGCGCTTTGAG 345
Db 244 GTGTTATCTTGAACCTGCGGTGCGGACGCGGCTTCTCAACCTGTATGCGCCCTCAAC 303
Qy 346 AGTACGCTTACTGATGAATCTCTGCGCTTTGGGAGTGTCTGTGCAAGATGTAAT 405
Db 304 ATCGGAGGACACTGCTCAGATGAGCGCTTCGGGAGCTGCTTGCAGAGCTGTGCTG 363
Qy 406 TCCATGATTTACTAACAATGTTCAACGACATCTTCACTTGAACATGATGAGCTGAGC 465
Db 364 GCCGTCGACACTAACAATCTTCTTCAGACATCTTCTTACCGGTATGAGCGTGAAC 423
Qy 466 CGCTACATTTGCGTGTGCAACCCCGTGAAGC-----TTTGAATTCGCGACACCTTGG 519
Db 424 CGATACCTGTGTGTCTGTGCGACCGTGAAGTTCGCCCAACATGCGCTTGGCGACCTAAC 483
Qy 520 AAGGCAAGATCATCAATATCTGATCTGCTGTGCTGTCTGATCTGTTGGCATCTTGTCA 579
Db 484 GGGGCGAAGTGTGCGAGCTGTGTGTGTGCTGAGGCTGACAGGCTCTGTTCTGCGCTTC 543
Qy 580 ATAGTCTTGAAGGACCAAGTCAAGGAGACGTCGATGATGATGATGATGATGATGATG 639
Db 544 TTCTCTTTCGCTGGGTCTA---CAGCAACGAGCTGCGAGTCCAAAGCTGTGGGCTGAGC 600
Qy 640 TTCCAGATGATGATCTCTCTGTGAGACCTTCTCATGAAGATCTGGGCTTTCATCTTT 699
Db 601 TTCCGCTGCGGCGGAGCGGTCTGTGTTCAAGGCGACCGT---GTCTACATTTGTGCTCTG 657
Qy 700 GCTTCTGTGATCTCTGTCTCTATCATCTGTCTGTCTCAACCCCTGATGATCTGTGCTTC 759
Db 658 GGCCTTCGTGTGCGCGGTGTGACCATCTGTGTGTCTTACACAGACCTCTGTGGCGAGCTG 717

Qy 760 AAGACGCTCGGCTCTTCTGTGCTCCGAGAAAGATCGCAACCTGCTAGATCAAC 819
Db 718 CGGCGCTGCGGCTCTCTGTGAGCTCAAGGCTCTAGGCAAGGCGGAGAGGTGACC 777
Qy 820 AGACTGTCTGT 879
Db 778 GTCTGTGCTGT 837
Qy 880 ATCTGT 939
Db 838 TCTGT 897
Qy 940 TTCTGATGCTGCTTATGCTTATACCAAGATGCTGATGCTTCTGATGCTTCTTCTT 999
Db 898 GTCTATCAGGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 957
Qy 1000 GATGAAACTTCAAGCGGTGTTCCG 1025
Db 958 GATGCAACTTCCGAAAGACTTCCG 983

RESULT 93

US-08-148-215A-3
; Sequence 3, Application US/08148215A
; Patent No. 5591602
; GENERAL INFORMATION:
; APPLICANT: O'Dowd, Brian F.
; TITLE OF INVENTION: Opioid Receptor: Compositions and Methods
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 No. 5591602th Clark Street, Suite 800
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60610

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/148,215A
FILING DATE: 05-NOV-1993
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: No. 5591602thrup, Thomas E.
REGISTRATION NUMBER: 33,268
REFERENCE/DOCKET NUMBER: OPIA003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-744-0090
TELEFAX: 312-755-4489

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
LENGTH: 1518 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:

NAME/KEY: CDS

LOCATION: 349..1347

US-08-148-215A-3

Query Match 18.2%; Score 210.4; DB 1; Length 1518;
Best Local Similarity 55.2%; Pred. No. 4.4e-42;
Matches 478; Conservative 0; Mismatches 376; Indels 12; Gaps 3;

Qy 166 CCGGCATCCCGGTATATATACAGCGGCTTACTCCGATGTTGTTGTTGGGCTTGTG 225
Db 472 CCGTTCCTTATATGCTCTCTGCGCCCGGTGACTCCGGATCTGTGTGGGCTGACT 531
Qy 226 GGCAACTGCTGTGATGTTGTGATCATCCGATACAAAGATGAAGACGACCAAC 285

```

Db      532  GCGAAGAGGCGCGATCTCTGTATCTTAAGAGGCGCCCAAGATGAACGGTACCAAC 591
Qy      286  ATTACATATTTAACTGGCTTTGGCAGATGTTAGTACTACAACATGCCCTTTGAG 345
Db      592  GTGTTCACTGAACTGGCGGTGGCCGACGGGGCTTTCAGCGTGGTACTGGCCGTCAAC 651
Qy      346  AGTACGGTCTACTGATGAATTCCTGGCTTTTGGGAGTGTCTGTGAAGATAGTAATT 405
Db      652  ATCGGAGGACACCTGCTCAAGTACGGCCCTTGGGGAGCTGCTTGAAGGTGTGCTG 711
Qy      406  TCCATTGATTAACAATGTTTCAACAGCATCTTCACTTGAACCATGATGAGCGTGAC 465
Db      712  GCCGTGACACATCAATCTTCTCCAGCATCTTCTAGCCGTATAGCGCTGAGAC 771
Qy      466  CGCTACATTCGCGGTGCGAACCCCGTGAAGC-----TTTGAAGCTTCGCAACCCCTTG 519
Db      772  CGATACCTGATGCTGTGGCCACCGTGAAGTCCCGCCACATGCCCTTGGCGGACCTAACCG 831
Qy      520  AAGCAAGATCATATATCTGCATCTGGCTGTGTGTATCTGTGGCATCTGTGCA 579
Db      832  GGGGGAAGGTGCGCAGCTGTGTGTGTGTGGCGGTGACGGTCTGGCTTGTGCTTC 891
Qy      580  ATAGCTTTGGAGGACCAAAAGTCAGGGAAGACGTGATGTCATTTAGTGTCTCTTGAG 639
Db      892  TTCTCTTTCGCTGGGCTCTA---CAGCAACAGAGCTGAGGTCCCAAGCTGTGGGCTGAGC 948
Qy      640  TTCCCAATGATGATGATCTCTGTGGGAGACCTTTTCAATGAAGATCTGGGCTTTCATCTTT 699
Db      949  TTCCCGTGGCCGAGCGGGGTCTGTTCAAAGGCCAACCGT---GTCTACACTTTTGTGCTCG 1005
Qy      700  GCGTTCGATGATCCCTGTCTCTATCATGCTGTGCTCAACCCCTGATATGCTGTGCTC 759
Db      1006  GCGTTCGATGATCCCTGTCTCTATCATGCTGTGCTCAACCCCTGATATGCTGTGCTC 1065
Qy      760  AAGAGCGTCCGCTCTTCTGTGCTCCGAGAGAAATTCGCAACCTGCGTGAATCAAC 819
Db      1066  CGGGCGGAGGCTCGCTCGCTGAGACCAAGCTCAGGAAGGCGAGGAGGTGAGC 1125
Qy      820  AGACTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 879
Db      1126  GTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1185
Qy      880  ATCCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 939
Db      1186  TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1245
Qy      940  TTCTGATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 999
Db      1246  GTCAATCAACAGCTCAAGTACGCAACTGCTGAGACCCCTTCTGTGTGTGTGTGTGT 1305
Qy      1000  GATGAAGATTTCAACGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1025
Db      1306  GATGCAACTTCCGAGAGAACTTCCG 1331

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RESULT 94
US-09-016-434-1480

Sequence 1480, Application US/09016434
Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESS: INCYTE PHARMACEUTICALS, INC.
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREMITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1480:
SEQUENCE CHARACTERISTICS:
LENGTH: 1518 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: g953234
US-09-016-434-1480

```

Query Match 18.2%; Score 210.4; DB 4; Length 1518;
Best Local Similarity 55.2%; Pred. No. 4.4e-42;
Matches 478; Conservative 0; Mismatches 376; Indels 12; Gaps 3;

```

Qy      166  CCGGCAATCCGCTGATCATCAAGCGGCTTACTCCGTAGTGTGTGTGTGTGTGTGTGT 225
Db      472  CCGTTCCTCTATGATGCTCTGCTCCGCGGTGATCTCCGGAATCTGTGTGTGTGTGTGT 531
Qy      226  GCGAATCGCTGTGATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 285
Db      532  GCGAAGAGGCGCGATCTCTGTATCTTAAGGCGCCCAAGATGAACGGTGAACCAAC 591
Qy      532  GTGTTCACTGAACTGGCGGTGGCCGACGGGCTTTCAGCGTGGTACTGGCCGTCAAC 651
Db      592  AGTACGGTCTACTGATGAATTCCTGGCTTTTGGGAGTGTCTGTGAAGATAGTAATT 405
Qy      346  AGTACGGTCTACTGATGAATTCCTGGCTTTTGGGAGTGTCTGTGAAGATAGTAATT 405
Db      652  ATCCGAGGACACCTGCTCAAGTACCTGCGCTTGGGGAGCTGCTGTGCAACCTGGTGTG 711
Qy      406  TCCATTGATTAACAATGTTTCAACAGCATCTTCACTTGAACCATGATGAGCGTGAC 465
Db      712  GCCGTGACACATCAATCTTCTCCAGCATCTTCTAGCCGTATAGCGCTGAGAC 771
Qy      466  CGCTACATTCGCGGTGCGAACCCCGTGAAGC-----TTTGAAGCTTCGCAACCCCTTG 519
Db      772  CGATACCTGATGCTGTGGCCACCGTGAAGTCCCGCCACATGCCCTTGGCGGACCTAACCG 831
Qy      520  AAGCAAGATCATATATCTGCATCTGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 579
Db      832  GGGGGAAGGTGCGCAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 891
Qy      580  ATAGCTTTGGAGGACCAAAAGTCAGGGAAGACGTGATGTCATTTAGTGTCTCTTGAG 639
Db      892  TTCTCTTTCGCTGGGCTCTA---CAGCAACAGAGCTGAGGTCCCAAGCTGTGGGCTGAGC 948
Qy      640  TTCCCAATGATGATGATCTCTGTGGGAGACCTTTTCAATGAAGATCTGGGCTTTCATCTTT 699
Db      949  TTCCCGTGGCCGAGCGGGGTCTGTGTTCAAAGCCAGCGT---GTCTACACTTTTGTGCTG 1005
Qy      700  GCGTTCGATGATCCCTGTCTCTATCATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 759

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Db      1006 GGGCTTCGCTGACCCGCTGAGCACTCTGTGTCTCTACACAGACCTCTCGGAGGCTG 1065
Qy      760 AAGAGCCGCGGCTCTCTTCTGCGCTCCGAGAGAAATCGAACCTCGTATGATTCACC 819
Db      1066 CGGGCGGCGGCTCTCGCTCGGAGCCAAAGGCTCTAGGCAAGGCCAGGAGGTGAC 1125
Qy      820 AGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 879
Db      1126 GTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1185
Qy      880 ATCTGTGAGAGCTCTGAGGAGCACTCCCAAGACAGCTGCTCTCTCAAGCTATTAC 939
Db      1186 TCTGTGCGGCGCTGACCAAGCACTGCGCCAGACCCCACTGCTATGATGCTTAC 1245
Qy      940 TTCTGCATCGCTTATAGGCTATACCAAGTAGCCGTAATCCATCTCTAGGCTTTCTT 999
Db      1246 GTCATACAGGCTCTACGTAAGCCAACTGTGCTGAAACCCCTTCTAGGCTTTCTA 1305
Qy      1000 GATGAAACTTCAAGCGGTGTTCCG 1025
Db      1306 GATGAAACTTCCGGAAGAACTTCCG 1331

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RESULT 95
US-09-170-496D-171
; Sequence 171, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 6555339- Endogenous, Constitutively Activated Human G Protein-
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496D
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 171
; LENGTH: 1002
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-170-496D-171

```

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Query Match      18.0%; Score 207.2; DB 4; Length 1002;
Best Local Similarity 55.0%; Pred. No. 2,3e-41;
Matches 476; Conservative 0; Mismatches 378; Indels 12; Gaps 3;

Qy      166 CCGGCGATCCGGCTATCATACCGCGGCTACTCCGTAAGTGTGCTGCGGCTTGTG 225
Db      124 CCGTTCCTTATGTGCTCTGCGCCGCGGTACTCCGGAATCTGTGCTGCGGCTGACT 183
Qy      226 GCGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 285
Db      184 GCGAACAAGCGCGCTATCTGTATCTTAAGGGGCCCAAGATGAAGCGTGACCAAC 243
Qy      286 ATTTAATATTTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 345
Db      244 GTGTTCATCTGAACCTGCGCGCTGCGCAAGGCTCTTCAAGCTGCTGCTGCTGCTAAC 303
Qy      346 AGTAGGCTCTATGATGATTAATTCCTGCGCTTTTGGGGAGTGTGCTGCAAGTATGTAAT 405
Db      304 ATCGGAGGACACTGCTGCAAGTACGCTTCCGAGGAGCTGCTGCAAGCTGCTGCTG 363
Qy      406 TCCATTGATTAACAAGATGTTCAACAGCATCTTCACTTGAACCATGATGAGCGTGGAC 465
Db      364 GCGGTCGACACTAACAATCTTCTCAAGCATCTTCTAGCCGATGAGCGTGGAC 423
Qy      466 GCGTACATGCTCGCTGTCGCAAGCGCTGAAAGC-----TTTGAAGCTTCCGACACCCCTTG 519
Db      424 CGATACCTGTGTGCTGCTGCGCAAGCGCTGAGGTCCTCCGCAATGCTCCTGCGGCACTTACCGG 483
Qy      520 AAGCGAAGATGATGATATCTGATCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCA 579

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Db      484 GGGGGAAGGTCGCGACGCTGTGTGTCTGCGGCGGTCACAGGTCCTGTCTGCGCTTC 543
Qy      580 ATATGCTTGGAGGCAACAAAGTCAAGGAGACGTCATGATGATGATGATGATGATGATGATGAT 639
Db      544 TTCTCTTTCGCTGCGCTGCTA---CAGCAACAGCTGCGAGGTCCTCAAGCTGTGCGCTGAGC 600
Qy      640 TTCCGAATGATGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 699
Db      601 TTCCGCTGCGGAGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 657
Qy      700 GCTTGTGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 759
Db      658 GCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 717
Qy      760 AAGAGCTGCGGCTCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 819
Db      718 CGGGCGGTCGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 777
Qy      820 AGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 879
Db      778 GTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 837
Qy      880 ATCTGTGAGAGCTCTGAGGAGCACTCCCAAGACAGCTGCTCTTCCAGCTATTAC 939
Db      838 TCTGTGCGGCTCTGACCAAGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 897
Qy      940 TTCTGCATCGCTTATAGGCTATACCAAGTAGCCGTAATCCATCTCTAGGCTTTCTT 999
Db      898 GTCATACAGGCTCTACGTAAGCCAACTGTGCTGAAACCCCTTCTAGGCTTTCTA 957
Qy      1000 GATGAAACTTCAAGCGGTGTTCCG 1025
Db      958 GATGAAACTTCCGGAAGAACTTCCG 983

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RESULT 96
US-09-530-880-5
; Sequence 5, Application US/09530880
; Patent No. 6524805
; GENERAL INFORMATION:
; APPLICANT: Stefano, George B.
; APPLICANT: Filman, Caterina
; TITLE OF INVENTION: OPIATE, CANNABINOID, AND ESTROGEN
; FILE REFERENCE: 09598-004001
; CURRENT APPLICATION NUMBER: US/09/530,880
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: PCT/US98/23944
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 60/065,043
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 441
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-530-880-5

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Query Match      17.7%; Score 204.8; DB 4; Length 441;
Best Local Similarity 67.7%; Pred. No. 6.4e-41;
Matches 287; Conservative 0; Mismatches 137; Indels 0; Gaps 0;

Qy      664 TGGGACCTCTTCAAGAGATGCTGCTTCTTCACTTCTGCTGCTGCTGCTGCTGCTGCTGCT 723
Db      6 TGGGAAACCTGCTGAAGATGTGTTTATCTTCCGCTTCAATATACGATGCTATC 65
Qy      724 ATCATGCTGCTCAACCTGATATCTGCTGCTCAAGAGCGTCCGCTCTTCTGCG 783
Db      66 ATTACCGTGTCTATGATGATGATATCTTGGCGCTCAAGAGTGTCCGATCTCTGCG 125
Qy      784 TCCGGAAGAAAGATCGAACCTCGTATGATCAACAGACTGTGCTGCTGCTGCTGCTGCTGCTGCA 843

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TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 68..1051
 US-08-148-215A-1

Query Match 15.2%; Score 175.6; DB 1; Length 1054;
 Best Local Similarity 51.6%; Pred. No. 1.2e-33;
 Matches 450; Conservative 0; Mismatches 419; Indels 3; Gaps 2;

```

QY 154 GCGCAGATCTCCCGGCGATCCCGGTCAATCAGCGGGGTCTACTCCGTAGTGTCTGC 213
DB 155 GCGCGCGCTGCGGGCGCGCGGTGGGTGACAGATTGTCTAGCGGTGATCTGCGGC 214
QY 214 GTGGGCTTGTGGGCACTCGGTGATCTGTCTGTGATCATCCGATACCAAGATGAAG 273
DB 215 GTGGGTCTGGCGGGCACTCCCGGTGTGTACGTGTGTGCGGGCGCGCATGAAG 274
QY 274 ACAGCAACCAATTTACATATTAACTGGCTTGGGAGATGCTTTAGTTACTACAAAC 333
DB 275 ACCGTACCAACCTGTCTCACTCACTGGGCATGCGAGAGCTCTTACGCTGTGTG 334
QY 334 ATGCCCTTCAAGAGTACGGTCTACTTGAATGATTCCTGGCCTTTTGGGAGTGTCTGTG 393
DB 335 CTGCCCATCAACATGCGCGACTTCTGCTGGCGGAGTGGCCCTTGGGGAGCTCATGTGC 394
QY 394 AAGATAGTAATTTCCATTGATTACTACCAATGTTTACCAGATCTTACCTTGAACATG 453
DB 395 AAGCTCATGTGGCTATGACACAGTAAACACCTTCTCCAGCCTTACTTCTCACCGTC 454
QY 454 ATGAGCGTGGACCGGTACATTTGCGGTGGCCACCCCGTGAAGGCTTTGACTTCGGACA 513
DB 455 ATGAGCGCGGACCGGTACTGTTGTGTGGTGGCCACTGCGGAG--TCGGCGCGGGTGGCG 512
QY 514 CCCTTGAAGGCAAGATCATCAATATCTGCATCTGGTGTCTGCTCATCTGTGGCATC 573
DB 513 GCGCGACTCAAGCGCGCGCGCGGGGTGAGCTGTGGCG--TGTGGGAGATGCTCAACTC 571
QY 574 TCTGCAATAGTCTTGGAGGCAACAAAGTCAAGGAAAGCTGATGTCAATGATGTCTC 633
DB 572 GTGCTGTGCGCTTGTGCAAGTCTTCCCGCGGTAGAGCAAGACAGGGCGCGCGCATGTC 631
QY 634 TTGCAATTTCCAGATGATGATCTCTGTGTGGAGCTTGTATGAATCTGCGCTTTC 693
DB 632 GTGCTAGTCTTTCGCAAGCGCGGAGGCTTGTGTGGCGCGAGCGCGCTTACACGCTC 691
QY 694 ATCTTGGCTTGTGATCCCTGTCTCATCATCATCTGTCTGTACACCTGATGATCTG 753
DB 692 GTGCTGGGCTTGTGCATCCCGGTGTGCACCATCTGTGTCTTATACCACTGCTGTGC 751
QY 754 GGTCTCAAGAGCGTCCGCTCTTCTGTGCTCCGAGAGAAAGATGCAACCTGCGTGA 813
DB 752 CGGCTGCAATGCGATCGGCTGTGAGACGCGCAAGGCGCTGAGGCGCGCCCAAGAGCG 811
QY 814 ATCAACAAGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 873
DB 812 GTGACCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 871
QY 874 ATATTCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 933
DB 872 CTGAGCAAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 931
QY 934 TATTACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 993
DB 932 TCTTCTTCTATACAGAGCTGTGATGCGCAAGCTGTCTTCAACCTTCTCTTACGCG 991
QY 994 TTTCTTGTGAAATCTTCAAGCGGTGTTCG 1025
DB 992 TTCCTGAGCGCGACTTTCGAGAAACCTCCG 1023

```

RESULT 99

US-09-016-434-1479
 Sequence 1479, Application US/09016434
 Patent No. 6500938

GENERAL INFORMATION:
 APPLICANT: Janice Au-Young
 TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
 TITLE OF INVENTION: PATHWAY GENE EXPRESSION
 NUMBER OF SEQUENCES: 1490
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 STREET: 3174 PORTER DRIVE
 CITY: PALO ALTO
 STATE: CALIFORNIA
 COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

CURRENT APPLICATION DATA:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Zeller, Karen J.

REGISTRATION NUMBER: 37,071

REFERENCE/DOCKET NUMBER: PA-0002 US

TELEPHONE: (650) 855-0555

TELEFAX: (650) 845-4166

INFORMATION FOR SEQ ID NO: 1479:

SEQUENCE CHARACTERISTICS:

LENGTH: 1596 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: GENBANK

CLONE: 9953232

US-09-016-434-1479

Query Match 15.2%; Score 175.6; DB 4; Length 1596;
 Best Local Similarity 51.6%; Pred. No. 1.4e-33;
 Matches 450; Conservative 0; Mismatches 419; Indels 3; Gaps 2;

```

QY 154 GCGCAGATCTCCCGGCGATCCCGGTCAATCAGCGGGGTCTACTCCGTAGTGTCTGC 213
DB 613 GCGCGCGTGGCGCGCGCGCTGGCGGTGCTGTACAGATTGTCTACGCGGTATCTGCGGC 672
QY 214 GTGGGCTTGTGGGCAATCTCGGTGATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 273
DB 673 GTGGGTGTGGGGCAATCTCGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 732
QY 274 ACAGCAACCAATTTACATATTAACTGGCTTGGGAGATGCTTTAGTTACTACAAAC 333
DB 733 ACCGTACCAACCTGTCTATCTCACTGGGCATGCGAGAGACTCTTACGCTGTGTG 792
QY 334 ATGCCCTTCAAGAGTACGGTCTACTTGAATGATTCCTGGCCTTTTGGGAGTGTCTGTG 393
DB 793 CTGCCCATCAACATGCGCGACTTCTGCTGGCGAGTGGCCCTTGGGGAGCTCATGTGC 852
QY 394 AAGATAGTAATTTCCATTGATTACTACCAATGTTTACCAAGATCTTCACTTGAACATG 453
DB 853 AAGCTCATGTGGCTATGACACAGTAAACACCTTCTCCAGCTTACTTCTTCAACGCTC 912
QY 454 ATGAGCGTGGACCGGTACATTTGCGGTGCGACCCCGTGAAGGCTTTGAGACTTCGACACA 513

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 30, 2004, 16:58:44 ; Search time 528 Seconds
(without alignments)
9284.887 Million cell updates/sec

Title: US-09-904-584-1
Perfect score: 1154
Sequence: 1 atgagcccccgcagccagat.....ccagtaagcagtcagtcgcga 1154

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Listing first 500 summaries

Database : N_Geneseq_29Jan04:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002s:*
- 7: geneseqn2003as:*
- 8: geneseqn2003bs:*
- 9: geneseqn2003cs:*
- 10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1146	99.3	1182	7	ACA56819 Human big
2	1146	99.3	1182	7	ABZ42678 Human opi
3	1146	99.3	1182	9	AAD58490 Human kap
4	1146	99.3	1182	9	ADE84861 Farnesyl
5	1143	99.0	1143	2	AAT90998 Human kap
6	1142	99.0	1142	2	AAT12550 Human kap
7	1137.8	98.6	1284	5	AAT90999 Human kap
8	1131.8	98.1	1143	5	AB198011 Non-endog
9	1001	86.7	1275	2	AAT92601 Human kap
10	910.8	78.9	1408	2	AAV49254 Mouse kap
11	910.8	78.9	1410	2	AAV75926 Mouse kap
12	910.8	78.9	2481	2	AAQ86725 Mammalian
13	869.6	75.4	1000	2	AAQ75931 Human kap
14	448	38.8	2135	5	AAAF85416 Nucleotid
15	446.4	38.7	1618	2	AAQ89222 Rat mu op
16	446.4	38.7	1618	2	AAQ89223 Transcrip
17	446.4	38.7	1618	3	AAAS9499 CDNA enco
18	443.4	38.4	2070	2	AAQ79199 Rat mu-su
19	436.4	37.8	2162	2	AAV61994 Human mu-
20	434.8	37.7	1239	6	ABBS54814 CDNA enco
21	434.8	37.7	1245	6	ABBS54813 CDNA enco
22	434.8	37.7	1431	6	ABBS54812 CDNA enco
23	434.8	37.7	1610	2	AAQ89226 Human mu

24	434.8	37.7	1610	3	AAAS9503 CDNA enco
25	434.8	37.7	2149	6	ABBS54815 CDNA enco
26	434.8	37.7	2160	2	AAQ93102 Human mu
27	434.8	37.7	2162	2	AAV61995 Human mu-
28	434.8	37.7	2162	2	AAV61986 Human mu-
29	434.8	37.7	2162	2	AAV61988 Human mu-
30	434.8	37.7	2162	2	AAV61984 Human mu-
31	434.8	37.7	2162	2	AAV61987 Human mu-
32	434.8	37.7	2162	2	AAV61980 Human mu-
33	434.8	37.7	2162	2	AAV61985 Human mu-
34	434.8	37.7	2162	2	AAV61989 Human mu-
35	434.8	37.7	2162	2	AAZ88470 Human mu
36	434.8	37.7	2162	6	ABK14953 Human mu
37	434.8	37.7	2162	7	ACAS6781 Human opi
38	434.8	37.7	2162	7	ABZ42697 Human opi
39	434.8	37.7	2162	9	ADCC21534 Human DM
40	434.8	37.7	2279	7	AAAD51226 Human REM
41	434.8	37.5	1176	7	AAAD50855 Human mu
42	433.2	37.5	1473	6	ABBS54816 CDNA enco
43	433.2	37.5	2162	2	AAV61991 Human mu-
44	433.2	37.5	2162	2	AAV61992 Human mu-
45	433.2	37.5	2162	2	AAV61993 Human mu-
46	433.2	37.5	1334	3	AAZ60728 CDNA enco
47	433.4	37.5	1346	3	AAZ60737 CDNA enco
48	433.4	37.5	1365	3	AAZ60736 CDNA enco
49	433.4	37.5	1423	3	AAZ60726 CDNA enco
50	433.4	37.5	1610	3	AAZ60741 CDNA enco
51	432.4	37.5	1729	3	AAZ60734 CDNA enco
52	431.6	37.4	1182	5	AB198013 Non-endog
53	431.6	37.4	1203	5	AB198012 Non-endog
54	430.8	37.3	2045	3	AAZ60735 CDNA enco
55	430.8	37.3	2229	2	AAV49252 Mouse mu
56	430.4	37.3	1149	6	ABX13057 Human MOR
57	429.2	37.2	1542	7	AAZ60729 CDNA enco
58	429.2	37.2	1981	5	AAAD1041 Murine de
59	429.2	37.2	1981	6	ABBS53445 DNA beque
60	427.6	37.1	1981	2	AAO56705 Partial s
61	422.6	36.6	1821	5	AAO56700 Sequence
62	422.6	36.6	1829	2	AAAD1035 Murine de
63	422.6	36.6	1829	6	ABBS53439 CDNA enco
64	422.6	36.6	2218	7	AAV49253 Mouse del
65	422.6	36.6	2219	7	AAV75085 Murine de
66	422.6	36.6	2272	2	AAQ75927 Mouse del
67	415.6	36.0	1176	7	AAAD50856 Human mod
68	411.4	35.6	2216	2	AAQ66656 Murine de
69	408.6	35.4	1773	7	ACAS6807 Human sig
70	408.6	35.4	1773	7	ABT34217 Human del
71	408.6	35.4	1773	7	ABV75086 Human del
72	408.6	35.4	1773	7	ABZ42658 Human opi
73	407	35.3	1119	5	AB198009 Non-endog
74	402.2	34.9	1197	7	AAAD50857 Human mod
75	395	34.2	1829	7	ABX94262 Human ORP
76	393.4	34.1	1805	6	ABBS53446 CDNA enco
77	393.4	34.1	1829	7	ABX94264 Human ORP
78	393.4	34.1	1829	7	ABX94263 Human ORP
79	393.4	34.1	1973	7	ACAS6793 Human sig
80	393.4	34.1	1973	9	ADCC40517 DNA deriv
81	393.4	34.1	2534	7	ABX94045 CDNA enco
82	393.4	34.1	2534	7	ABZ42709 Human opi
83	391.8	34.0	1113	5	AB198010 Non-endog
84	391.8	34.0	1829	7	ABX94260 Human ORP
85	387.6	33.6	1238	3	AAZ60727 CDNA enco
86	387.6	33.6	1257	3	AAZ60730 CDNA enco
87	384	33.3	1670	6	ABBS54825 DNA enco
88	377.6	32.7	1243	7	ABX94042 Rat orpha
89	377.6	32.7	1387	7	ABX94039 Rat orpha
90	377.6	32.7	1567	2	AAO89233 CDNA enco
91	377.6	32.7	1567	2	AAAS9510 CDNA enco
92	376	32.6	2706	2	AAQ92972 Rat opior
93	375.6	32.5	945	6	ABBS54811 CDNA enco
94	368	31.9	1452	2	AAAT90381 Rat metha
95	368	31.9	1452	2	AAAT89585 Rat orpha
96	368	31.9	1452	2	AAV56017 Rat metha

97	368	31.9	1452	3	AAZ91047	AAZ91047 Rat metha	C 170	188.2	16.3	348	4	AA124178
98	368	31.9	1452	4	AAH26613	AAH26613 Rat anti-	C 171	188.2	16.3	348	4	ABA69297
99	368	31.9	1452	5	AA515709	AA515709 Rat metha	C 172	188.2	16.3	348	4	ABA69297
100	367.8	31.9	1134	3	AAZ60659	AAZ60659 DNA encod	C 173	188.2	16.3	348	4	ABA51291
101	367.8	31.9	1330	2	AAQ75928	AAQ75928 Mouse opi	C 174	188.2	16.3	348	4	ABA36226
102	366.2	31.7	2600	6	AA172372	AA172372 KOR3 gene	C 175	188.2	16.3	348	4	AAK43397
103	357	30.9	1177	3	AAZ60658	AAZ60658 DNA encod	C 176	188.2	16.3	348	4	AAK17583
104	347.2	30.1	1228	7	ABX94043	ABX94043 Rat orpha	C 177	188.2	16.3	348	4	ABSA3018
105	347.2	30.1	1372	7	ABX94040	ABX94040 Rat orpha	C 178	188.2	16.3	348	5	ABSA09740
106	344.8	29.9	2600	2	AAQ90096	AAQ90096 Mouse Kap	C 179	188.2	16.3	348	6	ABSA17490
107	344.8	29.9	2600	2	ADD49196	ADD49196 Mouse Kap	C 180	188.2	16.2	1008	8	ACCT99883
108	336.2	29.1	1223	3	AAZ60656	AAZ60656 DNA encod	C 181	186.4	15.9	1155	9	ABDS2675
109	336.2	29.1	1283	3	AAZ60657	AAZ60657 DNA encod	C 182	184	15.2	1155	9	ABDS2675
110	336.8	29.1	1421	7	ABX94038	ABX94038 Rat orpha	C 183	181.8	15.8	348	6	ABSA69714
111	335.8	29.1	1566	7	ABX94037	ABX94037 Rat orpha	C 184	179.8	15.6	540	6	ABQ22580
112	327.4	28.4	2634	3	AAZ60653	AAZ60653 DNA encod	C 185	179.8	15.6	540	6	ABQ22581
113	327	28.3	1256	3	AAQ60654	AAQ60654 DNA encod	C 186	178.8	15.5	1000	6	ABK94683
114	321.8	27.9	829	2	AAQ56703	AAQ56703 Partial s	C 187	178.8	15.5	1000	7	ABX92985
115	319.6	27.7	830	5	AAAD11039	AAAD11039 Human mu	C 188	178.8	15.5	1000	7	ABX92985
116	319.6	27.7	830	5	ABSS51443	ABSS51443 Human opi	C 189	178.8	15.5	1000	7	ABT33305
117	291.2	25.2	2602	7	ABX94254	ABX94254 Human orp	C 190	178.8	15.5	1000	8	ACCT9856
118	289.6	25.1	1947	7	ABX94261	ABX94261 Human orp	C 191	178.8	15.5	1000	9	ADCS1932
119	268.8	23.3	3200	7	ABX94053	ABX94053 Rat orpha	C 192	177	15.3	987	6	ABK94565
120	268.8	22.3	8372	9	ABX94036	ABX94036 Rat orpha	C 193	177	15.3	987	7	ABT33314
121	257.4	22.3	1843	9	ADCB6876	ADCB6876 Human GPC	C 194	177	15.3	987	8	ACCT9865
122	243	21.1	2447	2	AAQ56702	AAQ56702 Partial s	C 195	177	15.3	987	8	ACCT9865
123	243	21.1	2447	5	AAAD11038	AAAD11038 Human Kap	C 196	176.8	15.3	993	7	ABT33331
124	243	21.1	2447	6	ABSS53442	ABSS53442 Human opi	C 197	176.8	15.3	993	8	ACCT9882
125	242.6	21.0	1317	7	ACSA6848	ACSA6848 Human sig	C 198	175.6	15.2	987	3	AAA30587
126	242.6	21.0	1427	6	AB168104	AB168104 Ovary can	C 199	175.6	15.2	987	6	ABK94959
127	241	20.9	1167	6	AA139556	AA139556 CDNA encod	C 200	175.6	15.2	987	7	ABZ42743
128	241	20.9	1167	7	ABZ42764	ABZ42764 Human som	C 201	175.6	15.2	987	9	ABZ42530
129	241	20.9	9190	6	AA139555	AA139555 Genomic D	C 202	175.6	15.2	1054	2	AAQ83681
130	240.4	20.8	599	6	ABK34413	ABK34413 Human CDN	C 203	175.6	15.2	1054	2	AAQ83681
131	239.4	20.7	1167	5	AB198027	AB198027 Non-endor	C 204	175.6	15.2	1596	7	ACSA6881
132	235	20.4	329	9	ADD49504	ADD49504 Human lun	C 205	175.2	15.2	1596	6	ABK48100
133	229.6	19.9	1176	8	ABZ42761	ABZ42761 Human som	C 206	172.4	14.9	987	3	AAA30712
134	229.6	19.9	1176	8	ADB67674	ADB67674 Human som	C 207	172.4	14.9	987	6	ADCC2688
135	229.6	19.9	1634	2	AAQ45553	AAQ45553 Human som	C 208	170.2	14.7	987	6	ABK94661
136	229.6	19.9	1634	2	ACSA6704	ACSA6704 Human sig	C 209	170.2	14.7	987	6	ADCS1928
137	226.6	19.6	1265	5	AAQ45654	AAQ45654 Murine so	C 210	170.2	14.7	1083	6	ABK94660
138	226.4	19.6	1176	5	AB198024	AB198024 Non-endor	C 211	170.2	14.7	1083	9	ADCS1926
139	221.8	19.2	1904	6	AB199251	AB199251 Mouse isc	C 212	169	14.6	1095	7	ABZ42765
140	221.2	19.2	1244	2	AAQ45656	AAQ45656 Murine so	C 213	169	14.6	1245	8	ADB67669
141	219.4	19.0	2518	3	AAZ60655	AAZ60655 DNA encod	C 214	169	14.6	4881	5	AAAS92481
142	216.4	18.8	1110	2	AAQ29155	AAQ29155 Pituitary	C 215	169	14.6	5133	5	ABSA92480
143	215.2	18.6	1023	6	AB161580	AB161580 Human GPR	C 216	167.4	14.5	1095	5	AB198028
144	215.2	18.6	1023	6	ABK94573	ABK94573 G protein	C 217	167.4	14.5	1285	9	ACSA6768
145	215.2	18.6	1023	7	ABX92900	ABX92900 Screening	C 218	167.4	14.5	1285	9	ADCC22031
146	215.2	18.6	1023	7	ABT33330	ABT33330 GPR7 119a	C 219	162.2	14.1	1257	7	ABZ42763
147	215.2	18.6	1023	8	ACCT99881	ACCT99881 Human GPR	C 220	162.2	14.1	1257	7	AAQ55958
148	215.2	18.6	1023	8	ADCS1942	ADCS1942 Human GPR	C 221	162.2	14.1	1296	2	AAQ45657
149	214.8	18.6	1110	7	ABZ42762	ABZ42762 Human som	C 222	162.2	14.1	1413	7	ACSA6723
150	214.8	18.6	1110	7	AAOT09250	AAOT09250 Human som	C 223	160.6	13.9	1257	5	AB198026
151	214.8	18.6	1351	2	AAQ45655	AAQ45655 Human som	C 224	160.4	13.9	726	2	AAAT77788
152	214.8	18.6	1351	2	AAQ45655	AAQ45655 Human sig	C 225	156.2	13.5	1796	2	AAQ45658
153	214.8	18.6	1510	9	ADCB6824	ADCB6824 Human GPC	C 226	156.2	13.5	1797	9	ABN85440
154	211.6	18.3	1110	5	AB198025	AB198025 Non-endor	C 227	156.2	13.5	1797	9	AAAS9961
155	210.4	18.2	999	6	AB161598	AB161598 Human GPR	C 228	153.4	13.3	1384	7	ABT41859
156	210.4	18.2	999	9	ABX92918	ABX92918 Screening	C 229	147	12.7	540	6	ABQ22578
157	210.4	18.2	999	9	ADCS1821	ADCS1821 Human GPR	C 230	147	12.7	540	6	ABQ22579
158	210.4	18.2	1002	3	AAA30590	AAA30590 Human G P	C 231	143.4	12.4	442	4	AA114990
159	210.4	18.2	1002	6	AB161563	AB161563 Human GPR	C 232	143.4	12.4	442	4	ABSA5723
160	210.4	18.2	1002	6	ABZ42744	ABZ42744 Human G P	C 233	143.4	12.4	442	4	AA136336
161	210.4	18.2	1002	9	ADCC22534	ADCC22534 Human G P	C 234	143.4	12.4	442	4	ABSA46180
162	210.4	18.2	1002	9	ACFS7976	ACFS7976 Human GPR	C 235	143.4	12.4	442	4	ABSA6342
163	210.4	18.2	1518	2	AAO83682	AAO83682 Eps11on o	C 236	143.4	12.4	442	4	AAK0381
164	210.4	18.2	164	7	ACSA6882	ACSA6882 Human sig	C 237	143.4	12.4	442	4	AAK04853
165	208	18.0	1898	6	ABN85443	ABN85443 Murine So	C 238	143.4	12.4	442	5	ABSA30020
166	207.2	18.0	1002	3	AAH30713	AAH30713 DNA encod	C 239	143.4	12.4	442	5	AA104755
167	207.2	18.0	1002	3	ADCC2690	ADCC2690 Human G P	C 240	143.4	12.4	442	6	ABSA04979
168	204.8	17.7	441	2	AAAS9781	AAAS9781 DNA encod	C 241	140.6	12.2	487	6	ABV99026
169	195	16.9	887	7	ABX94044	ABX94044 Rat orpha	C 242	138.6	12.0	467	6	ABV95333

389	100.4	8.7	2370	7	ABZ42640	Abz42640 Human C-C
390	100.4	8.7	2372	7	ABZ68884	Abz68884 Nucleotid
391	100.4	8.7	2382	4	AA503022	AA503022 Human dia
392	98.8	8.6	1068	2	AAV28385	AAV28385 Human MCP
393	98.6	8.5	1095	3	AAZ45993	AAZ45993 CDNA enco
394	98.4	8.5	1080	3	AA62483	AA62483 Monkey MC
395	98	8.5	1073	5	AA505847	AA505847 Fruit fly
396	98	8.5	1073	5	AA505847	AA505847 DNA encod
397	97.8	8.5	1116	7	ABT40235	ABT40235 Rat TIG2
398	97.8	8.5	1451	5	AA505853	AA505853 Fruit fly
399	97.8	8.5	1452	8	AA505858	AA505858 Fruit fly
400	97.2	8.4	980	3	AAA30879	AAA30879 Human 11c
401	97.2	8.4	1062	4	AAA91187	AAA91187 Human MCH
402	97.2	8.4	1062	4	AA413652	AA413652 Human mel
403	97.2	8.4	1062	4	AA47298	AA47298 Human etho
404	97.2	8.4	1062	5	AB197900	AB197900 Non-endog
405	97.2	8.4	1062	5	AB197924	AB197924 Non-endog
406	97.2	8.4	1062	6	AB197924	AB197924 Non-endog
407	97.2	8.4	1062	6	AB197924	AB197924 Non-endog
408	97.2	8.4	1062	6	AB197924	AB197924 Non-endog
409	97.2	8.4	1062	7	AA36795	AA36795 Human mel
410	97.2	8.4	1062	7	AA54242	AA54242 Human mel
411	97.2	8.4	1062	8	AA57670	AA57670 Human mel
412	97.2	8.4	1062	9	AA62453	AA62453 Human mel
413	97.2	8.4	1062	9	AA62453	AA62453 Human mel
414	97.2	8.4	1074	3	AA72923	AA72923 Human SLC
415	97.2	8.4	1074	3	AA72923	AA72923 Human SLC
416	97.2	8.4	1074	4	AA72923	AA72923 Human SLC
417	97.2	8.4	1074	4	AA72923	AA72923 Human SLC
418	97.2	8.4	1074	6	AA72923	AA72923 Human SLC
419	97.2	8.4	1074	6	AA72923	AA72923 Human SLC
420	97.2	8.4	1209	3	AA72923	AA72923 Human SLC
421	97.2	8.4	1209	7	AA72923	AA72923 Human SLC
422	97.2	8.4	1209	7	AA72923	AA72923 Human SLC
423	97.2	8.4	1209	7	AA72923	AA72923 Human SLC
424	97.2	8.4	1209	7	AA72923	AA72923 Human SLC
425	97.2	8.4	1209	7	AA72923	AA72923 Human SLC
426	97.2	8.4	1209	7	AA72923	AA72923 Human SLC
427	97.2	8.4	1209	7	AA72923	AA72923 Human SLC
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429	97.2	8.4	1209	7	AA72923	AA72923 Human SLC
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435	97.2	8.4	1209	7	AA72923	AA72923 Human SLC
436	97.2	8.4	1209	7	AA72923	AA72923 Human SLC
437	97.2	8.4	1209	7	AA72923	AA72923 Human SLC
438	97.2	8.4	1209	7	AA72923	AA72923 Human SLC
439	97.2	8.4	1209	7	AA72923	AA72923 Human SLC
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442	97.2	8.4	1209	7	AA72923	AA72923 Human SLC
443	97.2	8.4	1209	7	AA72923	AA72923 Human SLC
444	97.2	8.4	1209	7	AA72923	AA72923 Human SLC
445	97.2	8.4	1209	7	AA72923	AA72923 Human SLC
446	97.2	8.4	1209	7	AA72923	AA72923 Human SLC
447	97.2	8.4	1209	7	AA72923	AA72923 Human SLC
448	97.2	8.4	1209	7	AA72923	AA72923 Human SLC
449	97.2	8.4	1209	7	AA72923	AA72923 Human SLC
450	97.2	8.4	1209	7	AA72923	AA72923 Human SLC
451	97.2	8.4	1209	7	AA72923	AA72923 Human SLC
452	97.2	8.4	1209	7	AA72923	AA72923 Human SLC
453	97.2	8.4	1209	7	AA72923	AA72923 Human SLC
454	97.2	8.4	1209	7	AA72923	AA72923 Human SLC
455	97.2	8.4	1209	7	AA72923	AA72923 Human SLC
456	97.2	8.4	1209	7	AA72923	AA72923 Human SLC
457	97.2	8.4	1209	7	AA72923	AA72923 Human SLC
458	97.2	8.4	1209	7	AA72923	AA72923 Human SLC
459	97.2	8.4	1209	7	AA72923	AA72923 Human SLC
460	97.2	8.4	1209	7	AA72923	AA72923 Human SLC
461	97.2	8.4	1209	7	AA72923	AA72923 Human SLC

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XX  Combination of polynucleotide probes, useful as array elements in a
PT  microarray for monitoring the expression of a number of target
PT  polynucleotides.
XX  Claim 1; SEQ ID NO 1417; 65bp; English.
XX
CC  The invention relates to a combination which, comprises a number of
CC  polynucleotide probes comprising a sequence selected from one of the 1490
CC  sequences mentioned in the specification. The combination is useful as an
CC  array element in a microarray for monitoring the expression of a number
CC  of target polynucleotides. The microarray is particularly useful in the
CC  diagnosis and treatment of cancer and immunopathology and neuropathology.
CC  The microarray is useful in diagnostics and treatment regimens, drug
CC  discovery and development, toxicological and carcinogenicity studies,
CC  forensics and pharmacogenomics. The microarray is also useful for
CC  monitoring progression of diseases and for developing sophisticated
CC  profiles for the effects of currently available therapeutic drugs. The
CC  combination is also useful for purifying a subpopulation of mRNAs, cDNAs
CC  and genomic fragments and in research and diagnostic applications. The
CC  array can detect changes in expression in a large number of genes coding
CC  for different signaling pathway populations which can be used to diagnose
CC  various diseases including cancer e.g. adenocarcinoma and leukaemia,
CC  immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease
CC  and Parkinson's disease. The present sequence represents a polynucleotide
CC  probe of the invention. Note: The sequence data for this patent did not
CC  form part of the printed specification but was obtained in electronic
CC  format directly from USPTO at
CC  seqdata.uspto.gov/sequence.html?DocID=06500938B1
CC  XX
SQ  Sequence 1182 BP; 245 A; 345 C; 293 G; 299 T; 0 U; 0 Other;
    Query Match      99.3%; Score 1146; DB 7; Length 1182;
    Best Local Similarity 99.6%; Pred. No. 1.9e-271;
    Matches 1149; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
    1  ATGGAATCCCGGATCGATCTTCCGCGGGAGCGCGGCGCTTACCTCGCGCCCGAGCGGC 60
    14  ATGGAATCCCGGATCGATCTTCCGCGGGAGCGCTCGCGCTTACCTCGCGCCCGAGCGGC 73
    61  TGCCTGCCCCCGAAGAGCAGCGCGCTGTTCCCGGCTGGGCGGAGCGCCGAGCAAGCAGCG 120
    74  TGCCTGCCCCCGAAGAGCAGCGCGCTGTTCCCGGCTGGGCGGAGCGCCGAGCAAGCAGCG 133
    121  AGCGCCGCGCTCGAAGAGCAGCGCGCTGAGCGCGCGCATCTTCCCGCGCATCCCGGCTC 180
    134  AGCGCCGCGCTCGAAGAGCAGCGCGCTGAGCGCGCGCATCTTCCCGCGCATCCCGGCTC 193
    181  ATCATCAGGGGCGGTCTACTCCGTAGTTCGTGCGGGCTTGGTGGGCAACTCGCGTGTTC 240
    194  ATCATCAGGGGCGGTCTACTCCGTAGTTCGTGCGGGCTTGGTGGGCAACTCGCGTGTTC 253
    241  ATGTTGCGTATCATCGATACCAAAAGATGAGAAGAGCAACCAATTATTAATTTAAC 300
    254  ATGTTGCGTATCATCGATACCAAAAGATGAGAAGAGCAACCAATTATTAATTTAAC 313
    301  CTGGCTTTGGCAGATGCTTACTACTACCAACCATATGCTTTCAGAGTACGGTCTTACTTG 360
    314  CTGGCTTTGGCAGATGCTTACTACTACCAACCATATGCTTTCAGAGTACGGTCTTACTTG 373
    361  ATGAATTCCTGGGCTTTGGGGATGTCGTGCAAGATGTATATTTCCATTATTAATTAAC 420
    374  ATGAATTCCTGGGCTTTGGGGATGTCGTGCAAGATGTATATTTCCATTATTAATTAAC 433
    421  AACATGTTCAACAGATCTTCACTTGAACATGATAGAGGCGGATCACTTACCGG 480
    434  AACATGTTCAACAGATCTTCACTTGAACATGATAGAGGCGGATCACTTACCGG 493
    481  TGGCAACCCCGTGAAGGCTTTGAGCTTCCGACACCCCTTGAAGGCAAAAGATCAATATC 540
    494  TGGCAACCCCGTGAAGGCTTTGAGCTTCCGACACCCCTTGAAGGCAAAAGATCAATATC 553
    541  TGCATCTGGCTGCTGTGTCATCTGTGGCATCTCTGCAATGTATGCTTGGAGGCAACCAA 600

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DB  554  TGCATCTGGCTGCTGTCTGTGTCATCTGTGGCATCTCTGCAATGTCTTGGAGGCAACCAA 613
QY  601  GTCAGGAAAGACGTGATGTCAATTGAGTGCTCTTGGACGTTCCAGATGATGATCACTATCC 660
DB  614  GTCAGGAAAGACGTGATGTCAATTGAGTGCTCTTGGACGTTCCAGATGATGATCACTATCC 673
QY  661  TGGTGGGACCTTTTATGAAAGATCTGCGCTTTCATCTTGGCTTGTATCCCTGTCTTC 720
DB  674  TGGTGGGACCTTTTATGAAAGATCTGCGCTTTCATCTTGGCTTGTATCCCTGTCTTC 733
QY  721  ATCATCATGCTGTCTACACCTGTATGATCTGCGCTTCAAGAGGCTCGGCTCTTCT 780
DB  734  ATCATCATGCTGTCTACACCTGTATGATCTGCGCTTCAAGAGGCTCGGCTCTTCT 793
QY  781  GGCCTCCGAGAAAGATGCAACTGCGTAGATCACCAGCTGCTGTGTGTGTG 840
DB  794  GGCCTCCGAGAAAGATGCAACTGCGTAGATCACCAGCTGCTGTGTGTGTG 853
QY  841  GGAATCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
DB  854  GCGATTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 913
QY  901  AGCACTCCGACAGACAGCTGCTCTTCCAGCTATTAATTTCTGATCGCTTAGAGCTAT 960
DB  914  AGCACTCCGACAGACAGCTGCTCTTCCAGCTATTAATTTCTGATCGCTTAGAGCTAT 973
QY  961  ACCAAGCAGTATGCTGATCTTCTTCTACGCTTCTTGTGTAAGAACTTCAAGCGGTGT 1020
DB  974  ACCAAGCAGTATGCTGATCTTCTTCTACGCTTCTTGTGTAAGAACTTCAAGCGGTGT 1033
QY  1021  TTCCGGGACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1080
DB  1034  TTCCGGGACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1093
QY  1081  CGAATTAACAGTTACAGATCTGCTTACCTGAGAGGACATGATGGATGTAATAACAGTA 1140
DB  1094  CGAATTAACAGTTACAGATCTGCTTACCTGAGAGGACATGATGGATGTAATAACAGTA 1153
QY  1141  TGACTAGTGTGTGA 1154
DB  1154  TGACTAGTGTGTGA 1167

RESULT 2
AB242678
ID  AB242678 strand; DNA; 1182 BP.
XX
AC  AB242678;
XX
DT  04-MAR-2003 (first entry)
XX
DE  Human opioid receptor kappa 1 nucleotide SEQ ID NO:147.
XX
KW  G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW  G protein-coupled receptor; modulator; antibody; immune-related disease;
KW  growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW  immunological-related cell proliferative disease; autoimmune disease;
KW  Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW  osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW  graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW  psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW  mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW  hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KW  ulcer; gene; ds.
XX
OS  Homo sapiens.
XX
PN  WO200261087-A2.
XX
PD  08-AUG-2002.
XX
PF  19-DEC-2001; 2001WO-US050107.

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OS Homo sapiens.
 XX Key Location/Qualifiers
 FT CDS 14..1156
 FT /*tag=a
 FT /product="Human kappa opioid receptor 1 (KOR)"
 FT /note="The CDS is referred to as SEQ ID NO:21 in the
 FT specification"
 XX
 XX WO2003061573-A2.
 XX
 XX 31-JUL-2003.
 XX
 XX 16-JAN-2003; 2003WO-US001450.
 XX
 XX 18-JAN-2002; 2002US-0349511P.
 XX 18-FEB-2002; 2002US-0360500P.
 XX 15-MAR-2002; 2002US-0365041P.
 XX 19-APR-2002; 2002US-0374063P.
 XX 14-AUG-2002; 2002US-0403468P.
 XX 27-SEP-2002; 2002US-0414262P.
 XX 21-OCT-2002; 2002US-0419886P.
 XX 05-NOV-2002; 2002US-0423809P.
 XX 26-NOV-2002; 2002US-0429797P.
 XX
 XX (MILL-) MILLENNIUM PHARM INC.
 XX
 XX S1105-Santiago I, Karichet I;
 XX
 XX WPI; 2003-598705/56.
 XX P-P8DB; AAE38589.
 XX
 XX Identifying a compound for treating urological disorders, for example
 XX PT urinary incontinence by assaying the ability of the compound to modulate
 XX PT the nucleic acid expression or polypeptide activity.
 XX
 XX Diecloaure; Page 149-151; Opp; English.
 XX
 XX The present relates to a method for identifying a compound for treating
 XX CC urological disorders e.g., urinary incontinence including overactive/
 XX CC overensitive bladder, overflow urinary incontinence, stress urinary
 XX CC incontinence caused by dysfunction of the bladder, urethra or central or
 XX CC peripheral nervous system, prostatitis, benign prostatic hyperplasia,
 XX CC cancer of the prostate or kidney disorders. The method is also useful for
 XX CC modulating hyperplasia in a cell and treating a subject having a
 XX CC urological disorder. The invention is also used in gene therapy. The
 XX CC present sequence is human kappa opioid receptor 1 (KOR) DNA
 XX
 XX Sequence 1182 BP; 245 A; 345 C; 293 G; 299 T; 0 U; 0 Other;
 XX
 XX Query Match 99.3%; Score 1146; DB 9; Length 1182;
 XX Best Local Similarity 99.6%; Pred. No. 1.9e-271;
 XX Matches 1149; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 301 CTGGCTTGGAGATGATCTTTAGTTACTACCAACCATGACCCCTTCAGAGTACGGTCTACTTG 360
 DB 314 CTGGCTTGGAGATGATCTTTAGTTACTACCAACCATGACCCCTTCAGAGTACGGTCTACTTG 373
 QY 361 ATGAATTCCTGGCCCTTTTGGGGATGCTGTGCAAGATAGTAATTTCCATTGATTAATAC 420
 DB 374 ATGAATTCCTGGCCCTTTTGGGGATGCTGTGCAAGATAGTAATTTCCATTGATTAATAC 433
 QY 421 AACATGTTACCCAGATCTTCACTTGTACATGATGAGGTGAGCCGCTACATTGGCCGTG 480
 DB 434 AACATGTTACCCAGATCTTCACTTGTACATGATGAGGTGAGCCGCTACATTGGCCGTG 493
 QY 481 TGGCAACCCCGTGAAGGCTTTGGACTTCCGCAACACCTTGAAGGCAAGATCATATATAC 540
 DB 494 TGGCAACCCCGTGAAGGCTTTGGACTTCCGCAACACCTTGAAGGCAAGATCATATATAC 553
 QY 541 TGCATCTGGCTGCTGCTCATCTGTGTCATCTGTGCAATATGTCCTTGGAGGCAACAA 600
 DB 554 TGCATCTGGCTGCTGCTCATCTGTGTCATCTGTGCAATATGTCCTTGGAGGCAACAA 613
 QY 601 GTCAAGGAAAGACGTGATGTCAATTGAGTCTCTTGCAAGTTCCAGATGATGACTACTCC 660
 DB 614 GTCAAGGAAAGACGTGATGTCAATTGAGTCTCTTGCAAGTTCCAGATGATGACTACTCC 673
 QY 661 TGTGTGGACCTCTTCATGAAGATCTGCGCTTCATCTTGGCTGTGATCCCTGTCCTC 720
 DB 674 TGTGTGGACCTCTTCATGAAGATCTGCGCTTCATCTTGGCTGTGATCCCTGTCCTC 733
 QY 721 ATCATCATCTGCTGTACACCTGATGATCTGCTGTCAAGAGGCTCGGCTCTCTTCT 780
 DB 734 ATCATCATCTGCTGTACACCTGATGATCTGCTGTCAAGAGGCTCGGCTCTCTTCT 793
 QY 791 GGGTCCGAGAAAGATGCAACCTGCGTGAATGATGATGATGATGATGATGATGATGATG 840
 DB 794 GGGTCCGAGAAAGATGCAACCTGCGTGAATGATGATGATGATGATGATGATGATGATG 853
 QY 841 GCAATCTCTGCTGTGCTGCACTCCCATTCATGATTCATCTGCTGAGGCTCTGGGG 900
 DB 854 GCGATTTCTGCTGTGCTGCACTCCCATTCATGATTCATCTGCTGAGGCTCTGGGG 913
 QY 901 AGCACTCCCAAGACAGACAGTGTCTCTTCAAGCTTACTTGTGATGCTCTTGAAGCTAT 960
 DB 914 AGCACTCCCAAGACAGACAGTGTCTCTTCAAGCTTACTTGTGATGCTCTTGAAGCTAT 973
 QY 961 ACCAAGTGTGCTGATTCATCTTCAAGCTTACTTGTGATGCTCTTGAAGCTAT 1020
 DB 974 ACCAAGTGTGCTGATTCATCTTCAAGCTTACTTGTGATGCTCTTGAAGCTAT 1033
 QY 1021 TTCCGGGACTTGTCTTCACTGAAGATGAGATGAGAGCGGCAAGCACTAGCAGATGTC 1080
 DB 1034 TTCCGGGACTTGTCTTCACTGAAGATGAGATGAGAGCGGCAAGCACTAGCAGATGTC 1093
 QY 1081 CGAAATTAAGTTCAGATCTGCTTACCTGAGGAGCATGATGAGGATGAATTAACAGTA 1140
 DB 1094 CGAAATTAAGTTCAGATCTGCTTACCTGAGGAGCATGATGAGGATGAATTAACAGTA 1153
 QY 1141 TGACTTGTGTGGA 1154
 DB 1154 TGACTTGTGTGGA 1167

RESULT 4
 ADE84861
 ID ADE84861 standard; DNA; 1182 BP.
 XX
 XX ADE84861;
 AC
 XX 29-JAN-2004 (first entry)
 DT
 XX Farnesyl transferase inhibitor modulated leukemia associated gene #80.
 DE
 XX Farnesyl transferase inhibitor; gene expression;
 KW ss; cyclostatic; farnesyl transferase inhibitor; gene expression;

KM		quinolinone; leukemia; cancer.
XX		
OS	Homo sapiens.	
XX		
PN	WO200308129-A2.	
XX		
PD	08-MAY-2003.	
XX		
PF	30-OCT-2002; 2002MO-US034784.	
XX		
PR	30-OCT-2001; 2001US-0336997P.	
PR	30-OCT-2001; 2001US-0340081P.	
PR	30-OCT-2001; 2001US-0340938P.	
XX		
PA	30-OCT-2001; 2001US-0341012P.	
XX		
Pt	(ORTH) ORTHO CLINICAL DIAGNOSTICS INC.	
DR	Rapont M;	
XX		
XX	WPI, 2003-513497/48.	
PT	Determining whether a patient will respond to treatment with a farnesyl transferase inhibitor. By analyzing the expression of gene that is differentially modulated in the presence of the inhibitor.	
CC	Disclosure; SEQ ID NO 80; 346bp; English.	
CC	The invention relates to a method of determining whether a patient will respond to treatment with a farnesyl transferase inhibitor (FTI), by analyzing the expression of gene that is differentially modulated in the presence of an FTI. The method is useful for determining whether a patient will respond to treatment with a FTI such as (B)-6-(lamino(4-chlorophenyl)(1-methyl-1H-imidazol-5-yl)methyl]-4-(3-chlorophenyl)-1-methyl-2-(1H)quinolinone, monitoring the therapy of a patient, treating a patient with leukemia with FTI if the analysis indicates that the patient will respond. This sequence corresponds to a gene whose expression may be modulated in the presence of FTI.	
XX		
XX	Sequence 1182 BP; 245 A; 345 C; 293 G; 299 T; 0 U; 0 Other;	
SO		
Query Match	99.3%; Score 1146; DB 9; Length 1182;	
Best Local Similarity	99.6%; Pred. No. 1.9e-271;	
Matches 1149; Conservative	0; Mismatches 5; Indels 0; Gaps 0	
OY	1 ATGGAATCCCCCGATCCAGATCTTTCGCGGGGAGACCGGGCCTTAACCTGCAGCGGCC	60
DB	14 ATGGAATCCCCCGATCCAGATCTTTCGCGGGGAGACCGGGCCTTAACCTGCAGCGGCC	73
OY	61 TGCTGCGCCCCCAACGACGAGCGCTGTGTTCCCGGTGAGCGCCGACGCAACGAGC	120
DB	74 TGCTGCGCCCCCAACGACGAGCGCTGTGTTCCCGGTGAGCGCCGACGCAACGAGC	133
OY	121 AGCGCGCGGTCCGAGAGACCGCGAGCTGAGACCCCGGCAATCTCCCCGGCATCCCGGTC	180
DB	134 AGCGCGCGGTCCGAGAGACCGCGAGCTGAGACCCCGGCAATCTCCCCGGCATCCCGGTC	193
OY	181 ATCATCAACGCGAGGTCTACTCCGTAAGTTCGTCGTGGGCTTGAGTGGGAACTCGCTGTC	240
DB	194 ATCATCAACGCGAGGTCTACTCCGTAAGTTCGTCGTGGGCTTGAGTGGGAACTCGCTGTC	253
OY	241 ATGTTGCTGATCATCCGATACCAAGAATGAAGACGACAACCAATTATATTTAATC	300
DB	254 ATGTTGCTGATCATCCGATACCAAGAATGAAGACGACAACCAATTATATTTAATC	313
OY	301 CTGGCTTTGGCAGATGCTTTAGTTACTAACACCATGCCCCTTTACAGATAAGCTTACTTG	360
DB	314 CTGGCTTTGGCAGATGCTTTAGTTACTAACACCATGCCCCTTTACAGATAAGCTTACTTG	373
OY	361 ATGAATTCCTGGCCTTTGGGAGTGGCGTGGCAAGATGATATTTCAATTGATTAATCA	420
DB	374 ATGAATTCCTGGCCTTTGGGAGTGGCGTGGCAAGATGATATTTCAATTGATTAATCA	433
OY	421 AACATGTTACCAAGCATCTTCACTTGACCATGATAGAGTGGACCGCTACATATGCGGTC	480

Db	434	AACATGTTTCCACGAGATCTTCACTCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTG	493
Qy	481	TGCCACCCCGTGAAAGCTTTGGACTTTCGACACACCCCTTGAAGGAAAGATCATCAATATC	540
Db	494	TGCCACCCCGTGAAAGCTTTGGACTTTCGACACACCCCTTGAAGGAAAGATCATCAATATC	553
Qy	541	TGCATCTGGCTCTCTGCTCATCTCTTTGGACATCTTGCATATAGTCTTTGGAGGCACCAA	600
Db	554	TGCATCTGGCTCTCTGCTCATCTCTTTGGACATCTTGCATATAGTCTTTGGAGGCACCAA	613
Qy	601	GTACAGGAAAGAGTGCATGTCAATTGAGTGCCTCTTGAGTTCCGAGATGATGACTACTCC	660
Db	614	GTACAGGAAAGAGTGCATGTCAATTGAGTGCCTCTTGAGTTCCGAGATGATGACTACTCC	673
Qy	661	TGGTGGAGCCTCTTCATGAAGATCTGCGTCTTTCATCTTTGCTTGATCCCTGCTC	720
Db	674	TGGTGGAGCCTCTTCATGAAGATCTGCGTCTTTCATCTTTGCTTGATCCCTGCTC	733
Qy	721	ATCATCATGCTGTGCTTACACCTGTGATGATCTCGCGTCTCAAGAGCGTCCGCTCTTCT	780
Db	734	ATCATCATGCTGTGCTTACACCTGTGATGATCTCGCGTCTCAAGAGCGTCCGCTCTTCT	793
Qy	781	GGCTCCCGAAGAAAGATCGCAACCTGGTGGATCACACGCTGCTGGTGGTG	840
Db	794	GGCTCCCGAAGAAAGATCGCAACCTGGTGGATCACACGCTGCTGGTGGTG	853
Qy	841	GCAGTCTTCGTCGTGCTGAGACTCCATTGCATATTCATCTTGAGAGCTCTGGGG	900
Db	854	GCGGTTTTCGTGCTGCTGAGACTCCATTGCATATTCATCTTGAGAGCTCTGGGG	913
Qy	901	AGCAGCTTCCACAGCAGCTGCTCTCTCCAGCTATTAATCTTGATGCGCTTAGGCTAT	960
Db	914	AGCAGCTTCCACAGCAGCTGCTCTCTCCAGCTATTAATCTTGATGCGCTTAGGCTAT	973
Qy	961	ACCAACATTAAGCTTGAATCCCATTTCTCAAGCCTTTCTGATGAAACCTTCAAGCGGTG	1022
Db	974	ACCAACATTAAGCTTGAATCCCATTTCTCAAGCCTTTCTGATGAAACCTTCAAGCGGTG	1033
Qy	1021	TTCCGGGACTTCTGCTTTCACATGAAATGAGATGAGACGGCAGACCTAGCAGATC	1080
Db	1034	TTCCGGGACTTCTGCTTTCACATGAAATGAGATGAGACGGCAGACCTAGCAGATC	1093
Qy	1081	CGAAATACAGTTCAAGATCTGCTTACTGTAGGGACATCGATGGATGAATTAACAGTA	1140
Db	1094	CGAAATACAGTTCAAGATCTGCTTACTGTAGGGACATCGATGGATGAATTAACAGTA	1153
Qy	1141	TGACTTAGTCGTGA 1154	
Db	1154	TGACTTAGTCGTGA 1167	
RESULT 5			
AAT90998			
ID	AAT90998	standard; cDNA, 1143 BP.	
AC	AAT90998;		
XX	14-APR-1998	(first entry)	
XX	Human kappa opioid receptor cDNA.		
XX	Human kappa opioid receptor cDNA.		
KW	Selective target cell activation; G protein-coupled receptor; RASL;		
KW	gene therapy; cell proliferation; kappa opioid receptor; human;		
KW	transgenic animal; arrhythmia; bone disease; seizure;		
XX	vascular contraction; disease model; ss.		
XX	Homo sapiens.		
OS	Homo sapiens.		
PN	W09735478-A1.		
PD	02-OCT-1997.		


```
XX OS Homo sapiens.
XX FH Key
XX FT CDS
XX FT 1..1142
XX FT /tag= a
XX FT /product= "kappa opioid receptor"
XX FT /note= "incomplete termination codon"
XX PN MO9601898-A1.
XX PD 25-JAN-1996.
XX PF 07-JUL-1995; 95WO-FR000912.
XX PR 11-JUL-1994; 94FR-00008531.
XX PA (UYST-) UNIV PASTEUR STRASBOURG LOUIS.
XX PI Kieffer B, Simonin F;
XX DR WPI, 1996-097628/10.
XX DR P-PSDB; AAR88722.
XX PT New nucleic acid encoding the human Kappa opioid receptor - useful in
XX PT diagnosis and therapy, and for isolating receptor ligands and modulators.
XX PS Claim 3; Page 13-15; 30pp; French.
XX CC This sequence codes for the human kappa opioid receptor and was obtained
XX CC from two overlapping cDNA fragments isolated from a human placental cDNA
XX CC library. The fragments were amplified from the library using PCR primers
XX CC based on the sequence of human genomic clones which hybridised with a
XX CC murine delta receptor cDNA probe. Nucleotide probes derived from the
XX CC kappa opioid receptor coding sequence are useful for diagnosis of
XX CC neurological, cardio- vascular and psychiatric disorders associated with
XX CC opioid receptors
XX SQ Sequence 1142 BP; 236 A; 337 C; 283 G; 286 T; 0 U; 0 Other;
Query Match 99.0%; Score 1142; DB 2; Length 1142;
Best Local Similarity 100.0%; Pred. No. 1.8e-270;
Matches 1142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAGCTCCCGGATCAGATCTTCCGCGGAGCGCGGCGCTTACTGCGCCCGAGCGCC 60
DB 1 ATGAGCTCCCGGATCAGATCTTCCGCGGAGCGCGGCGCTTACTGCGCCCGAGCGCC 60
QY 61 TGCCGCGCCCGCAACAGAGCGCGCTGTTTCCGCGTGGCGAGCCCGAGCAACGCG 120
DB 61 TGCCGCGCCCGCAACAGAGCGCGCTGTTTCCGCGTGGCGAGCCCGAGCAACGCG 120
QY 121 AGCGCGGCTGGAGAGCGCGAGCTGAGAGCCCGGCAATCTCCCGGCAATCCGCGT 180
DB 121 AGCGCGGCTGGAGAGCGCGAGCTGAGAGCCCGGCAATCTCCCGGCAATCCGCGT 180
QY 181 ATCATCAGGCGGCTTACTCCGTAAGTCTTCGTCGCGGCTTGGGGAATCCGTGTC 240
DB 181 ATCATCAGGCGGCTTACTCCGTAAGTCTTCGTCGCGGCTTGGGGAATCCGTGTC 240
QY 241 ATGTCGATCATCCGATACCAAGATGAAGACAGAACCAACATTTACATATTATAC 300
DB 241 ATGTCGATCATCCGATACCAAGATGAAGACAGAACCAACATTTACATATTATAC 300
QY 301 CTGCGTTTGGCAGATGCTTTAGTTACTCAACCAATGCGCTTTACAGAGTACGCTT 360
DB 301 CTGCGTTTGGCAGATGCTTTAGTTACTCAACCAATGCGCTTTACAGAGTACGCTT 360
QY 361 ATGAATTCCTGCGCTTTGGGAGTGTCTGCAAGATGAATTAATTTCAATGATTATAC 420
DB 361 ATGAATTCCTGCGCTTTGGGAGTGTCTGCAAGATGAATTAATTTCAATGATTATAC 420
QY 421 AACATGTTACACAGATCTTCACTTGACCATGATGAGCGTGAACCGCTATATGCGGTG 480
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DB 421 AACATGTTACACAGATCTTCACTTGACCATGATGAGCGTGAACCGCTATATGCGGTG 480
QY 481 TGCCACCCCGTGAAGGCTTTGACTCCGACACACCTTTGAAGCAAGATCATCAATATC 540
DB 481 TGCCACCCCGTGAAGGCTTTGACTCCGACACACCTTTGAAGCAAGATCATCAATATC 540
QY 541 TGCAATCGGCGCTGTCTGATCTGTGGCAATCTTGCAATATGCTTGGAGGACCAAA 600
DB 541 TGCAATCGGCGCTGTCTGATCTGTGGCAATCTTGCAATATGCTTGGAGGACCAAA 600
QY 601 GTCAAGGAAGACGTGATGATGAGTGTCTCTGACAGTCCAGATGATGATGACTATCC 660
DB 601 GTCAAGGAAGACGTGATGATGAGTGTCTCTGACAGTCCAGATGATGATGACTATCC 660
QY 661 TGATGGGACCTTCTTATGAAGATCTGGCTTTTCACTTTGCTTGTGATCCCTGCTC 720
DB 661 TGATGGGACCTTCTTATGAAGATCTGGCTTTTCACTTTGCTTGTGATCCCTGCTC 720
QY 721 ATCATCATGCTGTGACACCTGATGATGATGATGATGATGATGATGATGATGATGAT 780
DB 721 ATCATCATGCTGTGACACCTGATGATGATGATGATGATGATGATGATGATGATGAT 780
QY 781 GGCCTCCGAGAGAAAGATCGCAACCTGCGTAGATCAACAGACTGCTGATGATGATG 840
DB 781 GGCCTCCGAGAGAAAGATCGCAACCTGCGTAGATCAACAGACTGCTGATGATGATG 840
QY 841 GCACTCTTGTGCTGTCTGAGTCCCATTCATCAATATTCATCTGTGAGAGCTTGGGG 900
DB 841 GCACTCTTGTGCTGTCTGAGTCCCATTCATCAATATTCATCTGTGAGAGCTTGGGG 900
QY 901 AGCACTCCGACAGACAGCTGCTCTCCAGATTAATCTTGATGCTTGGAGCTAT 960
DB 901 AGCACTCCGACAGACAGCTGCTCTCCAGATTAATCTTGATGCTTGGAGCTAT 960
QY 961 ACCAAGTATGCTGAATCCCATTTCTGACGCTTTCTTGAATGAATCTTCAAGCGGTG 1020
DB 961 ACCAAGTATGCTGAATCCCATTTCTGACGCTTTCTTGAATGAATCTTCAAGCGGTG 1020
QY 1021 TTCCGGGACTTGTGCTTTCCACTGAAGATGAGATGAGAGCGCGAGACATGAGATC 1080
DB 1021 TTCCGGGACTTGTGCTTTCCACTGAAGATGAGATGAGAGCGCGAGACATGAGATC 1080
QY 1081 CGAATACAGTTTCAAGATCCGCTTACCTGAGGAGCATGAGATGATGAATPAAACAGTA 1140
DB 1081 CGAATACAGTTTCAAGATCCGCTTACCTGAGGAGCATGAGATGATGAATPAAACAGTA 1140
QY 1141 TG 1142
DB 1141 TG 1142
RESULT 7
AAT90999
ID AAT90999 standard; cDNA; 1284 BP.
XX
XX AAT90999;
DE 14-APR-1998 (first entry)
XX
XX Human kappa opioid receptor modified cDNA.
XX Selective target cell activation; G protein-coupled receptor; RASL;
XX gene therapy; cell proliferation; kappa opioid receptor; human;
XX transgenic animal; arrhythmia; bone disease; seizure;
XX vascular contraction; disease model; ss.
OS Homo sapiens.
OS Synthetic.
OS Chimeric.
XX
XX Key Location/Qualifiers
FH sig_peptide 1..90
```



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FT      /tag= a
FT      /product= "prolactin signal sequence"
FT      mat_peptide
FT      91..1284
FT      /tag= b
FT      /product= "FLAG-KOR-HA fusion"
XX      WO9735478-A1.
XX      02-OCT-1997.
XX      25-MAR-1997; 97WO-US005334.
XX      26-MAR-1996; 96US-00622348.
XX      (REGC ) UNIV CALIFORNIA.
XX      Conklin BR;
XX      WPI; 1997-502739/46.
XX      P-PsDB; AAW30298.
XX      Selective activation of target cell expressing modified G protein coupled
XX      receptor - allows control of cellular proliferation, especially for
XX      amplification of transfected cells in gene therapy.
XX      Example 1; Page 77-79; 117pp; English.
XX      This cDNA sequence encodes a polypeptide (see AAW30298) comprising the
XX      human G protein-coupled kappa opioid receptor (KOR) (see also AAW30297)
XX      flanked by sequences that facilitate the detection and purification of
XX      recombinant KOR, and especially KOR RASSLS (see AAW30299), i.e. a
XX      receptor activated superiorly by a synthetic ligand. A novel method for
XX      selectively activating a target cell (TC) comprises: (i) introducing into
XX      the cell a nucleic acid sequence (I) that expresses a RASSL (A) and (ii)
XX      exposing the transfected cell to small synthetic molecules (B) that bind
XX      to and activate (A), inducing the G protein coupled cellular response
XX      associated with receptor activation. (A) has: (a) decreased binding
XX      affinity for a selected natural ligand of the native receptor; (b)
XX      binding affinity for (B); and (c) is activated by binding (B)
XX      sufficiently to produce the required cellular response. Also new are:
XX      transgenic cells including heterologous (I) in the genome; cellular
XX      implants comprising a TC transfected with (I); isolated (I); and
XX      transgenic animals expressing (A). Activation of (A) results, in vitro or
XX      in vivo, in cellular proliferation, or secretion of a cellular product,
XX      particularly a heterologous therapeutic protein encoded by a second
XX      inserted nucleic acid sequence. Particularly it is used to expand the
XX      relatively few cells that are successfully transfected during gene
XX      therapy procedures. Other responses that can be regulated are cell
XX      migration and contraction, or pigment production. In transgenic animals,
XX      expression or stimulation of (A) is designed to develop cardiac
XX      arrhythmia, symptoms of bone disease, seizures, vascular contractions,
XX      dementia, neurodegeneration etc., for use as models of these diseases
XX      (claimed). The transgenic animals are also used for production of
XX      improved food products (e.g. increased calcium content in eggshells or
XX      altered fat/lean ratios) or to control fertility or induce labour
XX      SQ      Sequence 1284 BP; 265 A; 377 C; 322 G; 320 T; 0 U; 0 Other;
Query Match      98.6%; Score 1137.8; DB 2; Length 1284;
Beat Local Similarity 99.8%; Pred. No. 2.1e-269;
Matches 1139; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY      2 TGGACTCCCGATCCAGATCTTCGCGGGAGACCGGGCCCTTACCTGCGCCCGAGCGCT 61
DB      113 TCGACTCCCGATCCAGATCTTCGCGGGAGACCGGGCCCTTACCTGCGCCCGAGCGCT 172
QY      62 GCGTGGCCCCCAACGACGAGCGCTGTTCCGCGGCTGGGCGAGGCCGACACGACGCA 121
DB      173 GCGTGGCCCCCAACGACGAGCGCTGTTCCGCGGCTGGGCGAGGCCGACACGACGCA 232
QY      122 GCGCGCGCTCGAGAGCGCGGACCTGAGACCGCGGACATCTTCCCGGCGCATCCGCGTCA 181
DB      233 GCGCGCGCTCGAGAGCGCGGACCTGAGACCGCGGACATCTTCCCGGCGCATCCGCGTCA 292

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QY      182 TCATCAGCGGCGGCTTACTCCAGTAGTTCGTGCGGGCTTGGGCGCACTCGGTGTCA 241
DB      293 TCATCAGCGGCGGCTTACTCCAGTAGTTCGTGCGGGCTTGGGCGCACTCGGTGTCA 352
QY      242 TGTTCGTGATCATCCGATACACAAAGATGAGACAGCAACCAATTTATCATATTTAAAC 301
DB      353 TGTTCGTGATCATCCGATACACAAAGATGAGACAGCAACCAATTTATCATATTTAAAC 412
QY      302 TGGCTTGGCAGATGCTTTAGTTACTACACCATGCGCTTTGAGTAGCGGTCTACTTGA 361
DB      413 TGGCTTGGCAGATGCTTTAGTTACTACACCATGCGCTTTGAGTAGCGGTCTACTTGA 472
QY      362 TGAATTCCTGGGCTTTGGGGATGTCGTGTGCAAGATGTAATTTCCATGATTTACTACA 421
DB      473 TGAATTCCTGGGCTTTGGGGATGTCGTGTGCAAGATGTAATTTCCATGATTTACTACA 532
QY      422 ACATGTTACACGACATCTTCACTTGACCATGATGAGCGTGAACCGCTACATTGCGGTG 481
DB      533 ACATGTTACACGACATCTTCACTTGACCATGATGAGCGTGAACCGCTACATTGCGGTG 592
QY      482 GCGACCCCGTGAAGGCTTTGACCTTCCGACACCCCTTGAGGCAAGATCATCATATCT 541
DB      593 GCGACCCCGTGAAGGCTTTGACCTTCCGACACCCCTTGAGGCAAGATCATCATATCT 652
QY      542 GCATCTGGCTGCTGTCGTCATCTGTTGGCATCTTCGCAATATCTCTTGGAGGACCAAG 601
DB      653 GCATCTGGCTGCTGTCGTCATCTGTTGGCATCTTCGCAATATCTCTTGGAGGACCAAG 712
QY      602 TTAGGGAAGACGTGATGTCATTTGATGTCCTCTTGCAGTTCCAGATGATGACTACTCT 661
DB      713 TTAGGGAAGACGTGATGTCATTTGATGTCCTCTTGCAGTTCCAGATGATGACTACTCT 772
QY      662 GGTGGACCTCTTCAATGAAGATCTGCTGTCATCTTGCCTTGTGATCCCTGTCTCA 721
DB      773 GGTGGACCTCTTCAATGAAGATCTGCTGTCATCTTGCCTTGTGATCCCTGTCTCA 832
QY      722 TCATCATGTCGTCGTCACACCCGATGATTCGCGCTCAAGACGTCGCGCTCTTCTCG 781
DB      833 TCATCATGTCGTCGTCACACCCGATGATTCGCGCTCAAGACGTCGCGCTCTTCTCG 892
QY      782 GCTCCGAGAGAAAGATGCAACCTGCGTAGATCACAGACTGTCGTGATGATG 841
DB      893 GCTCCGAGAGAAAGATGCAACCTGCGTAGATCACAGACTGTCGTGATGATG 952
QY      842 CAGTCTTGCTGCTGTCGTCGACCTCCATTCACATAATCAATCTGTGTGAGGCTTGGGGA 901
DB      953 CAGTCTTGCTGCTGTCGTCGACCTCCATTCACATAATCAATCTGTGTGAGGCTTGGGGA 1012
QY      902 GCACTCTCCACAGCAGACTGCTCTCCAGTATTTACTTTCGATCCGCTTAAGCTATA 961
DB      1013 GCACTCTCCACAGCAGACTGCTCTCCAGTATTTACTTTCGATCCGCTTAAGCTATA 1072
QY      962 CCAACGATAGCTGATCCATTTCTTCAAGCTTCTTGAATGAATCAAGCGGTGT 1021
DB      1073 CCAACGATAGCTGATCCATTTCTTCAAGCTTCTTGAATGAATCAAGCGGTGT 1132
QY      1022 TCCGGAGCTTGTGCTTCCACTGAAGATGAGATGAGGCGGACGACTAGCAGATGC 1081
DB      1133 TCCGGAGCTTGTGCTTCCACTGAAGATGAGATGAGGCGGACGACTAGCAGATGC 1192
QY      1082 GAAATACGTTTCAGATCTCTTTCCTGAGGGAATGATGGATGAATTAACCATGAT 1141
DB      1193 GAAATACGTTTCAGATCTCTTTCCTGAGGGAATGATGGATGAATTAACCATGAT 1252
QY      1142 G 1142
DB      1253 G 1253

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RESULT 8
 ABI98011
 ID ABI98011 standard; cDNA; 1143 BP.

XX	AB198011;
AC	
XX	18-FEB-2002 (first entry)
DT	
XX	
DE	Non-endogenous human GPCR cDNA, SEQ ID NO: 542.
XX	
XX	Human; G protein-coupled receptor; GPCR; non-endogenous; mutant;
KM	constitutively activated GPCR; agonist; disease; ss.
XX	
OS	Homo sapiens.
XX	Synthetic.
PM	MO200177172-A2.
XX	
PD	18-OCT-2001.
XX	
PF	05-APR-2001; 2001WO-US011098.
XX	
PR	07-APR-2000; 2000US-0195747P.
XX	
PA	(AREN-) ARENA PHARM INC.
PI	Lehmann-Brunsma K, Liaw CW, Lin I;
XX	
DR	WPI; 2001-648759/74.
XX	P-PsDB; ABB56375.
PT	Identifying agonists of G protein-coupled receptors (GPCRs) for use in
PT	disease treatment, comprises contacting candidate compounds with versions
XX	of GPCRs.
PS	
XX	Example 2; Page 344; 394dp; English.
CC	The invention relates to G protein-coupled receptors (GPCRs) for which
CC	the endogenous ligand has been identified. Non-endogenous constitutively
CC	activated versions of known GPCRs are used in the invention for the
CC	direct identification of candidate compounds as receptor agonists,
CC	inverse agonists or partial agonists. Such agonists are useful as
CC	therapeutic agents for diseases or disorders associated with GPCRs. The
CC	present sequence encodes a non-endogenous version of a known human GPCR
XX	
SEQ	Sequence 1143 BP; 238 A; 332 C; 284 G; 289 T; 0 U; 0 Other;
	Query Match 98.1%; Score 1131.8; DB 5; Length 1143;
	Best Local Similarity 99.4%; Pred. No. 5.9e-268;
	Matches 1136; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY	1 ATGGAAGTCCCCCGATTCAGATTCTTCCGGGGAGGCCGGCCTTAAGTGCGCCCGAGCGGC 60
DB	1 ATGGAAATCCCAGATTCAAGATCTTCCGGGGAGCGCTGGCCCTAAGTGCGCCCGAGCGGC 60
QY	TGCCGTGCCCCCAACAGAGAGCGCGCTGGTTTCCGGGTGGGCGGAGCCGAGCAAGCAAGCGC 120
DB	61 TGCCGTGCCCCCAACAGAGAGCGCGCTGGTTTCCGGGTGGGCGGAGCCGAGCAAGCAAGCGC 120
QY	121 AGCGCGGCTCGAGAGAGCGCGAGCTGAGAGCCCGGCAATCTCCCGGCAATCCCGGTC 180
DB	121 AGCGCGGCTCGAGAGAGCGCGAGCTGAGAGCCCGGCAATCTCCCGGCAATCCCGGTC 180
QY	181 ATCATCACGGGGTTACTCCGTAGTGTTCGTGCGGCTGGTGGGCAATCTCGTGGTC 240
DB	181 ATCATCACGGGGGTACTCCGTAGTGTTCGTGCGGCTGGTGGGCAATCTCGTGGTC 240
QY	241 ATGTTGCGATCATCCGATCCGATACCAAGAATGGAAGAGAGACAACCAATTACATAATTAAAC 300
DB	241 ATGTTGCGATCATCCGATCCGATACCAAGAATGGAAGAGAGACAACCAATTACATAATTAAAC 300
QY	301 CTGGCTTTGGAGAGATGCTTAGTAACTAACACCATGCGCTTTAGAGTAGCGTCTACTTG 360
DB	301 CTGGCTTTGGAGAGATGCTTAGTAACTAACACCATGCGCTTTAGAGTAGCGTCTACTTG 360
QY	361 ATGAATTCCTGGCCCTTTGGGAGATGCTGTGCAAGATAGTAATTTCCATTGATTACTAC 420

Db		361	ATGAATTCTGCGCTTTGGGGAGTGTGCTGCAAGAATGTAATTTCCATTGATTACTAC	420
Oy		421	AACATGTTACACAGCATCTTCACCTTGACACATGATGAGCGTGGACCGETAACATTCGCCGTG	480
Db		421	AACATGTTACACAGCATCTTCACCTTGACACATGATGAGCGTGGACCGETAACATTCGCCGTG	480
Oy		481	TGCCACCCCGTAGAAGGCTTTGGACTTTCGGCACACCCCTTGAAGGACAAGATCATCAATATC	540
Db		481	TGCCACCCCGTAGAAGGCTTTGGACTTTCGGCACACCCCTTGAAGGACAAGATCATCAATATC	540
Oy		541	TGCATCTGGCTGCTGTCTGTCAATCTGTGGCAATCTTGCAAAATGTCCTTGGAGGCACAA	600
Db		541	TGCATCTGGCTGCTGTCTGTCAATCTGTGGCAATCTTGCAAAATGTCCTTGGAGGCACAA	600
Oy		601	GTCAGGGAAGAAGTCGATGTCATTGAGAGTCCTTGACATTCGCCAGATGATGACTATCC	660
Db		601	GTCAGGGAAGAAGTCGATGTCATTGAGAGTCCTTGACATTCGCCAGATGATGACTATCC	660
Oy		661	TGGTGGAGACCTTTCATGAAAGATCTGCGTCTTTCATCTTTGCTTCGTGATCCCTGTCTCTC	720
Db		661	TGGTGGAGACCTTTCATGAAAGATCTGCGTCTTTCATCTTTGCTTCGTGATCCCTGTCTCTC	720
Oy		721	ATCATCATCTGCTGTCTAACCCTGTATGATCCTGGGTCTCAAAGAGGTCCGGCTCTTTCT	780
Db		721	ATCATCATCTGCTGTCTAACCCTGTATGATCCTGGGTCTCAAAGAGGTCCGGCTCTTTCT	780
Oy		781	GAGTCCCAGAGAAAAGATCGCAACCTGSGTAGATCAACAGACTGTCCTGSGTGGTGTG	840
Db		781	GAGTCCCAGAGAAAAGATCGCAACCTGSGTAGATCAACAGACTGTCCTGSGTGGTGTG	840
Oy		841	GCAGTCTTTCGTCTGTCTGTGAGATCTCCCATTTGCATATTTCAATCTTGATGAGAGCTTCTG	900
Db		841	GCGGTTTTTCGTCTGTCTGTGAGATCTCCCATTTGCATATTTCAATCTTGATGAGAGCTTCTG	900
Oy		901	AGCACTTCCACAGACAGCTGTCTCTCCAGCTATTACTTCTGATGTGCTTAGGCTAT	960
Db		901	AGCACTTCCACAGACAGCTGTCTCTCCAGCTATTACTTCTGATGTGCTTAGGCTAT	960
Oy		961	ACCAACAGTAGCCGTGAATCCCATCTCTAGCGCTTTCTTGATGAAAACTTCAAGCGGTGT	1020
Db		961	ACCAACAGTAGCCGTGAATCCCATCTCTAGCGCTTTCTTGATGAAAACTTCAAGCGGTGT	1020
Oy		1021	TTCCGGGAGCTTCTGCTTCCAATAAGATGAGATGAGAGCGGACAGACCTAGCAGAGTCTC	1080
Db		1021	TTCCGGGAGCTTCTGCTTCCAATAAGATGAGATGAGAGCGGACAGACCTAGCAGAGTCTC	1080
Oy		1081	CGAAATACAGTTCCAGATCTGTCTTAACCTGAGGGACATCCATGGGATGAATAAACCMGTAT	1140
Db		1081	CGAAATACAGTTCCAGATCTGTCTTAACCTGAGGGACATCCATGGGATGAATAAACCMGTAT	1140
Oy		1141	TGA 1143	
Db		1141	TGA 1143	
RESULT 9				
XX	ID	AAT92601	standard; cDNA, 1275 BP.	
XX	AC	AAT92601;		
XX	DT	14-APR-1998	(first entry)	
DE	XX	Human kappa opioid receptor prototype RASSL ORI DNA.		
XX	KW	Selective target cell activation; G protein-coupled receptor; RASSL;		
KW		gene therapy; cell proliferation; kappa opioid receptor; human;		
KW		transgenic animal; arrhythmia; bone disease; seizure;		
KW		vascular contraction; disease model; ss.		
DS	OS	Homo sapiens		
DS		Synthetic.		

OS Chimeric.
XX Key Location/Qualifiers
FH sig_peptide 1..90
FT /*tag= a
FT /product= "prolactin signal sequence"
FT mat_peptide 91..1284
FT /*tag= b
FT /product= "FLAG-modified KOR-HA fusion"
FT misc_feature 702..787
FT /*tag= c
FT /note= "delta opioid receptor sequence"
XX MO9735478-A1.
XX 02-OCT-1997.
XX PF 25-MAR-1997; 97WO-US005334.
XX 26-MAR-1996; 96US-00622348.
XX (RESC) UNIV CALIFORNIA.
XX Conklin BR;
XX WPI, 1997-502739/46.
XX P-PSDB; AAM30299.
XX Selective activation of target cell expressing modified G protein coupled
XX receptor - allows control of cellular proliferation, especially for
XX amplification of transfected cells in gene therapy.
XX Example 1; Page 80-82; 117pb; English.
XX
XX This cDNA sequence encodes RASBL OR1 (see AAM30299) a G protein-coupled
XX receptor that is activated superiorly by synthetic ligands. OR1 comprises
XX human G protein-coupled kappa opioid receptor (KOR) (see also AAM30297)
XX modified at 17 amino acid positions to contain the corresponding amino
XX acid of the delta opioid receptor. The OR1 polynucleotide was obtained by
XX site-directed mutagenesis of native human KOR cDNA (see AAT90998) and
XX includes flanking sequences that encode signal and epitope peptides to
XX facilitate the detection and purification of recombinant OR1. A novel
XX method for selectively activating a target cell (TC) comprises: (1)
XX introducing into the cell a nucleic acid sequence (I) that expresses a
XX RASBL (A) and (II) exposing the transfected cell to small synthetic
XX molecules (B) that bind to and activate (A), inducing the G protein
XX coupled cellular response associated with receptor activation. (A) has:
XX (a) decreased binding affinity for a selected natural ligand of the
XX native receptor; (b) binding affinity for (B); and (c) is activated by
XX binding (B) sufficiently to produce the required cellular response. Also
XX new are: transgenic cells including heterologous (I) in the genome;
XX cellular implants comprising a TC transfected with (I); isolated (I); and
XX transgenic animals expressing (A). Activation of (A) results, in vitro or
XX in vivo, in cellular proliferation, or secretion of a cellular product,
XX particularly a heterologous therapeutic protein encoded by a second
XX inserted nucleic acid sequence. Particularly it is used to expand the
XX relatively few cells that are successfully transfected during gene
XX therapy procedures. Other responses that can be regulated are cell
XX migration and contraction, or pigment production. In transgenic animals,
XX arrhythmia, symptoms of bone disease, seizures, vascular contractions,
XX dementia, neurodegeneration etc., for use as models of these diseases
XX (claimed). The transgenic animals are also used for production of
XX improved food products (e.g. increased calcium content in eggshells or
XX altered fat/lean ratios) or to control fertility or induce labour
XX
XX Sequence 1275 BP; 266 A; 373 C; 318 G; 318 T; 0 U; 0 Other;
XX
XX Query Match 86.7%; Score 1001; DB 2; Length 1275;
XX Best Local Similarity 93.1%; Pred. No. 8.5e-236;
XX Matches 1062; Conservative 0; Mismatches 70; Indels 9; Gaps 1;
XX
XX 2 TGGACTCCCGATCCAGATCTTCGCGGGAGACCGGCGCCCTACCTGCGCGCCGAGCGCCT 61

Db
113 TCGACTCCCGATCCAGATCTTCGCGGGAGACCGGCGCCCTACCTGCGCGCCGAGCGCCT 172
QY 62 GCTGCCCCCAACAGACAGCCGCTGTTTCCCGGTGGGGCGAGGCCGACAGCAAGGCA 121
Db 173 GCTGCCCCCAACAGACAGCCGCTGTTTCCCGGTGGGGCGAGGCCGACAGCAAGGCA 232
QY 122 GCGCCGCTCGAGAGACCGACAGCTGAGCCCGACATCTCCCGGCACTCCCGGTCA 181
Db 223 GCGCCGCTCGAGAGACCGACAGCTGAGCCCGACATCTCCCGGCACTCCCGGTCA 292
QY 182 TCATCAGCGCGGTCTACTCCGTAAGTTCGTGCGGGCTTGGTGGCAACTCGCTGTCA 241
Db 293 TCATCAGCGCGGTCTACTCCGTAAGTTCGTGCGGGCTTGGTGGCAACTCGCTGTCA 352
QY 242 TGTTCGTATCATCCGATACACAAAGATGAAAGACGACCAACATTTACATTTAAC 301
Db 353 TGTTCGTATCATCCGATACACAAAGATGAAAGACGACCAACATTTACATTTAAC 412
QY 302 TGGCTTGGAGAGATGCTTAACTTAAACCATGCGCTTCAAGATAGGTCGCTACTGA 361
Db 413 TGGCTTGGAGAGATGCTTAACTTAAACCATGCGCTTCAAGATAGGTCGCTACTGA 472
QY 362 TGAATTCCTGGCTTTTGGGAGTGTGCTGCAAGATGTAATTTCAATTGATTAACA 421
Db 473 TGAATTCCTGGCTTTTGGGAGTGTGCTGCAAGATGTAATTTCAATTGATTAACA 532
QY 422 ACATTTTACACAGCATCTTACCTTGACCATGATGAGCGTGAACCGCTACATGCGCGT 481
Db 533 ACATTTTACACAGCATCTTACCTTGACCATGATGAGCGTGAACCGCTACATGCGCGT 592
QY 482 GCCACCGCGTGAAGGCTTGGACCTTCGCAACACCTTGAAGGCAAAAGATCATCAATCT 541
Db 593 GCCACCGCGTGAAGGCTTGGACCTTCGCAACACCTTGAAGGCAAAAGATCATCAATCT 652
QY 542 GCATCTGCGCTGTCTGATCTGTTGGCATCTTGCATATGCTTGGAGGACCAAG 601
Db 653 GCATCTGCGCTGTCTGATCTGTTGGCATCTTGCATATGCTTGGAGGACCAAG 712
QY 602 TCAGGAGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 661
Db 713 CCGGGAGTGAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 763
QY 662 GGTGGAGCTCTTATGAAAGATCTGCGTTCATCTTGGCTTGGTATCCGTCCTCA 721
Db 764 ACTGGAGACGTGTACCAAGATCTGCGTTCATCTTGGCTTGGTATCCGTCCTCA 823
QY 722 TCATCATGCTGTCTACACACCTGATGATCTGCGTCTCAAGACGTCGCGCTCTTCTG 781
Db 824 TCATCATGCTGTCTACACACCTGATGATCTGCGTCTCAAGACGTCGCGCTCTTCTG 883
QY 782 GCTCCGAGAGAGATGCAACCTGCGTGAATCAACAGACTGTCGTGTGTGTG 841
Db 884 GCTCCGAGAGAGATGCAACCTGCGTGAATCAACAGACTGTCGTGTGTGTG 943
QY 842 CAGTTTGT 901
Db 944 CAGTTTGT 1003
QY 902 GCACCTCCACAGCAGACGCTCTCTCAGCTATTAATCTTGCATGCGCTTGAAGCTATA 961
Db 1004 GCACCTCCACAGCAGACGCTCTCTCAGCTATTAATCTTGCATGCGCTTGAAGCTATA 1063
QY 962 CCAACAGTAGTCTGATCCATCTCTAAGCTTCTTGTGATGAATACTTCAAGCGGTGT 1021
Db 1064 CCAACAGTAGTCTGATCCATCTCTAAGCTTCTTGTGATGAATACTTCAAGCGGTGT 1123
QY 1022 TCCGGAGCTTCTGCTTTCATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 1081
Db 1124 TCCGGAGCTTCTGCTTTCATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 1183
QY 1082 GAATATAGTTTCAAGATCTGCTTCACTGAGGAGATGATGATGATGATGATGATGAT 1141

Db 1184 GAAATACAGTTCAGATCTGCTTACCTGAGGAGCATGATGATGAATAAACAGATAG 1243
QY 1142 G 1142
Db 1244 G 1244

RESULT 10
AAV49254
ID AAV49254 standard; DNA; 1408 BP.
AAV49254;
AAV49254;
28-OCT-1998 (first entry)
XX Mouse kappa opiate receptor gene.
DE Mouse kappa opiate receptor gene.
XX Mouse; kappa opiate receptor; transgenic animal; mammal; identification;
KW exon; nervous tissue; pain; drug addiction; transplant rejection;
KW immunosuppressant; analgesic; morphine; side effect; ds.
XX
OS Mus sp.
XX Key Location/Qualifiers
FH 184. .1326
FT CDS /tag= a
FT /product= "kappa opiate receptor"

XX W09802534-A2.
XX 22-JAN-1998.
XX 11-JUL-1997; 97WO-FR001282.
XX 15-JUL-1996; 96FR-00008810.
XX (CNRS) CENT NAT RECH SCI.
XX
PI Kieffer BL, Matches HMD, Simonin F, Dierich A, Lemeur M;
XX WPI: 1998-110582/10.
DR P-PSDB; AAM44939.
XX
PT Transgenic animals defective in one type of opioid receptor - used to
PT identify agents for treatment of pain, drug addiction and transplant
PT rejection, lacking side effects of known opiate(s).
XX
XX Disclosure; Fig 13; 58pp; French.
XX
XX This sequence represents the gene encoding the mouse kappa opiate
XX receptor protein. The sequence is used to generate a transgenic non-human
XX mammal for identifying agents for treating disorders associated with
XX opiate receptors. In the mammal, the expression of the gene encoding the
XX opiate receptor is modified, particularly by the deletion of an exon
XX and/or insertion of a marker gene, e.g. the neomycin resistance gene,
XX into the sequence. Especially the expression of the gene is altered in
XX nervous tissue. The agents are potentially useful for treating severe
XX pain (chronic or acute), drug addiction and/or prevention or treatment of
XX transplant rejection (as immunosuppressants). The method may isolate and
XX identify powerful analgesics that lack morphine-like side effects

SO Sequence 1408 BP; 322 A; 359 C; 336 G; 391 T; 0 U; 0 Other;

Query Match 78.9%; Score 910.8; DB 2; Length 1408;
Best Local Similarity 86.8%; Pred. No. 1.3e-213;
Matches 1002; Conservative 0; Mismatches 152; Indels 0; Gaps 0;

QY 1 ATGACATCCCGGATCCAGATCTTCGCGGAGCCGCGGCTTACCTGCGCCCGAGCGCC 60
Db 184 ATGAGTCTCCCGATTCAGATCTTCGAGAGATTCAGGCGCTTACTGCTCCAGTCT 243
QY 61 TGCTGCCCCCAACAGAGCGCTGTTCCTCCGCTGGCGGAGCCCGAGACGAAACGCG 120
||||| ||||||| ||||| ||| ||||||| ||||||| |||

Db 244 TGCTTCTCCCAACAGACGCTTGTGTTCCCACTGGGAGATCCGACGATATGGC 303
QY 121 AGCGCCGCTCGAGAGAGCGCCAGCTGAGAGCCCGCGCATCTCTCCCGCCATCCCGTTC 180
Db 304 AGTGTGGGCTGAGAGATCAGCAGCTGAGTCCGCGCATCTCTCCGCGCATCTCTGTT 363
QY 181 ATCATCAGCGGCTTACTCTCGTAGTGTTCGTGAGGCTTGTGGGCAACTCGGTGCTC 240
Db 364 ATCATCAGCGGCTTACTCTGTGTATTTGTGTGGCTTATGTGGGCAATCTCTGCTC 423
QY 241 ATGTTCTGATCATTCGATACCAAGATGAAGACAGCAACCAATTTACATATTAAAC 300
Db 424 ATGTTGTATCATTCGATACCAAGATGAAGACCGCAACCAATTTACATATTAAAC 483
QY 301 CTGGCTTTGGAGATGCTTTAGTTACTATCAACCATGCCCTTTGAGAGTACGCTACTTG 360
Db 484 CTGGCTTTGGAGATGCTTTAGTTACTATCAACCATGCCCTTTGAGAGTACGCTACTTG 543
QY 361 ATGAATTCCTGGCCCTTTGGGATGTGCTGCAAGATAGTAATTTCCATTGATTTAC 420
Db 544 ATGAATTCCTGGCCCTTTGGGATGTGCTGCAAGATAGTAATTTCCATTGATTTAC 603
QY 421 AACATGTTCAACAGCATCTTCACTTGAACATGAATGAACGCTGACATTTGCCGTG 480
Db 604 AACATGTTCAACAGCATCTTCACTTGAACATGAATGAACGCTGACATTTGCCGTG 663
QY 481 TGCCACCCCGTGAAGGCTTTGAGCTTCGCGCACACCTTTGAAGGCAAGATCATATTC 540
Db 664 TGCCACCCCGTGAAGGCTTTGAGCTTCGCGCACACCTTTGAAGGCAAGATCATATTC 723
QY 541 TGCAATTCGCTGCTGTGCTCATCTGTTGGCATCTCTGCAATGATCTTGGAGGACCAA 600
Db 724 TGCAATTCGCTGCTGTGCTCATCTGTTGGCATCTCTGCAATGATCTTGGAGGACCAA 783
QY 601 GTCAGGGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
Db 784 GTCAGGGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 843
QY 661 TGTGTGGGACCTTTGATGAAGATGCTGCTTCACTTGGCTTCGATATCCGTGCTC 720
Db 844 TGTGTGGGACCTTTGATGAAGATGCTGCTTCACTTGGCTTCGATATCCGTGCTC 903
QY 721 ATCATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Db 904 ATCATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 963
QY 781 GGCCTCCGAGAGAAAGATTCGCAACTGCGTAGATCAACGACTGCTGTGTGTGTG 840
Db 964 GGCCTCCGAGAGAGAAAGATTCGCAACTGCGTAGATCAACGACTGCTGTGTGTGTG 1023
QY 841 GCAATCTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
Db 1024 GCAATCTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1083
QY 901 AGCACTTCCCAACAGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
Db 1084 AGCACTTCCCAACAGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1143
QY 961 ACCAAGATAGCTGAATTCCTGATTCCTGATTCCTGATTCCTGATTCCTGATTCCTG 1020
Db 1144 ACCAAGATAGCTGAATTCCTGATTCCTGATTCCTGATTCCTGATTCCTGATTCCTG 1203
QY 1021 TTCGGGACCTTTCCTTTCCTGATGAAGATGAGATGAGAGCGGAGACATGAGAGTGC 1080
Db 1204 TTTTGGGACCTTTCCTTTCCTGATGAAGATGAGATGAGAGCGGAGACATGAGAGTGC 1263
QY 1081 CGAATATCAAGTTGAGATTCCTGATTCCTGATTCCTGATTCCTGATTCCTGATTCCTG 1140
Db 1264 AGAATACAGATTCCTGATTCCTGATTCCTGATTCCTGATTCCTGATTCCTGATTCCTG 1323
QY 1141 TGACTAGTGTGA 1154
Db 1324 TGACTAGTGTGA 1337

RESULT 11
AA075926 standard; DNA, 1410 BP.
AA075926;
25-MAR-2003 (revised)
17-AUG-1995 (first entry)
Mouse kappa opioid receptor MORK1 cDNA.
Mouse kappa opioid receptor MORK1 cDNA.
Mouse; kappa; delta; mu; opioid receptor; brain; primer; PCR; amplify;
transmembrane domain; somatostatin; receptor; human; expression vector;
truncate; chimeric; assay; probe; ss.
Mus musculus.
Key Location/Qualifiers
FT CDS 186..1328
FT /tag= a
FT /product= "mouse kappa opioid receptor"
MO9428132-A2.
08-DEC-1994.
20-MAY-1994; 94MO-US005747.
20-MAY-1993; 93US-00066236.
30-JUL-1993; 93US-00100694.
05-NOV-1993; 93US-00147592.
(ARCH-) ARCH DEV CORP.
Bell GI, Relaine T, Yasuda K;
WPI, 1995-022804/03.
P-PSDB; AAR67669.
Polynucleotides and peptides derived from opioid receptor polypeptides -
PT for use in therapeutic compositions and in screening assays for useful
PT drug substances.
XX Claim 10; Page 207-211; 300bp; English.
PS The nucleotide sequence of the novel mouse kappa opioid receptor gene
XX MORK1. The gene was isolated from a mouse brain cDNA library using a
XX fragment (amplified from the cDNA library with primers AA075929-30) as a
XX probe. The primers are based on the conserved sequences present in the
XX second and third transmembrane domains of somatostatin (SRII) receptor
XX subtypes SSTR1, SSTR2 and SSTR3. The 1.2 kb part fragment from the mouse
XX kappa opioid receptor clone, lambda mal-1, was subcloned into the CMV
XX promoter-based expression vector pCMV-6b. The resultant construct pCMV-
XX mal-1 was transfected into COS-1 cells for protein production. The gene
XX encoding the opioid receptor can be used to produce complete, truncated
XX or chimeric opioid receptor proteins. The opioid receptors thus produced
XX are useful for the development of novel assays designed to select or
XX improve substances, capable of interacting with the opioid receptor
XX proteins, for use in diagnosis, drug design and therapeutic applications.
XX (Updated on 25-MAR-2003 to correct FN field.)
XX
SQ Sequence 1410 BP; 322 A; 360 C; 337 G; 391 T; 0 U; 0 Other;
Query Match 78.9%; Score 910.8; DB 2; Length 1410;
Best Local Similarity 86.8%; Pred. No. 1.3e-213;
Matches 1002; Conservative 0; Mismatches 152; Indels 0; Gaps 0;
QY 1 ATGAGCTCCCGATCAGATCTTCCGCGGAGCCGGGCTTACCTGCGCCCGGAGCGCC 60
DB 186 ATGAGTCCCGCATTCAGATCTTCCGAGGAGATCCAGGCCCTTACCTGCTCTCCAGTGT 245

QY 61 TGCCTGCCCCCAACAGACGCGCTGTGTTTCCCGGCTGGGCGGAGCCGACAGACGCGC 120
DB 246 TGCCTTCTCCCAACAGACGCGCTGTGTTTCCCGAAGTGGGAGAAATCCGACGTATATGCG 305
QY 121 AGCGCGGCTGGAGAGACGCGACGCTGGAGCCCGGACATCTTCCCGGCAATCCCGGTC 180
DB 306 AGTGTGGGCTCAGAGATCAGACGCTGGAGGTCCGGCGACATCTCTCCGCGCATCCCTGTT 365
QY 181 ATCATCAGCGGCGTCTACTCCGTAAGTGTTCGTCGCGGGGCTGGTGGGCGAACTCGCGTGC 240
DB 366 ATCATCAGCGGCGTCTACTCCGTAAGTGTTCGTCGCGGGGCTGGTGGGCGAACTCTCGGTC 425
QY 241 ATGTTCTGATCATCCGATACACAAAGATGAAGACAGCAACCAATTTACATATTAAAC 300
DB 426 ATGTTCTGATCATCCGATACACAAAGATGAAGACGCGCAACCAATTTACATATTAAAC 485
QY 301 CTGGCTTTGGCAGATGCTTTAGTTACTACACACCATGCCCCCTTTCAGAGTACGCTTACTTG 360
DB 486 CTGGCTTTGGCAGATGCTTTAGTTACTACACCATGCCCCCTTTCAGAGTACGCTTACTTG 545
QY 361 ATGAATTCCTGGCCCTTTGGGGAGTGTGCTGGGCAAGATAGTAAATTTCATTAATAC 420
DB 546 ATGAATTCCTGGCCCTTTGGAGATGTGTATGCAAGATTTGATTCATTAATAC 605
QY 421 AACATGTTACACGAGATCTTCACTTGAACATGATGAGCGTGGACCGCTACATTCGCGTG 480
DB 606 AACATGTTACACGAGATTTACCTTGAACATGATGAGTGTGACCGCTACATTCGCTG 665
QY 481 TGCACCCCGTGAAGGCTTTGGACTTCCGACACCCCTTGAAGGCAAGATCATATATC 540
DB 666 TGCACCCCGTGAAGGCTTTGGACTTCCGACACCCCTTGAAGGCAAGATCATATATC 725
QY 541 TGCATCTGGCTGCTGCTCATCTGTGTGGCATCTCTGCAATGTCTTGGAGGCAACCA 600
DB 726 TGCATTTGGCTTCTGGCATCATCTGTGTATATAGGATGATCTTGGAGGCAACCA 785
QY 601 GTCAGGAAAGACGTGATGTCAATGATGCTCTTGGACAGTTCCAGATGATGACTACTCC 660
DB 786 GTCAGGAAAGATGTGATGTCAATGATGCTCTTGGACAGTTCCAGATGATGATGATGCTC 845
QY 661 TGTGGGACCTTTCATGAAAGATCTGCGTCTTTCATCTTTCCTTGGTATCCCTGCTCTC 720
DB 846 TGTGGGACCTTTCATGAAAGATCTGCGTCTTTCATCTTTCCTTGGTATCCCAAGTCTCTC 905
QY 721 ATCATCATCTGTGCTAACAACCTGATGATCTGCGCTTCAAGAAGCTCCGCTCTTCT 780
DB 906 ATCATCATCTGTGCTAACAACCTGATGATCTGCGCTTCAAGAAGCTCCGCTCTCTCT 965
QY 781 GGCCTCCGAGAAAGATCGCAACCTGGGTAGGATCACAGACTGCTGAGTGGTGTG 840
DB 966 GGCCTCCGAGAAAGATCGCAACCTGGGTAGGATCACAGACTGCTGAGTGGTGTG 1025
QY 841 GCAGTCTTCTGCTGCTGCACTCCCAATTCATCATATTCATCTGAGGAGCTCTGGG 900
DB 1026 GCAAGTCTTCTGCTGCTGCACTCCCAATTCATCATATTCATCTGAGGAGCTCTGGG 1085
QY 901 AGCACTTCCACAGACAGCTGCTTCTTCACGCTTATCTTTCATGCTCTTAAAGCTAT 960
DB 1086 AGCACTTCCACAGACAGCTGCTTCTTCACGCTTATCTTTCATGCTCTTAAAGCTAT 1145
QY 961 ACCAAGATGAGCTGAATCCCATTTCTCAAGCCTTCTTGAAGAAACTTCAAGGGGT 1020
DB 1146 ACCAAGATGAGCTGAATCCCATTTCTCAAGCCTTCTTGAAGAAACTTCAAGGGGT 1205
QY 1021 TTTCCGGAATCTGCTTTCATCTGAAGATGAGATGAGCGGACAGACCTAGCAGATC 1080
DB 1206 TTTAGGAACTTCTGCTTCCATTAAGATGAGAAATGAGCGGACCAATATGAGTT 1265
QY 1081 CGAAATTAAGTTCAGGATCTGCTTACCTGAGGAGCATGATGGATGAATTAACAGTA 1140
DB 1266 AGAAACACAGATTCAGGATCTGCTTCAATGAGATGTGGAGGAGATGAATTAAGCAGTA 1325
QY 1141 TGACTAAGTCGTGGA 1154

Db 1326 TGACTAGTCGTGA 1339

RESULT 12

AA086725
ID AA086725 standard; cDNA; 2481 BP.

AC AA086725;

DT 01-DEC-1995 (first entry)

DE Mammalian kappa opioid receptor protein cDNA.

KM Mammalian kappa opioid receptor; mouse delta opioid receptor; analgesic; amplification; primer; rat; probe; E.coli; RT-PCR; hypnotic compound; ds.

OS Rattus rattus.

Key Location/Qualifiers

FT CDS 111..1253

FT /tag= a

FT /product= "kappa opioid receptor"

PN JP07070191-A.

PD 14-MAR-1995.

PF 30-JUL-1993; 93JP-00190261.

PR 09-JUL-1993; 93JP-00170591.

PA (TAKE) TAKEDA CHEM IND LTD.

DR WPI; 1995-144857/19.

XX P-PsDB; AAR72591.

XX Kappa opioid receptor protein and cells expressing it - useful for the

XX screening of compounds for analgesic and hypnotic properties.

XX Claim 2; Page 9-10; 15pp; Japanese.

XX The nucleotide sequence of the novel mammalian kappa opioid receptor

XX cDNA. The gene was isolated by amplifying a fragment from rat brain mRNA

XX by reverse transcriptase-PCR (RT-PCR) using primers AA086726-7 derived

XX from the mouse delta-opioid receptor gene. This fragment was cloned into

XX the plasmid pCR1 to produce pR1. The plasmid pR1 was used to probe a

XX rat brain DNA library in lambda ZAPII to obtain a clone of the rat kappa

XX opioid receptor gene, designated pKOPR2. This clone was introduced into

XX E.coli JM109 for production of the receptor protein. The receptor protein

XX is useful for screening of analgesic and hypnotic compounds including

XX peptides and proteins

XX Sequence 2481 BP; 629 A; 588 C; 544 G; 720 T; 0 U; 0 Other;

XX Query Match 78.9%; Score 910.8; DB 2; Length 2481;

XX Best Local Similarity 86.8%; Pred. No. 1.6e-213;

XX Matches 1002; Conservative 0; Mismatches 152; Indels 0; Gaps 0;

QY 1 ATGAGCTCCCGGATCCAGATCTTCCGCGGAGACCGGCGCTTACCTGCGCCCGAGCGCC 60

Db 111 ATGAGTCCCGGATCCAGATCTTCCGCGGAGACCGGCGCTTACCTGCGCTCCAGTGTCT 170

QY 61 TGCCTGCCCCCAACAGACGCGCTGTGTTCCCGGCTGGGCGGAGCCGACGACGACGCGC 120

Db 171 TGCCTACTCTCCCAACAGACGCTGTGTTCCCGGCTGGGCGGAGATCGGACGACATGCG 230

QY 121 AGCGCGGCTGGAGACGCGGAGCGCGGAGCGCGGACATCTCCCGGCGATCCCGGCTC 180

Db 231 AGTTGGGCTCCGAGAGACGACGCTGAGCCCGGCGACATCTTCCAGCCTATCCCTGT 290

QY 181 ATCATCAGCGGCTTACTCCGTAGTGTGTCGTGGGCTGGGAGCAATCGCTGTGTC 240

Db 291 ATCATCAGCGGCTTACTCCGTAGTGTGTCGTGGGCTGGGAGCAATCCGTGTGTC 350

QY 241 ATGTCGATCATCCGATACCAAGATGAAGACAGACCAACCATTTACATATTTAAC 300

Db 351 ATGTTGATCATCCGATACCAAGATGAAGACAGACCAACCATTTACATATTTAAC 410

QY 301 CTGGCTTTGGAGATGCTTTAGTTACTCAACCATGCGCTTTCAGAGTACGGTCTACTTG 360

Db 411 CTGGCTTTGGAGATGCTTTAGTTACTCAACCATGCGCTTTCAGAGTACGGTCTACTTG 470

QY 361 ATGAATTCCTGGCTTTGGGAGATGCTGTGCAAGATAGTAAATTTCCATGATTAATAC 420

Db 471 ATGAATTCCTGGCTTTGGGAGATGCTGTGCAAGATAGTAAATTTCCATGATTAATAC 530

QY 421 AACATGTTCAACAGATCTTACCTTGACATGATGAGCGTGGACCGCTTACATTTCCGCTG 480

Db 531 AACATGTTCAACAGATCTTACCTTGACATGATGAGCGTGGACCGCTTACATTTCCGCTG 590

QY 481 TGCCACCCCGTGAAGGCTTTGGAATCCGCAACCCCTTGAAGCAAGATCATATATTC 540

Db 591 TGCCACCCCGTGAAGGCTTTGGAATCCGCAACCCCTTGAAGCAAGATCATATATTC 650

QY 541 TGCACTTGGCTGCTGTCTCATCTGTTGGCATCTCTGCAATATGCTTTGGAGGCCCAA 600

Db 651 TGCACTTGGCTGCTGTCTCATCTGTTGGCATCTCTGCAATATGCTTTGGAGGCCCAA 710

QY 601 GTCAAGGGAAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660

Db 711 GTCAAGGGAAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 770

QY 661 TGTGGGAGCTCTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 720

Db 771 TGTGGGAGCTCTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 830

QY 721 ATCATCATGCTGTCTGATACCTGATGATGATGATGATGATGATGATGATGATGATGATG 780

Db 831 ATCATCATGCTGTCTGATACCTGATGATGATGATGATGATGATGATGATGATGATGATG 890

QY 781 GGCCTCCGAGGAAGATGCAACCTGGTGAAGATCAACAGACTGCTGCTGGTGGTGTG 840

Db 891 GGCCTCCGAGGAAGATGCAACCTGGTGAAGATCAACAGACTGCTGCTGGTGGTGTG 950

QY 841 GCAGCTTCTGCTGTCTGAGCTCCCATTCATTCATTCATTCATTCATTCATTCATTCATTC 900

Db 951 GCAGCTTCTGCTGTCTGAGCTCCCATTCATTCATTCATTCATTCATTCATTCATTCATTC 1010

QY 901 AGCACTTCCACAGACAGCTGCTCTCTCCAGCTATTAATCTTCTGATGCTCTTAGGCTAT 960

Db 1011 AGCACTTCCACAGACAGCTGCTCTCTCCAGCTATTAATCTTCTGATGCTCTTAGGCTAT 1070

QY 961 ACCAACAAGTACGCTGAATCCCATTCCTAGAGCTTCTTGAAGAAAATTGAAGCGGCTGT 1020

Db 1071 ACCAACAAGTACGCTGAATCCCATTCCTAGAGCTTCTTGAAGAAAATTGAAGCGGCTGT 1130

QY 1021 TTCCGGGACTTCTGCTTCACTGAAGATGAGATGAGACGCGCAGAGCATGACAGATC 1080

Db 1131 TTTCAGGACTTCTGCTTCACTGAAGATGAGATGAGACGCGCAGAGCATGACAGATC 1190

QY 1081 CGAATATACATTCAGAGATCTGCTTACCTGAGGAGATGATGAGATGATGATGATGATG 1140

Db 1191 AGAAACACAGTTCAAGATCTGCTTCACTGAGGAGATGATGAGATGATGATGATGATG 1250

QY 1141 TGACTAGTCGTGA 1154

Db 1251 TGACTAGTCGTGA 1264

RESULT 13

AA075931

ID AA075931 standard; DNA; 1000 BP.

XX AA075931;

AC

XX

```
DT 25-MAR-2003 (revised)
DT 18-AUG-1995 (first entry)
XX
DE Human kappa opioid receptor partial cDNA fragment.
XX
KM Mouse; kappa; delta; mu; opioid receptor; brain; primer; PCR; amplify;
KM transmembrane domain; somatostatin; receptor; human; expression vector;
KM truncate; chimeric; assay; probe; ss.
OS
XX Homo sapiens.
FH Key Location/Qualifiers
FT CDS 102..989
FT /tag= a
FT /product= "partial human kappa opioid receptor"
XX
FN W09428132-A2.
XX
PD 08-DEC-1994.
XX
PF 20-MAY-1994; 94WO-US005747.
XX
PR 20-MAY-1993; 93US-00066296.
PR 30-JUL-1993; 93US-00100694.
PR 05-NOV-1993; 93US-00147592.
XX
PA (ARCH-) ARCH DEV CORP.
PI Bell GI, Reisine T, Yasuda K;
XX
DR MPI; 1995-022804/03.
DR P-PSDB; AAR67672.
XX
FT Polynucleotides and peptides derived from opioid receptor polypeptides -
FT for use in therapeutic compositions and in screening assays for useful
FT drug substances.
XX
PS Claim 10; Page 236-239; 300pp; English.
XX
CC The partial nucleotide sequence of the novel human kappa opioid receptor
CC gene. The gene was isolated from a human brain hippocampus cDNA library
CC using a probe from the mouse kappa opioid receptor gene (AA075926). The
CC gene is missing the N-terminal sequence. The C-terminal sequence is very
CC similar to the mouse kappa opioid receptor sequence. Of the C-terminal
CC 293 amino acids, 281 residues are identical and 6 residues have
CC conservative substitutions. The gene encoding the human opioid receptor
CC can be placed in a suitable expression vector for production of the
CC protein in a cell. The opioid receptors thus produced are useful for the
CC development of novel assays designed to select or improve substances,
CC capable of interacting with the opioid receptor proteins, for use in
CC diagnosis, drug design and therapeutic applications. (Updated on 25-MAR-
CC 2003 to correct PN field.)
XX
SQ Sequence 1000 BP; 238 A; 253 C; 225 G; 278 T; 0 U; 6 Other;
Query Match 75.4%; Score 869.6; DB 2; Length 1000;
Best Local Similarity 97.5%; Pred. No. 1.5e-203;
Matches 891; Conservative 0; Mismatches 20; Indels 3; Gaps 1;
QY 244 TTCGTGATCATCGATTACACAAAGATGAGACAGCAACCAATTTACATATTTAAACCG 303
DB 87 TTCCTTTCTTTAGATACCAAGATGAGACAGCAACCAATTTACATATTTAAACCG 146
QY 304 GCTTGGCAGATGCTTTAGTACTACACCAATGCGCTTTAGAGTACGGTCTACTTGATG 363
DB 147 GCTTGGCAGATGCTTTAGTACTACACCAATGCGCTTTAGAGTACGGTCTACTTGATG 206
QY 364 AATTCTGCGCTTTGGGGATGCTGCTGCAAGATAGTAATTTCCATTATTAACAAC 423
DB 207 AATTCTGCGCTTTGGGGATGCTGCTGCAAGATAGTAATTTCCATTATTAACAAC 266
QY 424 ATGTTACACAGATCTTACCTTGACCATGATGAGCGGTGACCGCTACATTCGGGTGC 483
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DB 267 ATGTTACACAGATCTTCACTTTCATCATGATGAGCGTGACCGGTACATTCGGGTGC 326
QY 484 CACCCCGTAAGGCTTTTGAATTTCCGCAACCCCTGAAGGCAAAATCATTAATCTGC 543
DB 327 CACCCCGTAAGGCTTTTGAATTTCCGCAACCCCTGAAGGCAAAATCATTAATCTGC 386
QY 544 ATCTGGCTGCTGCTCATCTTGTGGCAATCTGTGCAATATGATCTTTGAGAGCAACAAGTC 603
DB 387 ATCTGGCTGCTGCTCATCTTGTGGCAATATGATCTTTGAGAGCAACAAGTC 446
QY 604 AGGGAAGAGCTGATGATGATGATGCTCTTTCAGAGTCCAGATGATGATGATGATGATG 663
DB 447 AGGGAAGAGCTGATGATGATGATGATGCTCTTTCAGAGTCCAGATGATGATGATGATG 506
QY 664 TGGGACCTTTTATGAAATCTGCGCTTTCATCTTTGCTTGGTATGATCCCTGCTCATC 723
DB 507 TGGGACCTTTTATGAAATCTGCGCTTTCATCTTTGCTTGGTATGATCCCTGCTCATC 566
QY 724 ATCATGCTGCTGATCACCTGATGATGCTGCTCAAGAGCGCTCGCTCTTTCGAC 783
DB 567 ATCATGCTGCTGATCACCTGATGATGCTGCTCAAGAGCGCTCGCTCTTTCGAC 626
QY 784 TCCCGAGAGAAAGATCGCAACCTGCGTAGAGATCACAGCTGCTCTGCTGCTGCTGCA 843
DB 627 TCCCGAGAGAAAGATCGCAACCTGCGTAGAGATCACAGCTGCTCTGCTGCTGCTGCA 686
QY 844 GTCTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 903
DB 687 GTCTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 746
QY 904 ACCCTCCACAGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 963
DB 747 ACCCTCCACAGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 806
QY 964 AACAGTAGCTGAATCCCATTTCTCTAGCGCTTTCTTGAATGAACCTTCAAGCGGTGTTTC 1023
DB 807 AACAGTAGCTGAATCCCATTTCTCTAGCGCTTTCTTGAATGAACCTTCAAGCGGTGTTTC 866
QY 1024 CGGGACTTCTGCTTTTCCACTGAAGATGAGAGTGAAGCGGACAGCACTTACGAGTCCCA 1083
DB 867 CGGGACTTCTGCTTTTCCACTGAAGATGAGAGTGAAGCGGACAGCACTTACGAGTCCCA 926
QY 1084 AATAAGTTCAAGATCCGCTTACCTGAGGAGCATGATG--GATGAATTAACAGTA 1140
DB 927 AATAAGTTCAAGATCCGCTTACCTGAGGAGCATGATGATGATGAATTAACAGTA 986
QY 1141 TGACTAGTCTGGA 1154
DB 987 TGACTAGTCTGGA 1000
RESULT 14
AAF85416
ID AAF85416 strand; cDNA to mRNA; 2135 BP.
XX
AC AAF85416;
XX
DT 23-JUL-2001 (first entry)
XX
DE Nucleotide sequence of a rat mu-subtype opiate receptor.
XX
KM mu-subtype opioid receptor; G protein; opioid; drug addiction; ss.
XX
OS Rattus rattus.
XX
FH Key Location/Qualifiers
FT CDS 157..1227
FT /tag= a
FT /product= "mu-subtype opiate receptor"
FT /transl_except= (pos: 157..159, aa: Met)
FT /transl_except= (pos: 160..162, aa: Arg)
FT /transl_except= (pos: 163..165, aa: Ser)
FT /transl_except= (pos: 166..168, aa: Glu)
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FT      /transl_except= (pos: 169, .171, aa: Pro)
FT      /transl_except= (pos: 232, .234, aa: Gly)
XX      US6225080-B1.
XX      PD
XX      01-MAY-2001.
XX      PF
XX      28-APR-1995; 95US-00430286.
XX      PR
XX      23-MAR-1992; 92US-00855286.
XX      26-FEB-1993; 93US-00026140.
XX      11-JUN-1993; 93US-00075447.
XX      PA
XX      (UHLG/) UHL G. R.
XX      (EPPL/) EPLER C. M.
XX      (WANG/) WANG J.
XX      PI
XX      Uhl GR, Epller CM, Wang J;
XX      DR
XX      WPI; 2001-342395/36.
XX      P-PSDB; AAB68440.
XX      PT
XX      Novel isolated DNA encoding mu-subtype opioid receptor protein which is
XX      useful for identifying other receptor subtypes, screening for mu opioid
XX      ligands and for understanding mechanisms of opioid action.
XX      PS
XX      Claim 1; Col 17-20; 51pp; English.
XX      CC
XX      The present sequence encodes a rat mu-subtype opioid receptor. The
XX      polynucleotide sequence is useful for producing a mu-type opioid receptor
XX      by standard recombinant techniques. The encoded protein is useful for
XX      producing monoclonal or polyclonal anti-receptor antibodies and to
XX      identify patterns of post-translational modifications and to elucidate
XX      associated G proteins. Mu receptor polynucleotides and polypeptides are
XX      useful in identifying other receptor subtypes, in screening for new
XX      opioid ligands and for understanding mechanisms of opioid action e.g.,
XX      drug addiction
XX      CC
XX      Sequence 2135 BP, 541 A, 590 C, 441 G, 563 T, 0 U; 0 Other;
XX      SQ
Query Match      38.8%; Score 448; DB 5; Length 2135;
Best Local Similarity 67.0%; Pred. No. 8.1e-100;
Matches 669; Conservative 0; Mismatches 320; Indels 9; Gaps 2;
QY      110 ACHGCAACGGCAGCCGCGCTCGAGAGAGCGGAGCGGCGGCACATCTCCCGG 169
DB      167 ACCGCAACCGGCTTGGCGGAGACAGCGCTGCGCTCAGACCGGCGGCTTCATG 226
QY      170 CCATCCCGGTCATCATCAGCGCGGTCTACTCCGTAGTGTTCGTCGCGCTTGGTGGCA 229
DB      227 TCACAGCATTTACATCATGAGCCCTCTACTCTATCGTGTGTAGTGGGCTCTTGGAA 286
QY      230 ACTCGTGTGTCATGTTCGTATCATCCGATACCAAGATGAAAGACAGCAACCAATTT 289
DB      287 ACTTCGCGTCATGTATGTATGTAAATACCAAAATGAAGATGCGCACCAACATCT 346
QY      290 ACATATTATTAACCTGCTTGGCAGATGCTTACTTACTTCAACCAATGCCCCCTTCAAGTA 349
DB      347 ACATTTTCAACCTTGTCTGCGCAGCGCTTACCGACGACGATACCTGCCCTTTCAGAGTG 406
QY      350 CGGTCTACTAGTGAATTCCTGCGCTTTTGGGGATGTGCTGTGCAAGATAGTAATTTCA 409
DB      407 TCAACTACCTGATGGAGAAATGGCCCTTGGAAACATCCCTTCAAGATGTGATCTCAA 466
QY      410 TTGATTACTACCAATGTTCAACAGCATCTTCAACCTTACCAATGATGAGGTGAGCCGCT 469
DB      467 TAGATTACTACCAATGTTCAACAGCATATTCACCCCTGACACATGAGGTGAGCCGCT 526
QY      470 ACATTGCGGTGCGCAACCGCGTGAAGGCTTGGACTTCGACACACCTTGAAGCAAGA 529
DB      527 ACATTGTGTCTGCGCAACCGCGTGAAGGCTTGGACTTCGACACACCTTGAAGCAAGA 586
QY      530 TCATCAATATCTGATCTGCTGTGTGTATCTGTGTGCAATCTCTGCAATAGTCTTGG 589

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DB      587 TCGTCAACGTCTGCAACGTGATCTCTCTCTGTCATCGGCTGCTGTAATGTTCAATGG 646
QY      590 GAGGCAACCAAGTACGAGGAAGAGCTGCATGTCTTAGTGTCTCTTGCAGATTTCCAGATG 649
DB      647 CAACCAACAAATATACAGCAGAGGGTC-----CATGATGACCTTCAAGCTTCCACC 700
QY      650 ATGACTACTCTCTGTGGGACCTCTTTCATGAAGATCTGCTGTCATCTTGGCTTCTGTA 709
DB      701 CAACCTGTACTGAGAAACCTGCTC---AAATCTGTGTTTATCTTGGCTTTCATCA 757
QY      710 TCCCTGTCTTCATCATCATGCTCTGTACACCTTGATGATCTGCTCTCAAGCGCTCC 769
DB      758 TGCCGCTCTCATCATCATCATCTGTGTGTACGGCTGATGATCTTACGACTCAAGAGCGTTC 817
QY      770 GGCCTCTTTCGTGCTCCCGAGAAAGAAATGCGCAACCTGCGATGATACCAAGACTGGTCC 829
DB      818 GCATGCTATCGGGCTCCAAAGAAAGACAGAAATCTGCGAGATCACCCGATGGTGC 877
QY      830 TGTGTGTGTGGGAGTCTGCTGCTGTGTGAACTCCCATTCACATATTCATCTGTGTTG 889
DB      878 TGTGTGTGTGGGAGTCTGATTTATGCTGTGTGTGAGCCCATTCACATCATGTCATCA 937
QY      890 AGGCTTGGGAGGACCTCCACAGCACAGCTGCTCTCCAGCTATTAATCTTGCATCG 949
DB      938 AAGCGCTGATCAGATTCAGAAACCAATTTAGACCGCTTCTGCGCACTTGCATTTG 997
QY      950 CCTTAGGCTATACCAACAGTATGCGTGAATCCCATTTCTAGCCCTTCTGATGAAACT 1009
DB      998 CTTGGGTTTACACGAACAGCTGCTCGTAATTCAGTTCTTTAGCGCTTCTGATGATAAACT 1057
QY      1010 TCAAGCGGTGTTTCCGGACTTCTGCTTTCCATGAAAGATGAGATGGAGCGGAGACA 1069
DB      1058 TCAACGATGCTTACAGAAAGTTTGTGATCCCAACCTGTCCACATCGAAGCAAAAAT 1117
QY      1070 CTAGCAGATCCGAATACAGTTACAGATCTCTGCTTAC 1107
DB      1118 CCATCTGAGTCCGTCAGAAACATGAGGAACATCCCTCC 1155

RESULT 15
AA089222
ID      AA089222 standard; cDNA, 1618 BP.
XX
XX      AA089222;
AC      25-MAR-2003 (revised)
DT      20-OCT-1995 (first entry)
XX
XX      Rat mu opioid receptor cDNA.
DE      Mu opioid receptor; MOR-1; gene therapy; diagnostic; ss.
XX
XX      Rattus sp.
OS
XX
XX      Key Location/Qualifiers
FH      CDS 214..1410
FT      /*tag= a
XX
XX      WO9507983-A1.
XX      23-MAR-1995.
XX      13-SEP-1994; 94WO-US010358.
XX      13-SEP-1993; 93US-00120601.
XX      (INDV ) UNIV INDIANA FOUND.
XX      PA
XX      Yu L;
XX      WPI; 1995-131351/17.
XX      P-PSDB; AAR71964.
DR

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QY 170 CCATCCGGGTCATCATCAGGCGGCTCTACCTCGTAGTGTGCTGGGCTTGGTGGCA 229
DB 410 TCACAGCATTCATCATCATGAGCCCTTACTATCTATGCTGTGTGTGGGCTCTTGGAA 469
QY 230 ACTGCGTGTGATGTTGCTGATTCATCCGATACACAAAGATGAAGACAGCAACCAATTT 289
DB 470 ACTTCGTGTGATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 529
QY 290 ACATATTTAACCTGGCTTGGGAGATGTCTTGTAGTACTACAAACATGCGCTTTCAGAGTA 349
DB 530 ACATTTTAACTTCTCTGGGAGACGCTTGTAGCAACAGTACACTGCGCTTTCAGAGTG 589
QY 350 CGGTCTACTGTAGTAATTCCTGGCCTTTTGGGAGATGTCTGTGCAAGTATGATTTTCA 409
DB 590 TCACTTACTCTGATGGGAACATGGCCCTTCGGAAACATCTCTGCAAGATGTGTGTGTCA 649
QY 410 TTGATTTACTACAACTGTTCACAGCATCTTCACTTACACATGTATGAGCGTGAACGCT 469
DB 650 TAGATTACTACAACTGTTCACAGCATATTCACCTCTGCAACATGAGCGTGAACGCT 709
QY 470 ACATTGCGGTGTGACCCCGTGAAGGCTTGTGACCTTGCACACCTTGAAGGCAAGA 529
DB 710 ACATTTCTGTCTGTGACCCAGTCAAGCCCTGTGATTCCTGTACCCCGAATATGCAAAA 769
QY 530 TCATCAATATCTGATCTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 589
DB 770 TGTCTAAGCTGTGCAACTGTGATCTCTCTCTGTGCACTGTGTGTGTGTGTGTGTGTGT 829
QY 590 GAGGACCAAAATCAGGGAAGACGTGATGTGATGTGAGTGTCTTGTGACCTTCCAGATG 649
DB 830 CAACACCAAAATACAGGAGGAGGCTC-----CATGATTTGACCTTCACTTCTCCACC 883
QY 650 ATGACTACTCTGTGTGAGACTCTTTCATGAGATGTGCTGTCTTCACTTGTGCTGTGA 709
DB 884 CAACCTGTGATCTGTGAGAACTGTCTC---AAATCTGTGTCTTGTATCTTGTGTGTGTCA 940
QY 710 TCCCTGTCTCTCATCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 769
DB 941 TCCCATCTCTCATCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1000
QY 770 GGTCTCTTCTGTGCTGTGAGGAGAAAGATCGCAACCTGTGTGTGTGTGTGTGTGTGTGT 829
DB 1001 GATGTGTATCTGTGCTGTGAGGAGAAAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1060
QY 830 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 889
DB 1061 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1120
QY 890 AGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 949
DB 1121 AAGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1180
QY 950 CCTTAGCTATATCAACAGTAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1009
DB 1181 CTTTGGGTATACAGAACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1240
QY 1010 TCAAGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1069
DB 1241 TCAAGGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1300
QY 1070 CTAGCAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1107
DB 1301 CCACTGAGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1338

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RESULT 17
 ID AAAS9499
 XX AAAS9499 standard; cDNA; 1618 BP.
 AC AAAS9499;
 XX
 DT 14-NOV-2000 (first entry)

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XX DE cDNA encoding a mu opioid receptor polypeptide.
XX mu opioid receptor; transcription regulatory polypeptide;
XX opiod receptor-like polypeptide; ss.
XX Rattus sp.
XX Key Location/Qualifiers
XX CDS 214..1410
XX FT /*tag= a
XX FT /product= "mu opioid receptor (AAB07864)"
XX FT 339..1235
XX CDS /*tag= b
XX /note= "alternative reading frame which encodes a
XX polypeptide (AAB07865) with a zinc finger motif"
XX
XX US6103492-A.
XX
XX 15-AUG-2000.
XX
XX 07-JUL-1997; 97US-00889108.
XX
XX 08-MAR-1993; 93US-00056886.
XX 13-SEP-1993; 93US-00120601.
XX 13-SEP-1994; 94US-00305518.
XX
XX (INDV ) UNIV INDIANA.
XX
XX Yu L;
XX
XX MPI: 2000-542550/49.
XX P-PSDB; AAB07864, AAB07865.
XX
XX Novel nucleic acids encoding mu opioid receptor for expressing large
XX quantities opiod receptors which are useful for screening and evaluating
XX subtype-selective drugs and as probes or primers.
XX
XX Example 1; Col 89-92; 86pp; English.
XX
XX The present sequence encodes a mu opioid receptor protein. The
XX specification also describes a transcription regulatory polypeptide and
XX an opiod receptor-like polypeptide. Human mu opiod receptor, which may
XX polynucleotides are useful as a source of probes and primers, which may
XX be used as diagnostic tools to detect normal and abnormal DNA sequences
XX in DNA derived from patients cells. They are also used as a means for
XX detecting and isolating other members of the polypeptide family and
XX related polypeptides from a DNA library potentially containing such
XX sequences. The polynucleotide is used for preparing large quantities of
XX opiod receptor which on expression in microorganism can be useful for
XX evaluating subtype-selective drugs
XX
XX Sequence 1618 BP; 390 A; 486 C; 370 G; 372 T; 0 U; 0 Other;
XX
XX Query Match 38.7%; Score 446.4; DB 3; Length 1618;
XX Best Local Similarity 66.9%; Pred. No. 1.8e-99;
XX Matches 668; Conservative 0; Mismatches 321; Indels 9; Gaps 2;
XX
QY 110 ACAGCAAGGAGGAGCGCGGCTCGGAGAGCGGAGCTGTGAGCCCGGACATCTCCCGG 169
DB 350 ACCGCAAGCGGCTTGGCGGGAACAGACCTGTGTGCTTCAACCGGAGCCCTTCCATGG 409
QY 170 CCATCCGGGTCATCATCAGGCGGCTCTACCTCGTAGTGTGCTGGGCTTGGTGGCA 229
DB 410 TCACAGCATTCATCATCATGAGCCCTTACTATCTATGCTGTGTGTGGGCTCTTGGAA 469
QY 230 ACTGCGTGTGATGTTGCTGATTCATCCGATACACAAAGATGAAGACAGCAACCAATTT 289
DB 470 ACTTCGTGTGATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 529
QY 290 ACATATTTAACCTGGCTTGGGAGATGTCTTGTAGTACTACAAACATGCGCTTTCAGAGTA 349
DB 530 ACATTTTAACTTCTCTGGGAGACGCTTGTAGCAACAGTACACTGCGCTTTCAGAGTG 589

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QY	CGGTACTCTTGATGAATTCCTGGCCCTTTGGGGATGTGCTGGCAAGATGATTAATTC	409
Db	580 TCACTTACTCTGATGGGAACATGGCCCTTCGGAACCATCTCTGGCAAGATGATTA	649
QY	410 TTGATTACTACACATGTTTCCACAGCATCTTCACTTGCATCGATGAGCGTGACCGCT	469
Db	650 TAGATTACTACACATGTTTCCACAGCATTAATTCACCTCTGCACCATGAGCGTGACCGCT	709
QY	470 ACATTGGCGTGTGCCACCCCGTGAAAGGCTTTGGACTTCCGACACCCCTTGAAAGGC	529
Db	710 ACATTGGCTGTGCCACCCAGTCAAAAGCCCTCGAATTTCCGTATCCCCCGAAATG	769
QY	530 TCATCAATATATCGCATCTGGCTGCTGTGTATCTGTTGGCATCTCTGCAATAGTCCTTG	589
Db	770 TCGTAAAGCTGTGCACCTGATCTCTCTCTTCTGCGCATGGCTGTGCTGTGAATGTTCA	829
QY	590 GAGGCACCAAAAGTCAAGGAGACGTCGATGATTTAGTAGTGCTCTTGGCAGTTCC	649
Db	830 CAACCAACAAATACAGGACGGGGTC-----CATGATTTGCACCTCAAGTTCTCC	883
QY	650 ATGATTACTCTCTGTGGGACCTCTTCAATGAGATCTGGCTTTCAATCTTTGCTTC	709
Db	884 CAACCTGGTACTGGGAGAACTGCTC-----AAATCTGTGTCTTTATCTTCGCTT	940
QY	710 TCCCTGTCTCTATATATCATCGTCTGTCTACACCTGATATATCTGGGTCTCA	769
Db	941 TGGCGATCTCTATATATCACTGTGTATAGGGCTGATATCTTACGACTCAAGAG	1000
QY	770 GAGCTCTTTCGTGGCTCCCGAGAAAGATCGCAACCTGGGTAGGATTCACCA	829
Db	1001 GCATGCTATCGGGCTCCCAAGAAAAGACAGAAATCTGGGACGATCACCGGAT	1060
QY	830 TGTGTGTGTGGCACTCTTTCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	889
Db	1061 TGT	1120
QY	890 AGGCTCTGTGGGAGACCTTCCACAGCACAGCTGCTCTTCCAGCTATTA	949
Db	1121 AAGCGCTATATCAAGATTCAGAAACCAATTCAGACCGTTTCTGGGACCTT	1180
QY	950 CCTTAGGCTATATCAACAGTAGCTGAATCCCATCTCTAGACGCTTTCTTGAT	1009
Db	1181 CTTTGGGTTTACAGAACAGCTGCTGTATTCAGTTCTTTAGCGCTTCTTGAT	1240
QY	1010 TCAACGGGTGTTTCCGGGACTTCTGTCTTCCATGAAATGAGATGAGACGG	1069
Db	1241 TCAACGATGCTTCAAGAGGTTCTGTGATCCCAACTCGTCCACGATCGAA	1300
QY	1070 CTAGCAGATCCGAAATACAGTTCCAGATCTCTGTAC	1107
Db	1301 CCATCTGAGTCCGTGAGAACATTAAGGAAATCCCTTC	1338

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RESULT 18
AAQ79199
ID AAQ79199 standard; cDNA, 2070 BP.
XX
AC
XX AAQ79199;
XX
DT 25-MAR-2003 (revised)
DT 19-APR-1995 (first entry)
XX
DE Rat mu-subtype opioid receptor cDNA.
XX
KW Mu-subtype opioid receptor; MSOR; drug addiction; ds.
XX
OS Rattus rattus.
XX
FH Key
FT CDS
FT
FT /product= "Mu-subtype_opioid_receptor"

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XX	EP612845-A2.
PN	
XX	
PD	31-AUG-1994.
XX	
PF	09-FEB-1994; 94EP-00101968.
XX	
PR	26-FEB-1993; 93US-00026140.
XX	
PA	(AMCY) AMERICAN CYANAMID CO.
PI	
Pt	Eppler CM, Shieh H, Zysk JR, Corbett MJ;
PT	
XX	
DR	WPI, 1994-265963/33.
DR	P-P8DB; AAR65188.
CC	
CC	Pure mu-type opioid receptor protein - and nucleic acid coding for it.
PS	Claim 1, Fig 11, 39pp; English.
XX	
CC	AAR65188 is the rat mu-subtype opioid receptor protein purified from rat
CC	brain membranes, with biotinyl-b-endorphin (AAR5666) as its ligand. It
CC	is encoded by the nucleotide sequence AAQ7919 which was synthesized
CC	using AAQ71022 and AAQ71023 as PCR primers. AAR65188 is useful for
CC	identifying other receptor subtypes' for screening new opioid ligands,
CC	and for studying mechanisms of opioid action, e.g. drug addiction.
CC	(Updated on 25-MAR-2003 to correct PN field.)
SQ	
	Sequence 2070 BP; 526 A; 564 C; 423 G; 557 T; 0 U; 0 Other;
Query Match	38.4%; Score 443.4; DB 2; Length 2070;
Best Local Similarity	66.6%; Pred. No. 1.1e-98;
Matches	668; Conservative 0; Mismatches 326; Indels 9; Gaps 2;
OY	105 GCCCGACGACAGCAGCGAGCGGGCTGGAGAGACGGCAGGTGGAGCCCGGCACATCTC 164
Db	97 GTCTGAACCGACCGGGCTTGGCGGAAACGACAGCTTGCCCTCAAGACCAGCATCTTC 156
OY	165 CCCGCCATCCCGGTCAATCACGGCGGTACTCCGTAGTGTTCGTGGGCTTGGT 224
Db	157 CATGGTCAACGACATTACCATCATAGCGCCCTCTACTCTATCGTGTGTAGTGGGCTCTT 216
OY	225 GGGCAATCGTGGTCACTGTTCTGTGATCATCCGATACCAAAGATGAAGACGACAACCA 284
Db	217 CGAAAACCTCTCGTGCATGTATGTATGTGAATACCAAAAATGAAGACTGCCAACAA 276
OY	285 CATTACATATTTTAACCGTGGCTTTGGCGAGATGCTTAGTACTCAACATGACCCCTTCA 344
Db	277 CATCTACATTTTCAACTCTGCTTGGCGAGACGCTTAGCGACAGTACACTGCTCTTCCA 336
OY	345 GAGTACGGTCTACTTGTATGAATTCCTGGCCCTTTTGGGGATGTCGTGCAAGATAGTAT 404
Db	337 GAGGTCAACGACCTGATGGGAATAGGCCCTTGGAAACATTCCTGTGCAAGATGTGAT 396
OY	405 TTCAATTGATTACTACCAACATGTTCCACGATCTTCACTTGAACATGATGAGCGTGA 464
Db	397 CTCAATGATTACTACCAACATGTTCCACGATATTCACCTCTGCAACATGAGCGTGA 456
OY	465 CGCGTACATTGGCGGTGGCCACCCCGTGAAGGCTTTGGACCTTGGCACACGCTTGAAGGC 524
Db	457 CGCGTACATTGGCTGTGGCCACCCGATGAAGCCCTGTGATTTCCGTACCCCCGAAATGC 516
OY	525 AAAGATCATCAATAATCTGCATCTGTGCTGTGTCATCTGTGGCATCTCTGCATATAGT 584
Db	517 CAANAATGTCACAGCTGTGCAACTGTGATCTCTCTTGGSCATGGGTCTGCTGAATGTT 576
OY	585 CCTTGAAGGACCAAAAGTCAGGGAAGAAGCTGATGTCAATTGATGCTCTTGCAGTTGCC 644
Db	577 CATGGCAACCACAAAAAATACAGGCGAGGGGTCC-----ATNATGTGCAACCTTCACGTTCTC 630
OY	645 AGATGATGATCACTACCTCGGTGGGACCTTTCATGAAGATCTGCGCTTCATCTTGGCTT 704
Db	631 CCACCCAACTGTGTACTGGGAACTGTGCT--AAATCTGTGTCTTTATCTTGGCTTT 687

Qy 872 ACATATTCATCTGCTGGAGGCTCTGGGGAGACCTCCACAGACAGCTGCTCTCCA 931
Db 890 ACATTTAGCTATCATTTAAAGCTTGGTTTCAATCCAGAAACTGTTCCAGACTGTT 949
Qy 932 GCTATTACTTCTGCATGCGCTTAGGCTATACCAAGTAGCCTGAATCCATTCTTAG 991
Db 950 CTGGCAGCTTCTGCATGCTCTAGGTTACACAAACAGCTGCTCAACCCAGTCTTTATG 1009
Qy 992 CTTTCTTGATGAAACCTTCAAGCGGTGTTCCGGGACTTCTCTCTTCCACTGAAGATGA 1051
Db 1010 CATTTCTGATGAAACTTCAACGATCTTCAGAGAGTCTGTATCCCAACTCTTTCGA 1069
Qy 1052 GGATGACGGGACAGCACTAGACAGTCCGAAATA 1087
Db 1070 ACATGAGCAACAAACCTCACTGGAATTCGTGAGA 1105

RESULT 21
ABS54813
ID ABS54813 standard; cDNA; 1245 BP.
XX
AC ABS54813;
XX
DT 11-DEC-2002 (first entry)
XX
DE cDNA encoding human mu2 opioid receptor fused to mu1 2KB sequence.
XX
KW Human; mu1; opioid receptor; gene; ss; morphine; receptor;
KW intracellular calcium.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 1..1245
FT /"tag= a
FT /product= "Mu1/mus opioid receptor fusion protein"
FT /transl_except= (pos:1185..1187,aa:Leu)
XX
XX W0200268594-A2.
XX
XX 06-SEP-2002.
XX
XX 22-FEB-2002; 2002MO-US005452.
XX
XX 22-FEB-2001; 2001US-0270479P.
XX PR 05-DEC-2001; 2001US-0336677P.
XX
XX (RESU-) RES FOUND SUNY.
XX
XX Cadet P, Stefano GB;
XX
XX WPI: 2002-706977/76.
XX P-PSDB; AB932260.
XX
XX New isolated nucleic acid molecule encoding a polypeptide having mu3
XX PT opiate receptor activity, useful as research tools for exploring the
XX PT interactions, molecular mechanisms and relationship of morphine with the
XX PT mu3 opiate receptor.
XX
XX Claim 5; Page 29-30; 52pp; English.
XX
XX This invention relates to a novel nucleic acid molecule encoding a
XX CC polypeptide having mu3 opiate receptor activity. Mu opioid receptors
XX CC exhibit a high binding specificity for morphine. The invention also
XX CC comprises a method for identifying a mu3 opiate receptor agonist or
XX CC antagonist. The nucleic acids and polypeptides of the invention are
XX CC useful as research tools for exploring the interactions of morphine
XX CC with the mu3 opiate receptor, the molecular mechanisms by which morphine
XX CC induces intracellular calcium concentration changes and the relationship
XX CC of mu3 opiate receptors with other mu opioid receptors. They are also
XX CC useful for identifying a mu3 opiate receptor agonist or antagonist. The

CC Present sequence represents a cDNA sequence encoding human mu1/mu2 opioid
CC receptor fusion protein of the invention
XX
SQ Sequence 1245 BP; 308 A; 356 C; 248 G; 333 T; 0 U; 0 Other;
Query Match 37.7%; Score 434.8; DB 6; Length 1245;
Best Local Similarity 66.3%; Pred. No. 1,2e-96;
Matches 660; Conservative 0; Mismatches 327; Indels 9; Gaps 2;
Qy 92 CCGGCTGGGCGGAGCCGAGACGACGCGCGGCTGGAGAGACGCGCACTGAGC 151
Db 125 CCGAGCCATGCGGCTCCGAGCCGACCGACCTGGGGCGGAGAGACAGCTGCGCTCCGA 184
Qy 152 CCGGCGACATCTCCCGGCGCATCCGGTCAATCAACGGGGGTCTACTCCGTAGTGTTCG 211
Db 185 CCGGCACTCCCTCCATGATACCGGCAATCAAGATCAATGCGCTCTACTCATGCTGTGCG 244
Qy 212 TCGTGGGCTTGTGGGCACTCGCTGGTCAATGTTCCGATCATCCGATACACAAAGATGA 271
Db 245 TGGTGGGGGCTCTTGGGAACTTCTGCTCATGATGATGATGATGATGATGATGATGATG 304
Qy 272 AGACAGCAACCAACATTTACATATTTAACCTGCTTTGGCAGATGCTTTAGTTACTACAA 331
Db 305 AGACTGCCAACCAATCTACATTTTCAACCTTGCTGCGCAGATGCTTAGCCACACGTA 364
Qy 332 CCAAGCCCTTTCAGAGTACGCTACTGTATGAAATTCCTGGGCTTTTGGGGATGCTGT 391
Db 365 CCGTCCCTTTCAGAGTACGCTACTGTATGAAATTCCTGGGCTTTTGGGGATGCTGT 424
Qy 392 GCAAGATGATTAATTTCAATGATTTACTACAACTGTTCAACAGATCTTACCTTGACCA 451
Db 425 GCAAGATGATGATCTCATGATTTACTATATGTTACAGATGTTACAGCATATTCACCTT 484
Qy 452 TGATGACGGTGAACCGCTACATTTGCGTGGCCACCCCGTGAAGGCTTTGACTTCGCA 511
Db 485 CCAATGAGTGTGATTCATATTCATTCAGCTGCGACCCCTGCAAGGCTTTAGATTCGTA 544
Qy 512 CACCTTGAAGGCAAGATCATCAATATGATGATGCTGCGCTGCTGATCATGCTTGGA 571
Db 545 CTCGCCGAAATGCGAAATTTATCAATGCTGCAACTGATATCTCTTTAGCCATTTGTC 604
Qy 572 TCTCTGCAATAGTCTTGGAGGACCAAAAGTCAAGGAGACGTGATGATTTAGTGTCT 631
Db 605 TTCCTGTAATGTTCAATGCTGTAACAACAAATACAGGCAAG-----TTCATATGATTTGA 658
Qy 632 CCTTGCAGTTCCAGATGATGACTACTCTGCTGGGACCTCTTATGAAGATGCTGCT 691
Db 659 CACTAACATTTCTCATTCACACCTGGTACTGGGAAACCTGCG---TGAAGATCTGTGTT 715
Qy 692 TCATCTTTCGCTTCGATCCGTCCTCATCATCATGCTGCTTACACCCGATGATGATCC 751
Db 716 TCATCTTTCGCTTCATTAATGCTGCTCATCATCATTAACGCTGTGCTATGAGATGATCT 775
Qy 752 TCGCTCAAGAGCGTCCGCTCTTCTGAGCTCCGAGAGAAAGATCGCAACTGCGTA 811
Db 776 TCGGCTCAAGAGTCCGCTCATGCTCTCTGCTCCAAAGAAAGGACAGAAATCTTCGAA 835
Qy 812 GGATACCAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 871
Db 836 GGATACCAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 895
Qy 872 ACATATTCATCTGCTGGAGGCTCTGGGAGACCTCCACAGACAGCTGCTCTCTCA 931
Db 896 ACATTTAGCTATCATTTAAAGCTTGGTTTCAATCCAGAAACTGTTCCAGACTGTT 955
Qy 932 GCTATTACTTCTGCATGCGCTTAGGCTATACCAAGTAGCCTGAATCCATTCTTAG 991
Db 956 CTGGCAGCTTCTGCATGCTCTAGGTTACACAAACAGCTGCTCAACCCAGTCTTTATG 1015
Qy 992 CTTTCTTGATGAAACCTTCAAGCGGTGTTCCGGGACTTCTCTCTTCCACTGAAGATGA 1051
Db 1016 CATTTCTGATGAAACTTCAACGATGCTTCAGAGAGTCTGTATCCCAACTCTTCTCA 1075

Qy	392	CGAAGATGTATTTCCATTTATTAATTAATTAACAATGTTACAGAGATCTTCACTTTGACCA	451
Db	637	GCAAGATATGTATCTCCATAGATTAATAATATTTTCAACGAAATTTCAACCTCTTGCA	696
Qy	452	TGATAGCGGTGAGACCGGTACATTTGCCGTGTGCCACCCCGTGAAGGCTTTGACCTTCCGCA	511
Db	697	CCATGAGTGTGATGATACATATGCAAGTCTGCAACCTGTACAGGCGCTTAATTTCCGTA	756
Qy	512	CACCTTTGAAGGCAGAAAGATCATCAATATCTGCATCTGGCTGTGTGTCATCTGTTGGCA	571
Db	757	CTCCCCGAAATGCCCAAAATTAATCAATGCTGCACTGGATCTCTCTTTCAAGCAATTTGTC	816
Qy	572	TCTGTCAATATGCTCTTTGAGGCAACAAAGTACAGGGAAGACGTGCATGTCATTTGATGTC	631
Db	817	TTCTGTATATGTCATATGCTACACAAATTAACGGCAAG-----TTCCATATAGTTGA	870
Qy	632	CCTTGCACTTCCAGATATGACTAATCTCCTGTGTGGACCTCTTCAATGAAGATCTGCTCT	691
Db	871	CACTAACATTTCTCTATCCACACTGTGATCTGGGAAACCTCG--TGAAGATCTGTGTT	927
Qy	692	TCATTTTGGCTTGTGTGATTCCTGTCCATCATGATGTCGTGCTACACCGTATGATCC	751
Db	928	TCATTTTGGCTTCTTAATATGCAAGTCTCATATTAACGTGTGCTATATGACCTGATGATCT	987
Qy	752	TGCGTCTCAAGAGCGTCCGCGCTCTTTGTGCTCCGAGAGAAAGATGCAACTTGCGTA	811
Db	988	TGCGCTCAAGAGTGTCCGCAATGCTCTCTGCTCCAAAGAAAGACAGGAATTTTCGAA	1044
Qy	812	GGATTCACAGACTGCTCTGTGTGTGTGTGGCAATCTTGTGTCTGTGTGACTCCCATTC	871
Db	1048	GGATTCACAGAGTGTGTGTGTGTGTGGTGTGTGTATCATGCTGTGTGGAATCTCCATTC	1107
Qy	872	ACATATTCATCTGTGTGAGGCTCTGGGGAAGCACCTCCACAGCAACAGCTGCTCTTCCA	931
Db	1108	ACATTTAGTATCATTAAGCTTTGTTTACAATCCAGAAACATACGTTCCAGACTGTTT	1167
Qy	932	GCTATTAATTTGTGCATGTGCTTAAGGCTATTAACCAACATGATGCTGAATCCATTTCTTACG	991
Db	1168	CTTGACATTTGTGCATGTGCTCTCAAGGTATACAAACAGCTGCTCAACCAAGCTCTTTATG	1227
Qy	992	CCTTCTCTGATGAAAACTTCAAGCGGTGTTTCCGGAACCTTGTGCTTTCACTGAAGATGA	1055
Db	1228	CATTTCTGGAATGAATACTTCAACAGATCTCTTCAAGAGATTTCTGTATCCCAACTCTTCCA	1287
Qy	1052	GGATGAGCGGAGAGACATGACAGATGTCGAAATA	1087
Db	1288	ACATTTGAGCAACAAATCTCACTCCAAATTCGTCACA	1323

RESULT	27
AAV61995	
ID	AAV61995 standard; cDNA; 2162 BP.
XX	
XX	AAV61995;
XX	
D7	11-JAN-1999 (first entry)
XX	
DE	Human mu-opioid receptor cDNA variant 11.
XX	
KM	Mu-opioid receptor; variant; polymorphism; mutant; detection; disease
KM	predisposition; addiction; analgesic; anaesthetic; anti-addictive;
KM	psychopharmaceutical agent; diagnostic; side effect; drug; opiate;
KM	cocaine; inherited alcoholism; human; ss.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
FX	
FX	Key
FX	CDS
FX	Location/Qualifiers
FX	213..2040
FX	/*tag= a
FX	/product= "mu-opioid receptor"
FX	502..503
FX	misc feature

FT	/*tag=	b	
FT	/note=	"Site of intron 1"	
FT		855..856	
FT	/*tag=	c	
FT	/note=	"Site of intron 2"	
FT		1376..1377	
FT	/*tag=	d	
FT	/note=	"Site of intron 3"	
FT		1613	
FT	/*tag=	e	
FT	/note=	"Wild type G is replaced by C"	
PN			
XX	W09833937-A2.		
XX			
XX	06-AUG-1998.		
PD			
XX			
PF	02-FEB-1998;	98WO-DE000382.	
XX			
PR	03-FEB-1997;	97DE-01003925.	
XX			
PA	(DELBL-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.		
PI			
XX	Hoehle M, Wendel B;		
DR			
XX	WPI; 1998-437487/37.		
PT			
PT	New genomic and cDNA sequences encoding human mu-opioid receptor - used,		
PT	e.g. to predict pre-disposition to addiction and for development of		
PT	analgesics, anaesthetics and anti-addiction agents.		
XX			
PS	Claim 8; Page; 26pp; German.		
XX			
CC	This sequence encodes a novel human mu-opioid receptor in which a G		
CC	nucleotide at position 1613 of the wild-type sequence represented in		
CC	AAV61984 is replaced by a C. The wild type receptor and its variants,		
CC	polymorphisms and mutants are used in a method for detecting		
CC	predisposition to disease, particularly addictive disease, by isolating		
CC	cDNA from a sample, genotyping selected positions and comparing with a		
CC	reference DNA. Such sequences are used to develop analgesic, anaesthetic,		
CC	anti-addictive and psychopharmaceutical agents, to construct genes and		
CC	vectors, particularly for pharmaceutical development, to develop		
CC	diagnostic kits for predicting risk of addiction, response to analgesics		
CC	or anaesthetics, or development of side effects from a drug. Particular		
CC	applications are to determine risk of addiction to opiates or cocaine, or		
CC	of developing inherited alcoholism. Note: This sequence is not		
CC	represented in the specification and has been constructed from the wild-		
CC	type sequence represented in AAV61984 in accordance with the		
CC	specification		
XX			
XX			
SQ	Sequence 2162 BP; 562 A; 566 C; 457 G; 575 T; 0 U; 2 Other;		
Query Match	37.7%; Score 434.8; DB 2; Length 2162;		
Best Local Similarity	66.3%; Pred. NO. 1.4e-96;		
Matches 660; Conservative	0; Mismatches 327; Indels 9; Gaps 2		
92	CCGGCTGGGCGCGAAGCCGACGCAACGCGCGCGCTCGGAGAGACCGGAGCTGAGAC	151	
DB	337 CCGACCATGGGCTCCGAAACCGCACCAACCTGGGCGGAGAGACGCTGTGCGCTCGGA	396	
97	152 CCGGCGCATCTCCCGGCGCATCCCGGTCATCATCAGCGGCGGTCTACTCCGTAAGTTCG	211	
DB	397 CCGGCAAGCTTCATGATGTCAGCGGCGCATCAGATCATGAGCCCTTACTTCATCGGTGCG	456	
97	212 TCGTGGGCTTGGTGGGCACTCGCTGTCGATCTCGATCATCGGATCAACCAAGATGA	271	
DB	457 TGGTGGGCTCTTGGGAAACTTCTGTGTCATGATGATGATGTCAGATACCAAGATGA	516	
97	272 AGACGACCAACCAATTTAATATTTAACTGGCTTTGGAGATGCTTTAGTTACTACAA	331	
DB	517 AGACTGCCCAACCATCTACATTTTCAACCTTGTCTGGCAGATGCCCTTACACACAGTA	576	
97	332 CCATGCGCTTTCAAGATACGGTCTACTGATGAATTCCTGGCCTTTTGGGATGTGCTGT	391	

Db	577	CCCTG	CCCTTCCAGAGTGTGAATTA	CTTAATGGAAACATGG	CCATTGGAAACATCTCTT	636
Qy	392	GCAAGATAGTAATTTCCATTGATTA	CTTACAACTGTTCA	CCAGCATCTTCA	CCCTTGACCA	451
Db	637	GCAGAGTATGATCTCCATAGATTAC	TATTAACATGTTCA	CCAGCATTA	CCCTTGCA	696
Qy	452	TGATGAGCGTGAACGGCTACAT	TGGCGTGGCA	CCCGGTGAAAGGTTTGACTTCCGA		511
Db	697	CCATGAGTGTGATGCATACATTTGA	CTGCGCAC	CCCTGTCAAGGCTTAAATTTCCGTA		756
Qy	512	CACCTTTGAAGGCAAAAGATCAT	CAATATCTGCA	CTGGCTGTGTCATCTGTTGACA		571
Db	757	CTCCCCGAATATGCAAAATTTAT	CAATGTCGCA	CACTGATTCCTCTTCA	GGCATTGGTC	816
Qy	572	TCTTGCAATAGTCTCTTGAGGCA	CCAAAGTCA	GGGAAAGTCGATGTCA	TGATGAGTCT	631
Db	817	TTCTGTATATGTTCAATGCTTAC	CAACAAATATAC	AGGCAAGG-----TTCCATATGATTTGA		870
Qy	632	CCCTGACATGCCAGATGATGACT	ACTCTGTGGGACCTCTTCA	TGATGAGATCTGGTCT		691
Db	871	CACATAACATTTCTCTATTCAC	ACTGTGTA	CTGGGAAACCTTCG---TGAAGATCTGTGTT		927
Qy	692	TGATCTTTGCTTCCGTGATCC	CTGTCTCATCATCATGTCTG	CTTACACCTGATGATCC		751
Db	928	TCATCTTGCCCTTCAATTATG	CCAGTCTCATATTA	CCCTGTGCTAATGGA	CTGATGATCT	987
Qy	752	TGCGTCTCAAGAGCGTCCGGCT	CTCTTCTGGGCTCCCGA	GAGAAAGATGCAACCTGGCGTA		811
Db	988	TGCGGCTCAAGAGTGTCCGCA	TGCTCTCTG	CTCCAAAGAAAGACAGAAATCTTTCGA		1047
Qy	812	GGATCACACGACTGTCTGTGTG	TGTGGCAGTCTTGTGCTGTG	CTGAGACTCCATTC		871
Db	1048	GGATCACACGAGATGTGTGTG	TGTGGTGTGCTGTGTCAT	CGTCTGTGGA	CTTCCATTC	1107
Qy	872	ACATATTCATCCTGTGAGAG	GCCTCGGGAGACCTCC	ACAGCAAGTGTCTCTCCA		931
Db	1108	ACATTTAGTCAATCAATTAAG	CTTGTGTTCATATCC	CGAAACTACGTTCC	AGACTGTTT	1167
Qy	932	GCTATTACTTTCGATCGCTT	AGGCTATACCA	CAGATGAGCTGATCC	ATTCCTACG	991
Db	1168	CTTGCACCTTCTGCAATGTG	CTTAAGTTACAA	CAAGCGTCAACCA	AGTCTTTANG	1227
Qy	992	CCTTCTTGATGAAAACTTCA	AGCGGTGTTCCGGAC	CTTGTGCTTTTCA	CTGAAGATGA	1051
Db	1228	CATTTCTGATGAAAACTTCA	AGCATGCTTCA	GAGATTTGATTC	CAACCTCTTCCA	1287
Qy	1052	GGATGAGCGGACAGCACTA	GCAGTCCGAAATA	1087		
Db	1288	ACATTGAGCAACAAATCTCA	CTCGAATTCGTCACA	1323		
RESULT 28						
AAV61986	AAV61986 standard, cDNA, 2162 BP.					
AAV61986;						
11-JAN-1999	(first entry)					
Human mu-opioid receptor cDNA variant 2.						
Mu-opioid receptor; variant; polymorphism; mutant; detection; disease; prediagnosis; addition; analgesic; anaesthetic; anti-addictive; psychopharmacological agent; diagnostic; side effect; drug; opiate; cocaine; inherited alcoholism; human; ss.						
Homo sapiens.						
Synthetic.						
Location/Qualifiers						
80						
Key						
mutation						
/*tag= e						
/note= "Wild type C is replaced by T"						

FT	CDS	213..2040
FT	/tag=	a
FT	/product=	"mu-opioid receptor"
FT	misc_feature	502..503
FT	/tag=	b
FT	/note=	"Site of intron 1"
FT	misc_feature	855..856
FT	/tag=	c
FT	/note=	"Site of intron 2"
FT	misc_feature	1376..1377
FT	/tag=	d
FT	/note=	"Site of intron 3"
XX		
PX	WO9833937-A2.	
XX		
PD	06-AUG-1998.	
PF	02-FEB-1998;	96WO-DE000382.
PR	03-FEB-1997;	97DE-01003925.
PA	(DEIB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.	
PI	Hoehe M., Wendel B;	
DR	WPI; 1998-437487/37.	
PT	New genomic and cDNA sequences encoding human mu-opioid receptor - used,	
PT	e.g. to predict pre-disposition to addiction and for development of	
PS	analgesics, anaesthetics and anti-addiction agents.	
PS	Claim 8; Page; 26pp; German.	
XX		
CC	This sequence encodes a novel human mu-opioid receptor in which a C	
CC	nucleotide at position 80 of the wild-type sequence represented in	
CC	AAV61984 is replaced by a T. The wild type receptor and its variants,	
CC	polymorphisms and mutants are used in a method for detecting	
CC	predisposition to disease, particularly addictive disease, by isolating	
CC	DNA from a sample, genotyping selected positions and comparing with a	
CC	reference DNA. Such sequences are used to develop analgesic, anesthetic,	
CC	anti-addictive and psychopharmaceutical agents, to construct genes and	
CC	vectors, particularly for pharmaceutical development, to develop	
CC	diagnostic kits for predicting risk of addiction, response to analgesics	
CC	or anaesthetics, or development of side effects from a drug. Particular	
CC	applications are to determine risk of addiction to opiates or cocaine, or	
CC	of developing inherited alcoholism. Note: This sequence is not	
CC	represented in the specification and has been constructed from the wild-	
CC	-type sequence represented in AAV61984 in accordance with the	
CC	specification	
SQ		
SQ	Sequence 2162 BP; 562 A; 564 C; 458 G; 576 T; 0 U; 2 Other;	
	Query Match	37.7%; Score 434.8; DB 2; Length 2162;
	Best Local Similarity	66.3%; Pred. No. 1.4e-96;
	Matches 660; Conservative 0; Mismatches 327; Indels 9; Gaps 2	
OY	92	CCGCGTGGGCGCAGACCCGACAGCAACGGCAGCGCGCTGCAGAGACGCCAGCTGAGC 151
DB	337	CCGACCATTATGCGGTCCGAACCGCACCAACTGGCGGGAGAGAACAAGCTTGCTCCGA 396
OY	152	CCGGGCAATCTCCCGGSCCATCCCGGCATCATCAACGGCGGTCTACTCCGTAAGTTGG 211
DB	397	CCGGCAGTCCTCTCATATGATCAACGGCCATCAAGATATAGCCCTTACTCCATCGTAGCG 456
OY	212	TCTGTGGCTTGTGGGCAACTCGCTGATCATGTTCTGTATCATCGATACCAAGAATGA 271
DB	457	TGTGTGGGCTCTTGAAAACCTTCTGTGCATGATATGTGATTTGTCAAGATACCAAGAATGA 516
OY	272	AGACAGCAACCAATTTACTATTTAACCTGGCTTTGGCGAATGCTTTAGTTACTACA 331
DB	517	AGACTGACACCAATCTACTATTTCAACCTTGCTGGCAGATGCCCTTACACCAAGTA 576
OY	332	CGATGCCCTTCAAGTAGGTCTACTATTGATGAATTCCTGGCCTTTTGGGAGATGTGCT 391

	Key	Location/Qualifiers
FT	CDS	213..2040
TT		/*tag= a
Oy	333	CCATGCGCCTTTCAGAGTACGAGTCTTACTGTGATGAATTCGAGCCTTTGGGGAGTGGCTG 391
Db	577	CCCTGCGCCTTCCAGAGTGTGAATTACTCTAATGGGAACATGGCCATTGGAACCATCTTT 636
Oy	392	GCAAGATGATTAATTTCCATTGATTACTTAACAATGTTCAACAGCATCTTCAACCTTGACA 451
Db	637	GGAAAGTATGTATCTCCATAGATTACTTAATAAGTGTCAACAGCATTAATCAACCTCTGCA 696
Oy	452	TGATGAGCGTGGACCGCTACATTGGCGGTGGCAACCCCGTGAAAGGCTTTGGACTTCGCA 511
Db	697	CCATGAGTGTATTCGATTCATTTGACATTCGACCTTCGCAACCTGTCAAGGCTTATGATTCGTA 756
Oy	512	CACCCCTTGAAGGCAAAAGATCATCAATATTCGATCTGGCTGTCTGTCATCTGTGTGGCA 571
Db	757	CTCCCGCAAAATGCCAAAATTTATCAATGTCTGGCAACTGGAATTCCTCTTCAAGCATTTGGTC 816
Oy	572	TCTCTGCAATTAAGTCTTGGAGGCAACCAAGTCAGGGAAAGCGTCGATGTCAATTGAGTGTCT 631
Db	817	TTCTGTATATGTTCAATGGCTTACCAACAAAATAACAGGCAAGG-----TTCCATATGATTTGTA 870
Oy	632	CCCTGACAGTCCCAAGATGATGACTACTCTGGGCGGAGCCTCTTCATGAAAGATCTGGCTC 691
Db	871	CACCTAACAATCTCTCATCCAACTGGTACTGGAAAACTTCG---TGAAGATCTGTGTT 927
Oy	692	TCATCTTTGCTTTCGTGATCCCTGTCTCTCATCATCATATGCTGTGCTACACCCCTGATATCC 751
Db	928	TCATCTTTCGCTTCATTTATGCCAGTGCATCATTAACGTTGTATGAGACTGATGATCT 987
Oy	752	TGCGCTCAAGAGCGCTCCGGCTCTTTCTGGGCTCCCGAGAAAGAAATGCGAACCTGGCTGA 811
Db	988	TGCGCTCAAGAGTGTCCGCAATGCTCTCTGGCTCCAAAGAAAAGACAGAAATCTTGCAGAA 1047
Oy	812	GGATCACCAGACTGTCTCTGTGTGTGTGTGGCAGTCTTGTCTGTCTGTGAGACTCCCATTC 871
Db	1048	GGATCACCAGAGATGTGTCTGTGTGTGTGTGGCTGTGTATATGTCGTGTGAGACTCCCATTC 1107
Oy	872	ACATATTCATCTCTGTGTGAGGCTCTGGGAGAGCACTCCCAACGCAAGCTGCTCTCTCCA 931
Db	1108	ACATTTAGTATCTATTAAAGCTTGGTTAACATCCCAAGAACTGACGTTCCAGACTGTGTT 1167
Oy	932	GCTATTACTCTGTCATCGCCTTAGGCTATTACCAACAGTAGCTGAATCCCATTCCTCAAG 991
Db	1168	CTTGGCACTTCTGCAATTCCTCTAGATTACAAACAGCTGCTCAACCAAGTCTTTATATG 1222
Oy	992	CCTTTCTTGATGAATACTTCAAGCGGTGTTCGGGACTTGTGCTTTCACATGAAGATGA 1051
Db	1228	CATTTCTGATGAATAACTTCAACAGCATGCTTCAAGAGATTCGTATCCAACTCTTCCA 1287
Oy	1052	GGATGAGCGGACAGCAGCTAGCAGAGTCCGAAATA 1087
Db	1288	ACATTTAGCAACAAATCTCACTCGAATTCGTGAGA 1323
RESULT 30		
ID	AAV61984	
	AAV61984 standard; cDNA; 2162 BP.	
XX	AAV61984;	
AC		
XX		
DT	11-JAN-1999	(first entry)
DE		Human mu-opioid receptor cDNA.
XX		
XX		Human mu-opioid receptor cDNA.
OS		Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;
KW		predisposition; addiction; analgesic; anaesthetic; anti-addictive;
KW		psychopharmaceutical agent; diagnostic; side effect; drug; opiate;
KW		cocaine; inherited alcoholism; human; ss.
XX		
XX		
OS		Homo sapiens.
XX		
XX		

FT		/product= "mu-opioid receptor"
FT	misc_feature	502..503
FT		/*tag= b
FT		/note= "Site of intron 1"
FT	misc_feature	855..856
FT		/*tag= c
FT		/note= "Site of intron 2"
FT	misc_feature	1376..1377
FT		/*tag= d
FT		/note= "Site of intron 3"
XX		
XX		
PN	WO9833937-A2.	
PD		
XX	06-AUG-1998.	
XX		
PF	02-FEB-1998;	98WO-DE000382.
XX		
PR	03-FEB-1997;	97DE-01003925.
XX		
PA	(DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.	
XX		
P1	Hoehe M, Mendel B;	
DR	WPI; 1998-437487/37.	
XX		
PT	New genomic and cDNA sequences encoding human mu-opioid receptor - used,	
PT	e.g. to predict pre-disposition to addiction and for development of	
XX	analgesics, anaesthetics and anti-addiction agents.	
PS	Claim 8; Page 14-15; 26pp; German.	
XX		
CC	This sequence encodes a novel human mu-opioid receptor. This sequence and	
CC	its variants, polymorphisms and mutants are used in a method for	
CC	detecting predisposition to disease, particularly addictive disease, by	
CC	isolating DNA from a sample, genotyping selected positions and comparing	
CC	with a reference DNA. Such sequences are used to develop analgesic,	
CC	anaesthetic, anti-addictive and psychopharmaceutical agents, to construct	
CC	genes and vectors, particularly for pharmaceutical development, to	
CC	develop diagnostic kits for predicting risk of addiction, response to	
CC	analgesics or anaesthetics, or development of side effects from a drug.	
CC	Particular applications are to determine risk of addiction to opiates or	
CC	cocaine, or of developing inherited alcoholism	
SQ	Sequence 2162 BP; 562 A; 565 C; 458 G; 575 T; 0 U; 2 Other;	
	Query Match	37.7%; Score 434.8; DB 2; Length 2162;
	Best Local Similarity	66.3%; Pred. No. 1.4e-96;
	Matches 660; Conservative	0; Mismatches 327; Indels 9; Gaps 2
OY	92	CCGGCTGGGCGAGGCCGACAGCAACGGCAGCGCCGCTCGAGAGAGCGCGACTGGAGC 151
DY	337	CCGACCATTGCCTGTCCGAHCGCACCAAACCTGGGGGGAGAGACGCTTGCCCTCGA 396
OY	152	CCGCGACATCTCCCGGCGATCCCGGCATCATCAGCGCGGTTACTCCGTAGTGTTCG 211
DY	397	CCGGCAGTCCCTCATGTATACAGGCAATCAGATCAGATCAGGCCCTTACTCATGTGTGCG 456
OY	212	TGCTGGGCTGTGGTGGGCAACTCGCTGGTCATGTTCTGTGATCATCCGATACAAAAGTGA 271
DY	457	TGCTGGGGCTCTTCGAAACTTCTTGATCATGTATGTGATGTGCATACCAAGAATGA 516
OY	272	AGACAGCAACAACATTATACATATTAACTGGGCTTTGGAGATGCTTAAGTTACTACAA 331
DY	517	AATCTGCCAACACATCTACATTTTCAACCTTGTCTGGGAGATGCTTAGCCACAGTA 576
OY	332	CCATGCCCTTTCAGATACGGTCTACTGTGATGAATTCCTGGCCCTTTTGGGATGTGCTGT 391
DY	577	CCCTGCCCTTCAGAGTGTGAATTACCTAATGGGAMATGGCCATTGGAACATCCTTT 636
OY	392	GGAATATGTATTTTCCATTATCTACCAACATGTTACACAGATCTTCACTTGACCA 451
DY	637	GGAATATGTATTTTCCATTATCTACCAACATGTTACACAGATCTTCACTTGACCA 696

OY	452	IGATGAGCGTGGACCGCTACATTCGCCGTGTGCCACCCCGTGAAAGCTTTGGACTTCCGCA	511
Db	697	CCATAGAGTTGATGATATCATTTGACATGTGCGCACCCCTGTCAAGGCTTAGATTTCCGTA	756
OY	512	CACCCCTGGAAGGCAAAAGATCATCATATCTGCATCTGGCTGCTGCTCATCTGTTGGCA	571
Db	757	CTCCCCGAATATCCCAAAATTTATCAATGTTCGCAATCGAATCCTCTCTTTACGCCATTTGGTC	816
OY	572	TCTCTGCATAATGTCCTTGGAGGACCAAAAGTCAGGAGAGACGTGCAATGTCATTTAGTGTCT	631
Db	817	TTCCGTATGTTTCATGGCTACAAACAAAATACAGGCAAG-----TTCATATGATTTGTA	870
OY	632	CCTTGCAATTCOCNAATATGATGACTACTCCTGGTGGGACCTCTTCACTGAAGATCTGCTCT	691
Db	871	CACTAACATTTCTCTATCCAACCTGTGTACTGTGGAAAACTGTG--TGAAGATCTGTGTTT	927
OY	692	TCATCTTTGCCCTTCGTGATCCCTGTCTCTCATCATCATGCTCTGTCTAACCCCTGATGATCC	751
Db	928	TCATCTTGCCCTTCAATTATATGCCAGTGTCTATTAATACGTGTGCTATGGAACCTGATGATCT	987
OY	752	TGCGTCTCAAGAAGCGTCCGGCTCTCTTTCTGGCTCCCGAGAGAAAGTGGCAACTGGCTGA	811
Db	988	TGCGGCTCAAGAGTGTCCGCAATGCTCTCTGCGCTCCAAAAGAAAGACAGAAATCTTCGAA	1047
OY	812	GGATCACCAGACTGTGCTCCGGTGGTGGTGGGACGCTTGCTGGCTGCTGGATCTCCCATTC	871
Db	1048	GGATCACCAAGATGTGTGTGGTGGTGGTGGTGTGTATCGTGTGCTGGATCTCCCATTC	1107
OY	872	ACATAATTCATCCTGTGTGAGAGGCTCTGGGAGAGCACCTCCACAGCAAGCTGTCTCTCCCA	931
Db	1108	ACATTTACGTCATCATTTAAAGCTTTGGTTACAAATCCAGAAACATACGTTCCAGACTGTTT	1167
OY	932	GCTATTAATTTCTGCATGCGCTTTAGGCTATACCAACATGATGCTGAATCCATTTCTTACG	991
Db	1168	CTTGGCACTTTCGACTGTCTCTAGGTATACAAACAGCTGCTCAACCAAGCTCTTTATG	1227
OY	992	CCTTTCTTGATGAAAACCTTCAAGCGGTGTTCCTGGGACCTTCTGCTTTCCACTGAAGATGA	1051
Db	1228	CATTTCTGATGAAAACCTTCAACAGATCCTTCAGAGATTTCTGTATCCCAACTCTTCCA	1288
OY	1052	GGATGAGCGGCGAGACACTGACAGAGTCCGAATA	1087
Db	1288	ACATTTGAGCAACAAAACCTCACTCGAATTTGTCACA	1323

	RESULT 32
AAV61990	
ID	AAV61990 standard; cDNA, 2162 BP.
XX	
AC	AAV61990;
DT	11-JAN-1999 (first entry)
XX	
DE	Human mu-opioid receptor cDNA variant 6 .
KM	Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;
KM	predisposition; addiction; analgesic; anaesthetic; anti-addictive;
KM	psychopharmaceutical agent; diagnostic; side effect; drug; opiate;
XX	cocaine; inherited alcoholism; human; ss.
OS	Homo sapiens.
XX	Synthetic.
FT	
FT	Location/Qualifiers
FT	CDS 213..2040
FT	/tag= a
FT	/product= "mu-opioid receptor"
FT	330
FT	/tag= e
FT	/note= "wild type A is replaced by G"
FT	502..503
FT	/tag= b
misc_feature	
FT	

FT		/note= "Site of intron 1"
FT	misc_feature	855..856
FT		*tag= C
FT		/note= "Site of intron 2"
FT	misc_feature	1376..1377
FT		*tag= d
FT		/note= "Site of intron 3"
PX		
PN	WO9833937-A2.	
XX		
XX	06-AUG-1998.	
PD		
PF	02-FEB-1998;	98WO-DE000382.
PX		
PR	03-FEB-1997;	97DE-01003925.
PA	(DEIB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.	
XX		
PI	Hoehle M., Wendel B;	
DR	WPI; 1998-437487/37.	
XX		
PT	New genomic and cDNA sequences encoding human mu-opioid receptor - used,	
PT	e.g. to predict pre-disposition to addiction and for development of	
PT	analgesics, anaesthetics and anti-addiction agents.	
PX		
PS	Claim 8; Page; 26pp; German.	
CC	This sequence encodes a novel human mu-opioid receptor in which an A	
CC	nucleotide at position 330 of the wild-type sequence represented in	
CC	AAV61984 is replaced by a G. The wild type receptor and its variants,	
CC	polymorphisms and mutants are used in a method for detecting	
CC	predisposition to disease, particularly addictive disease, by isolating	
CC	DNA from a sample, genotyping selected positions and comparing with a	
CC	reference DNA. Such sequences are used to develop analgesic, anesthetic,	
CC	anti-addictive and psychopharmaceutical agents, to construct genes and	
CC	vectors, particularly for pharmaceutical development, to develop	
CC	diagnostic kits for predicting risk of addiction, response to analgesics	
CC	or anaesthetics, or development of side effects from a drug. Particular	
CC	applications are to determine risk of addiction to opiates or cocaine, or	
CC	of developing inherited alcoholism. Note: This sequence is not	
CC	represented in the specification and has been constructed from the wild-	
CC	type sequence represented in AAV61984 in accordance with the	
CC	specification	
XX		
SQ	Sequence 2162 BP; 561 A; 565 C; 459 G; 575 T; 0 U; 2 Other;	
	Query Match 37.7%; Score 434.8; DB 2; Length 2162;	
	Best Local Similarity 66.3%; Pred. No. 1.4e-96;	
	Matches 660; Conservative 0; Mismatches 327; Indels 9; Gaps 2	
OY	92	CCGGCTGCGGCCGAGCCCGACGCAACGCGCAGCGCGTTCGAGAGACGCGAGCTGAGNC 151
Db	337	CCGACCATGCGGGTCCGGAACCGCACCAACTGGGCGGGAGAGACAGCTGTGCCTCCGA 396
OY	152	CCGGCGCATATTCCTCCCGGCATATCCCGGTATCATACGCGCGGTCTAATCCGTAATTTTG 211
Db	397	CCGGCAGTCCCTCATATATCAACGCGCATACAGATCAAGCCCTTACTCCATCGGTGCG 456
OY	212	TGCGGGCTTGTTGGGCAACTCGTGTGTCATGTTGCGTATCATCCGATACCAAGAATGA 271
Db	457	TGTTGGGGCTTCTGGAAAATTCTCTGTGTCATGTAATGTGATGTGTGATACACCAAAGATGA 516
OY	272	AGACAGCAACAACATTTACATATTTAACCTGGCTTTGGCGAGATGCTTTAGTTACTACAA 331
Db	517	AGACTGACACCAACATCTTACATTTTCAACCTGCTCGACAGATGCCCTTACCCACAGTA 576
OY	332	CCATGACCTTTTCAGAGTAGGTCTACATTTGATGATTCCTGGCCCTTTTGGGAGTAGTGCT 391
Db	577	CCCTGCCCCCTTCCAGAGTGTGATTAATCTTAATGGAAACATGGCCATTGGAAACATTCCTTT 636
OY	392	GCAAGATAGTAATTTTCATTGATTACTAACATGTTTCAACGAGCATCTTCACTTGACCA 451

Db 637 GCAAGATAGTATCTCCATAGATTACTATAATGTTACACAGATATTACCCCTTGCA 696
 Qy 452 TGATGACGTGGAGCCGCTACATTGCGGTGCGCAACCCGTTGAAGCTTTGGACGCA 511
 Db 697 CCAAGAGTGTGATCGATACATTCGATGCTGCAACCCCTGTAAAGCCCTTAATATTCGCTA 756
 Qy 512 CACCCCTTGAAGGCAAGATCATCAATATCTCATCTGAGCTGCTGTGCTCATCTGTGCA 571
 Db 757 CTCCCCGAAATGCCAAATTTATCAATGTCTGCAATGATCTCTCTTGACGCAATGGTC 816
 Qy 572 TCTGTCAATAGTCTTGTGAGGACCAAAAGTCAGGAAAGACGTGATCATTTAGATGCT 631
 Db 817 TTCCTGTAATGTTCATGGCTACAAACAAATACAGGCAAGG-----TTCATATGATTTGA 870
 Qy 632 CTTTGCAAGTCCGAGATGATGACTACTCTGTGTGGAGCCTTTTATGAAATCTGGCT 691
 Db 871 CACTAACATTCCTCATTCGCAACCTGTGACTGGAAACCTGG---TGAAGATCTGTGTTT 927
 Qy 692 TCATCTTGTGCTTGTGATCCCTGTGCTCATCATCATCTGCTGCTACACCCGTGATGATCC 751
 Db 928 TCATCTTGTGCTTGTGATTCGCAATGCTCATCATCTGCTGCTGCTGCTGCTGCTGCTGCT 987
 Qy 752 TGCCTTCAGAGGCGTCCGCTCTTCTGTGCTCCGAGAGAAAGATGCAACCTGCGTA 811
 Db 988 TGGCCCTCAAGAGTGTCCGATGCTCTGTGCTCCAAAGAAAGACAGAAATCTTGAA 1047
 Qy 812 GGATCACCAGACTGCTCTGTGTGTGGCAGTCTTCTGTGCTGCTGCACTCCCATTC 871
 Db 1048 GGATCACCAGAGT 1107
 Qy 872 ACATATTCATCTGCTGTGAGGCTCTGCGGAGACACCTCCACAGACAGCTGCTCTGCA 931
 Db 1108 ACATATTCATCTGCTGTGAGGCTCTGCGGAGACACCTCCACAGACAGCTGCTCTGCA 1167
 Qy 932 GCTATTCATCTGCTGTGAGGCTCTGCGGAGACACCTCCACAGACAGCTGCTCTGCA 991
 Db 1168 CTTGGCACTTGTGATGCTCTGATGCTCTGATGCTCTGATGCTCTGATGCTCTGATGCT 1227
 Qy 992 CTTTCTTGTGATGAAACTTCAAGGGGTGTTCGCGAGCTTGTCTTCTCACTGAAGATGA 1051
 Db 1228 CATTTCGATGAAACTTCAAGGGGTGTTCGCGAGCTTGTCTTCTCACTGAAGATGA 1287
 Qy 1052 GGATGAGCGGCGAGACGCTGACAGAGTCCGAATA 1087
 Db 1288 ACATTGAGCAACAAACTCACTGCAATTCGTGCA 1323

RESULT 33

AAV61985 standard; cDNA, 2162 BP.

AAV61985;

11-JAN-1999 (first entry)

Human mu-opioid receptor cDNA variant 1.

Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;
 predilection; addiction; analgesic; anaesthetic; anti-addictive;
 psychopharmacological agent; diagnostic; side effect; drug; opiate;
 cocaine; inherited alcoholism; human; ss.

Homo sapiens.

OS Synthetic.

Location/Qualifiers

/tag= e
 /note= "Wild type G is replaced by T"
 /tag= a
 /product= "mu-opioid receptor"

CDS 213..2040
 /product= "mu-opioid receptor"

misc_feature 502..503

FT /*tag= b
 FT /note= "Site of intron 1"
 FT misc_feature
 FT 855..856
 FT /tag= c
 FT /note= "Site of intron 2"
 FT misc_feature
 FT 1376..1377
 FT /tag= d
 FT /note= "Site of intron 3"
 XX W0983937-A2.
 XX 06-AUG-1998.
 XX 02-FEB-1998; 98WC-DE000382.
 XX 03-FEB-1997; 97DE-01003925.
 PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
 PI Hoehe M, Wendel B;
 XX WPI; 1998-437487/37.
 DR
 XX
 XX
 PT New genomic and cDNA sequences encoding human mu-opioid receptor - used,
 PT e.g. to predict pre-disposition to addiction and for development of
 PT analgesics, anaesthetics and anti-addiction agents.
 XX
 PS Claim 8; Page; 26pp; German.
 XX
 XX This sequence encodes a novel human mu-opioid receptor in which a G
 CC nucleotide at position 41 of the wild-type sequence represented in
 CC AAV61984 is replaced by a T. The wild type sequence and its variants,
 CC polymorphisms and mutants are used in a method for detecting
 CC predilection to disease, particularly addictive disease, by isolating
 CC DNA from a sample, genotyping selected positions and comparing with a
 CC reference DNA. Such sequences are used to develop analgesic, anaesthetic,
 CC anti-addictive and psychopharmacological agents, to construct genes and
 CC vectors, particularly for pharmaceutical development, to develop
 CC diagnostic kits for predicting risk of addiction, response to analgesics
 CC or anaesthetics, or development of side effects from a drug. Particular
 CC applications are to determine risk of addiction to opiates or cocaine, or
 CC of developing inherited alcoholism. Note: This sequence is not
 CC represented in the specification and has been constructed from the wild-
 CC type sequence represented in AAV61984 in accordance with the
 CC specification
 CC
 XX
 XX Sequence 2162 BP; 562 A; 565 C; 457 G; 576 T; 0 U; 2 Other;
 SQ
 Query Match 37.7%; Score 434.8; DB 2; Length 2162;
 Best Local Similarity 66.3%; Pred. No. 1.4e-96;
 Matches 660; Conservative 0; Mismatches 327; Indels 9; Gaps 2;
 Qy 92 CCGGCTGGGCGAGCCCGACAGCAACGCGCGGCTCGAGAGCGCGAGCTGAGC 151
 Db 337 CCGACCATGGGCTGCGACGCAACGCGGCGGAGAGACAGCCTGTGCCCTCGCA 396
 Qy 152 CCGGCAATCTCCCGGCAATCCCGGTATCATCAGCGCGGTATCTCTAGTGTTCG 211
 Db 397 CCGGCAATCTCCCGGCAATCCCGGTATCATCAGCGCGGTATCTCTAGTGTTCG 456
 Qy 212 TCGTGGGCTGTGGGCAATCGGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 271
 Db 457 TCGTGGGCTGTGGGCAATCGGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 516
 Qy 272 AGACAGCAACCAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTA 331
 Db 517 AGACTGCAACCAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTA 576
 Qy 332 CCATGCGCTTTCAAGAGTGTCTACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 391
 Db 577 CCGTGGCGCTTCAAGAGTGTCTACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 636
 Qy 392 GCAAGATAGTAATTTCAATGATTACTACAAAGATTTACACAGATCTTACCTTGACA 451

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Db      637  GCAAGATGATGATCTCCATAGATTACTATAACATGTTACACAGATATTCAACCCCTGCA 696
Qy      452  TGATGAGGTGGAACCGCTACATTCGCGTGTGCGACCCCGTGAAGCTTTGAGCTTCCGCA 511
Db      697  CCATGAGGTGATGATGATACATTCGATGCTCCACCCCGTGAAGCCCTTAAATTTCCGTA 756
Qy      512  CACCTTGAAGGCAAAAGATCATCAATATCTGATCTGCTGTGCTGCTGATCTGTTGCA 571
Db      757  CTCCCCGAAATGCCAAATTTATCAATGTCTGCACTGATCTCTCTTCAAGCCATTGCTC 816
Qy      572  TCTCTGCAATAGTCTTGGAGGACCAAAAGTCAGGAAAGACGTGATGATTTAGTGTCT 631
Db      817  TTCCGTATATGTTATGATGCTACAAACAAATACAGGCAAGG-----TTCCATGATTTGTA 870
Qy      632  CCTTGACGTTCCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 691
Db      871  CACTAACATTTCTCTATCTCAACCTGTGTACTGGGAAACCTG---TGAAATCTGTGTCTT 927
Qy      692  TCATCTTTCCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 751
Db      928  TCATCTTTCCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 987
Qy      752  TGGCTCTCAAGAGCGTCCGCTCTCTTCTGCTCCGAGAGAAAGATCGCAACCTGCGTA 811
Db      988  TGGCTCTCAAGAGCGTCCGCTCTCTTCTGCTCCGAGAGAAAGATCGCAACCTGCGTA 1047
Qy      812  GGATCACACAGCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 871
Db      1048  GGATCACACAGCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1107
Qy      872  ACATATTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 931
Db      1108  ACATATTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1167
Qy      932  GCTATTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 991
Db      1168  CTGGCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1227
Qy      992  CCTTTCTGATGAAACCTTCAAGCGGCTTCCGCGGCTTCTGCTTCCACTGAAGTGA 1051
Db      1228  CATTTCTGATGAAACCTTCAAGCGGCTTCCGCGGCTTCTGCTTCCACTGAAGTGA 1287
Qy      1052  GGATGAGCGGCGAGAGCACTAGCAGAGTCCGAAATA 1087
Db      1288  ACATGAGCAACAAACTCCACTGCAATGTGTGCA 1323

RESULT 34
AAV61989
ID      AAV61989 standard; cDNA; 2162 BP.
XX
XX      AAV61989;
XX
XX      11-JAN-1999 (first entry)
XX
XX      Human mu-opioid receptor cDNA variant 5.
XX
XX      Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;
XX      predilection; addiction; analgesic; anaesthetic; anti-addictive;
XX      psychopharmacological agent; diagnostic; side effect; drug; opiate;
XX      cocaine; inherited alcoholism; human; ss.
XX
XX      Homo sapiens.
XX      Synthetic.
XX
XX      Key      Location/Qualifiers
XX      CDS      213..2040
XX      FT      /*tag= a
XX      FT      /product= "mu-opioid receptor"
XX      FT      229
XX      FT      /*tag= e
XX      FT      /note= "Wild type C is replaced by T"

```

```

FT      misc_feature      502..503
FT      /*tag= b
FT      /note= "Site of intron 1"
FT      misc_feature      855..856
FT      /*tag= c
FT      /note= "Site of intron 2"
FT      misc_feature      1376..1377
FT      /*tag= d
FT      /note= "Site of intron 3"
XX
XX      WO9833937-A2.
XX
XX      06-AUG-1998.
XX
XX      02-FEB-1998; 98WO-DE000382.
XX
XX      03-FEB-1997; 97DE-01003925.
XX
XX      (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX
XX      Hoehe M, Wendel B;
XX
XX      WPI; 1998-437487/37.
XX
XX      New genomic and cDNA sequences encoding human mu-opioid receptor - used,
XX      p.e.g. to predict pre-disposition to addiction and for development of
XX      analgesics, anaesthetics and anti-addiction agents.
XX
XX      Claim 8; Page; 26pp; German.
XX
XX      This sequence encodes a novel human mu-opioid receptor in which a C
XX      nucleotide at position 229 of the wild-type sequence represented in
XX      AAV61984 is replaced by an T. The wild type receptor and its variants,
XX      polymorphisms and mutants are used in a method for detecting
XX      predilection to disease, particularly addictive disease, by isolating
XX      DNA from a sample, genotyping selected positions and comparing with a
XX      reference DNA. Such sequences are used to develop analgesic, anaesthetic,
XX      anti-addictive and psychopharmacological agents, to construct genes and
XX      vectors, particularly for pharmaceutical development, to develop
XX      diagnostic kits for predicting risk of addiction, response to analgesics
XX      or anaesthetics, or development of side effects from a drug. Particular
XX      applications are to determine risk of addiction to opiates or cocaine, or
XX      of developing inherited alcoholism. Note: This sequence is not
XX      represented in the specification and has been constructed from the wild-
XX      type sequence represented in AAV61984 in accordance with the
XX      specification
XX
XX      Sequence 2162 BP; 562 A; 564 C; 458 G; 576 T; 0 U; 2 Other;
XX
XX      Query Match      37.7%; Score 434.8; DB 2; Length 2162;
XX      Best Local Similarity 66.3%; Pred. No. 1.4e-96;
XX      Matches 660; Conservative 0; Mismatches 327; Indels 9; Gaps 2;
XX
Qy      92  CCGGCTGGGCGGACCCGACAGCAACGGGCGGCTGAGAGAGCGGAGCTGAGAC 151
Db      337  CCGACCCATGCGGATCGGACCGGACCAACCTGCGGAGAGAGACGCTGCTCCGCA 396
Qy      152  CCGGCGACATCTCCCCGGGATCCCGGTATATACAGCGGCTTACTCCGATGTTG 211
Db      397  CCGGCGATCTCTTCATGATGACGGGATCAGCATGATGATGATGATGATGATGATGATG 456
Qy      212  TCGTGGGCTTGGTGGGCAACCTGCTGATGATGATGATGATGATGATGATGATGATGATG 271
Db      457  TGGTGGGCTCTTGGGAACTTCCGCTGATGATGATGATGATGATGATGATGATGATGATG 516
Qy      272  AGACAGCAACCAACATTTATGATTTTAACTGGCTTTGGAGATGCTTATTAACA 331
Db      517  AGACTGCGACCAACATTTATGATTTTCAACTTGTCTGGAGATGCTTATTAACA 576
Qy      332  CCATGCGCTTTAGAGTACGCTGATGATGATGATGATGATGATGATGATGATGATGATG 391
Db      577  CCTGCGCTTTCAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 636

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QY 392 GCAAGATAGTAATTCATTTGATTTACTACAACTGTCACAGCATCTTACCTTGACCA 451
 DB 637 GCAGATAGTATGATCTCCATAGTTACTATACATGTTCCAGCATATTCACCTCTGCA 696
 QY 452 TGATGAGGTGAGACCGCTACATATGCGGTGTCACCCCGTGAAGCTTTGACCGCA 511
 DB 697 CCATGAGTGTGATGATGATACATGCAAGTCGTCACCCCTGTCAAGGCTTAGATTCGGA 756
 QY 512 CACCTTGAAGGCAAGATCATCATATCTGATCTGCTGTGTCATCTGTTGGCA 571
 DB 757 CTCGCCGAATGTCGCAAAATTTATCAATGTCGCACTGATCTCTCTTCAGCATTTGGTC 816
 QY 572 TCTCTGCAATAGTCTTGTGAGGACCAAGTACAGGGAAGACGTGATGATGATGCT 631
 DB 817 TTCCTGTAATGTTCTATGCTACACAAATATACAGGCAAG-----TTCATAGATGTA 870
 QY 632 CTTTGACAGTCTCCAGATGATGATCTATCTGCTGAGGACCTTTCATGAGATCTGCT 691
 DB 871 CACTAATCTCTCATCAACCTGTGTACTGGAAACCTCG--TGAAGATCTGATTT 927
 QY 692 TCATCTTTCCTTCTGATCTCTGCTGCTCATCATGCTGCTGCTACACCTGATGATCC 751
 DB 928 TCATCTTTCCTTCTGATCTCTGCTGCTCATCATGCTGCTGCTGCTGCTGATGATCT 987
 QY 752 TGCGCTCAAGAGCGTCCGCGCTCTTTCGCTCCGAGAGAAATGSCAACCTGCGTA 811
 DB 988 TGCGCTCAAGAGTGTCCGCACTGCTCTCTGCTCCAAAGAAAGACAGGAATCTTCGA 1047
 QY 812 GGATCACCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 871
 DB 1048 GGATCACCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1107
 QY 872 ACATATTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 931
 DB 1108 ACATATTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1167
 QY 932 GCTATTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 991
 DB 1168 CTTGCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1227
 QY 992 CTTTCTTGTATGAAATCTTCAAGCGGTGCTTCCGGAGACTTCTGCTTTCATGAAATGA 1051
 DB 1228 CATTCTGATGAAATCTTCAAGCGGTGCTTCCGGAGACTTCTGCTTTCATGAAATGA 1287
 QY 1052 GGATGAGCGGACAGCACTAGCAAGTCCGAATA 1087
 DB 1288 ACATTGAGCAACAAATCTCCTGCAATTCGTGCA 1323

RESULT 37
 ACAS6781
 ID ACAS6781 standard; cDNA; 2162 BP.
 ACAS6781;
 06-JUN-2003 (first entry)

Human signalling pathway polynucleotide probe SEQ ID NO 1379.
 Human; probe; ss; array element; Parkinson's disease;
 signalling pathway population; cancer; adenocarcinoma; leukaemia;
 immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.
 Homo sapiens.
 OS
 PN US6500938-B1.
 PD 31-DEC-2002.
 PF 30-JAN-1998; 98US-00016434.
 PR 30-JAN-1998; 98US-00016434.
 XX

PA (INCY-) INCYTE GENOMICS INC.
 PI Au-Young J, Seilhamer JI;
 DR WPI; 2003-352189/33.
 PT Combination of polynucleotide probes, useful as array elements in a
 PT microarray for monitoring the expression of a number of target
 PT polynucleotides.
 PS Claim 1; SEQ ID NO 1379; 65bp; English.
 XX
 CC The invention relates to a combination which, comprises a number of
 CC polynucleotide probes comprising a sequence selected from one of the 1490
 CC sequences mentioned in the specification. The combination is useful as an
 CC array element in a microarray for monitoring the expression of a number
 CC of target polynucleotides. The microarray is particularly useful in the
 CC diagnosis and treatment of cancer and immunopathology and neuropathology.
 CC The microarray is useful in diagnostics and treatment regimens, drug
 CC discovery and development, toxicological and carcinogenicity studies,
 CC forensics and pharmacogenomics. The microarray is also useful for
 CC monitoring progression of diseases and for developing sophisticated
 CC profiles for the effects of currently available therapeutic drugs. The
 CC combination is also useful for purifying a subpopulation of mRNAs, cDNAs
 CC and genomic fragments and in research and diagnostic applications. The
 CC array can detect changes in expression in a large number of genes coding
 CC for different signalling pathway populations which can be used to diagnose
 CC various diseases including cancer e.g. adenocarcinoma and leukaemia,
 CC immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease
 CC and Parkinson's disease. The present sequence represents a polynucleotide
 CC probe of the invention. Note: The sequence data for this patent did not
 CC form part of the printed specification but was obtained in electronic
 CC format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?DocID=06500938B1
 CC
 SQ Sequence 2162 BP; 563 A; 566 C; 455 G; 576 T; 0 U; 2 Other;

Query Match 37.7%; Score 434.8; DB 7; Length 2162;
 Best Local Similarity 66.3%; Pred. No. 1.4e-96;
 Matches 660; Conservative 0; Mismatches 327; Indels 9; Gaps 2;

QY 92 CCGGCTGGGCGGAGCCGACAGCAAGCGAGCGCGCTCGAGAGACGCGCAGTGGAGC 151
 DB 337 CCGAGCCATGCGGTGCTGCAACCGCACCACTGGGGGAGAGACAGCCGTGCCCTCCGA 396
 QY 152 CCGGCAATCTCCCGGCGCATCCGGTCAATCAACGGCGGTCTACTCTCGATGTTGG 211
 DB 397 CCGGCAATCTCCCGGCGCATCCGGTCAATCAACGGCGGTCTACTCTCGATGTTGG 456
 QY 212 TCGTGGGCTGTGTTGGGCAATCGCTGTCATGTTGTATCATCCGATACAAAGATGA 271
 DB 457 TGTGTGGGCTCTTGGGAAATCTGCTGTCATGATGATGATGATGATGATGATGATGATGAT 516
 QY 272 AGACAGCAACCAATTTACATATTTAACTGCTGTTGGCAGATGCTTAGTACTACAA 331
 DB 517 AGACTGCCAACCAATCTACATTTTCAACCTTGTCTGCGAATGCTTTAGGCCAACAGTA 576
 QY 332 CCATGCGCTTTCAGAGTACGCTTACCTGATGATGATGATGATGATGATGATGATGATGAT 391
 DB 577 CCCTGCGCTTTCAGAGTACGCTTACCTGATGATGATGATGATGATGATGATGATGATGAT 636
 QY 392 GCAAGATAGTAATTTCCATGATTTACTACAAATGTTTACCGAGATCTTACCTTGACCA 451
 DB 637 GCAGATAGTATGATCTCCATAGTTACTATACATGTTCCAGCATATTCACCTCTGCA 696
 QY 452 TGATGAGGTGAGACCGCTACATATGCGGTGTCACCCCGTGAAGCTTTGACCGCA 511
 DB 697 CCATGAGTGTGATGATGATACATGCAAGTCGTCACCCCTGTCAAGGCTTAGATTCGGA 756
 QY 512 CACCTTGAAGGCAAGATCATCATATCTGATCTGCTGTGTCATCTGTTGGCA 571
 DB 757 CTCGCCGAATGTCGCAAAATTTATCAATGTCGCACTGATCTCTCTTCAGCATTTGGTC 816

QY	1052	GGATGGAGGGGACAGACACTGACAGACTCCGAATA	1087
Db	1288	ACATTGACACAAACTCCATCTCGATTCTGTGAGA	1323
RESULT 40			
AAD51226			
ID	AAD51226	standard; cDNA; 2279 BP.	
XX			
AC	AAD51226;		
XX			
DT	02-APR-2003	(first entry)	
XX			
DE	Human REMAP-7 cDNA.		
XX			
KM	Human; receptor and membrane-associated protein; REMAP; arteriosclerosis;		
KM	cell proliferative disorder; atherosclerosis; polycythaemia vera; cancer;		
KM	cirrhosis; hepatitis; paroxysmal nocturnal haemoglobinuria; psoriasis;		
KM	primary thrombocytopaenia; developmental disorder; mental retardation;		
KM	renal tubular acidosis; neurological disorder; Alzheimer's disease;		
KM	Parinson's disease; anaemia; reproductive disorder; autoimmune disorder		
KM	interfally; inflammatory disorder; acquired immune deficiency syndrome;		
KM	AlDS; epilepsy; allergy; asthma; autoimmune thyroiditis; Crohn's disease;		
KM	contact dermatitis; diabetes mellitus; glomerulonephritis; osteoporosis;		
KM	Goodpasture's syndrome; gout; Graves' disease; Hashimoto's thyroiditis;		
KM	irritable bowel syndrome; multiple sclerosis; Reiter's syndrome; uveitis;		
KM	osteoarthritis; pancreatitis; rheumatoid arthritis; Sjogren's syndrome;		
KM	gene therapy; virucide; protozoacide; fungicide; gene; ss.		
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	CDS	19..1407	
FT		/*tag= a	
FT		/product= "Human REMAP-7 protein"	
FT	sig_peptide	19..87	
FT		/*tag= b	
FT	mat_peptide	88..1404	
FT		/*tag= C	
FT		/product= "Human mature REMAP-7 protein"	
XX			
PN	WO200294990-A2.		
XX			
PD	28-NOV-2002.		
XX			
PF	16-MAY-2002; 2002WO-US015899.		
XX			
PR	18-MAY-2001; 2001US-0292197P.		
PR	08-JUN-2001; 2001US-0297012P.		
PR	21-JUN-2001; 2001US-0300582P.		
PR	22-JUN-2001; 2001US-0300495P.		
PR	28-JUN-2001; 2001US-0301992P.		
PR	14-DEC-2001; 2001US-0340542P.		
XX			
PA	(INCY-) INCYTE GENOMICS INC.		
PI	Lal PG, Warren BA, Xu Y, Duggan BM, Honchell CD, Kallick DA;		
PI	Baughn MR, Tang YT, Yue H, Bandman O, Jones KA, Becha SD, Iran UK;		
PI	Au-Young JK, Griffin JA, Zebatjadian Y, Lee EA, Elliott VS;		
PI	Thangavelu K, Ramkumar J, Lu Y, Hatalla AJA, Walla NK, Ison CH;		
PI	Thomson M, Swarnakar A, Yang J, Richardson TW, Emerling BM, Yao MG;		
PI	Cocks BG, Sanjwalala B, Mason PM, Gandhi AR, Li JX, Forsythe IU;		
PI	Gururajan R, Gierzen KU;		
XX			
XX	WPI: 2003-129423/12.		
DR	P-PSDB; AAE33476.		
XX			
PT	New human receptors and membrane-associated proteins and nucleic acids,		
PT	useful for diagnosing, treating or preventing inflammatory disorder, e.g.		
PT	AIDS, allergy or anemia, multiple sclerosis, osteoarthritis, cancer or		
XX	hepatitis.		

[illegible]


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OS Synthetic.
XX Key location/Qualifiers
FH CDS 213..2040
FT /tag= a
FT /product= "mu-opioid receptor"
FT /tag= b
FT /tag= b
FT /note= "Site of intron 1"
FT mutation 666
FT /tag= e
FT /note= "Wild type A is replaced by G"
FT /tag= c
FT /tag= c
FT /note= "Site of intron 2"
FT /tag= d
FT /note= "Site of intron 3"
XX MO983937-A2.
XX 06-AUG-1998.
XX 02-FEB-1998; 98WO-DE000382.
XX 03-FEB-1997; 97DE-01003925.
XX (DEIB-) DEIBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX Hoehe M, Wendel B;
XX WPI: 1998-437487/37.
XX
XX New genomic and cDNA sequences encoding human mu-opioid receptor - used,
XX e.g. to predict pre-disposition to addiction and for development of
XX analgesics, anaesthetics and anti-addiction agents.
XX
XX Claim 8; Page; 26pp; German.
XX
XX This sequence encodes a novel human mu-opioid receptor in which an A
XX nucleotide at position 666 of the wild-type sequence represented in
XX AAV61994 is replaced by a G. The wild type receptor and its variants,
XX polymorphisms and mutants are used in a method for detecting
XX predisposition to disease, particularly addictive disease, by isolating
XX DNA from a sample, genotyping selected positions and comparing with a
XX reference DNA. Such sequences are used to develop analgesic, anaesthetic,
XX anti-addictive and psychopharmaceutical agents, to construct genes and
XX vectors, particularly for pharmaceutical development, to develop
XX diagnostic kits for predicting risk of addiction, response to analgesics
XX or anaesthetics, or development of side effects from a drug. Particular
XX applications are to determine risk of addiction to opiates or cocaine, or
XX of developing inherited alcoholism. Note: This sequence is not
XX represented in the specification and has been constructed from the wild-
XX type sequence represented in AAV61984 in accordance with the
XX specification
XX
SQ Sequence 2162 BP; 561 A; 565 C; 459 G; 575 T; 0 U; 2 Other;
Query Match 37.5%; Score 433.2; DB 2; Length 2162;
Best Local Similarity 66.2%; Pred. No. 3.5e-96;
Matches 659; Conservative 0; Mismatches 328; Indels 9; Gaps 2;
QY 92 CCGGCTGGGCGGAGCCCGAGCAAGGAGGCGCGGCTCGGAGAGAGCGGCAAGCTGAGAC 151
DB 337 CCGACCCGATCGCGATCGGAACCCGACCAACCTGCGGAGAGAGAGAGCGCTGTCGCA 396
QY 152 CCGGCGACATCTCCCGGCGCATCCGCGTATCATACGCGGCTACTCCGAGTGTTCG 211
DB 397 CCGGCGATCTCTCATGATCATGCGCGCATCATGCGCTCTTACTCATCGTGTGG 456
QY 212 TCGTGGGCTGTGGGCAACTGCTGTCATGTTCGATCATCGCATCAAGATGA 271
DB 457 TGGTGGGCTCTTCCGAAACTTCTCGTGTATGTATGTTCGATCATCAAGATGA 516

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QY 272 AGACAGCAACCAACATTTACATATTTACCTGGCTTTGGCAGATCTTTAGTTACTACAA 331
DB 517 AGACTGCCAACCAACATTTACATTTTCAACCTTGTCTGTGGCAGATCTTTAGCACCAGTA 576
QY 332 CCATGCCCTTTACAGATACGGCTCTATGATGAATTTCTGGCTTTGGGAGTGTCTGT 391
DB 577 CCTGCCCTTCCAGATGTGATTAATTAATTAATGGAACATGGCCATTTGGAACATCTTT 636
QY 392 GCAAGATGTGAATTTCCATTTGATTTACTACAAATGTTTCAACGACATCTTCACTTGACA 451
DB 637 GCAAGATGTGATCTCCATTAATTAATTAATGATGATGATGATGATGATGATGATGATGAT 696
QY 452 TGATGAGGTGAGACCGCTACATTTGCGGTGGCAACCCGTTGAGGCTTGGACCTCCGA 511
DB 697 CCAATGATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 756
QY 512 CACCTTTGAGGCAAGATCATATATATGATGATGATGATGATGATGATGATGATGATGATGAT 571
DB 757 CTCCCCGAAATGCCAAATTTATCAATGTCGAACTGGATCCTCTTCAAGCATTTGGTC 816
QY 572 TCTGTCAATAGTCTTGGAGGACCAAAAGTCAGGAAAGAGCTGATGATGATGATGATGATGAT 631
DB 817 TTCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 870
QY 632 CTTGCAATGTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 691
DB 871 CACTAACATCTCTCATCAACCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 927
QY 692 TCATCTTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 751
DB 928 TCATCTTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 987
QY 752 TCGCTCAAGAGGCTCGGCTCTTGTGCTCCGAGAGAAAGATGCAACCTGCTGA 811
DB 988 TCGGCTCAAGAGGCTCGGCTCTTGTGCTCCGAGAGAAAGATGCAACCTGCTGA 1047
QY 812 GGATCAGCAGATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 871
DB 1048 GGATCAGCAGATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1107
QY 872 ACATATTCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 931
DB 1108 ACATATTCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1167
QY 932 GCTATTTACTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 991
DB 1168 CTTGCACTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1227
QY 992 CTTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1051
DB 1228 CATTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1287
QY 1052 GGATGAGGCGGAGAGCACTAGAGAGTCCGAATA 1087
DB 1288 ACATTGAGCAACAAATCTCACTGCAATTCTGCA 1323

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RESULT 44
AAV61992
ID AAV61992 standard; cDNA, 2162 BP.

AAV61992;

11-JAN-1999 (first entry)

Human mu-opioid receptor cDNA variant 8.

Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;
predisposition; addiction; analgesic; anaesthetic; anti-addictive;
psychopharmaceutical agent; diagnostic; side effect; drug; opiate;
cocaine; inherited alcoholism; human; ss.

```
OS Homo sapiens.
XX Synthetic.
FH Key
FT CDS
FT 213..2040
FT /tag= a
FT /product= "mu-opioid receptor"
FT 502..503
FT /tag= b
FT /note= "Site of intron 1"
FT 655..656
FT /tag= c
FT /note= "Site of intron 2"
FT 1006
FT /tag= e
FT /note= "Wild type G is replaced by A"
FT 1376..1377
FT /tag= d
FT /note= "Site of intron 3"

W09833937-A2.
PD 06-AUG-1998.
PF 02-FEB-1998; 98MO-DE000382.
PR 03-FEB-1997; 97DE-01003925.
PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
PI Hoehe M, Wendel B;
DR WPI, 1998-437487/37.
PT New genomic and cDNA sequences encoding human mu-opioid receptor - used,
PT e.g. to predict pre-disposition to addiction and for development of
PT analgesics, anaesthetics and anti-addiction agents.
XX
XX Claim 8; Page; 26pp; German.
XX
XX This sequence encodes a novel human mu-opioid receptor in which a G
XX nucleotide at position 1006 of the wild-type sequence represented in
XX AAV61984 is replaced by an A. The wild type receptor and its variants,
XX polymorphisms and mutants are used in a method for detecting
XX predisposition to disease, particularly addictive disease, by isolating
XX DNA from a sample, genotyping selected positions and comparing with a
XX reference DNA. Such sequences are used to develop analgesic, anaesthetic,
XX anti-addictive and psychopharmaceutical agents, to construct genes and
XX vectors, particularly for pharmaceutical development, to develop
XX diagnostic kits for predicting risk of addiction, response to analgesics
XX or anaesthetics, or development of side effects from a drug. Particular
XX applications are to determine risk of addiction to opiates or cocaine, or
XX of developing inherited alcoholism. Note: This sequence is not the wild-
XX type sequence represented in AAV61984 in accordance with the
XX specification
XX
XX Sequence 2162 BP; 563 A; 565 C; 457 G; 575 T; 0 U; 2 Other;
XX
XX Query Match 37.5%; Score 433.2; DB 2; Length 2162;
XX Best Local Similarity 66.2%; Pred. No. 3.5e-96;
XX Matches 659; Conservative 0; Mismatches 328; Indels 9; Gaps 2;
```

```
Db 457 TGTGGGGCTCTTGGAAACTTCTGGGTCATGTATGTATGTGCATACCAAGATGA 516
Qy 272 AGACAGCAACCAATTTACATATTTAACCTGGCTTGGAGATGCTTATGTTACTACA 331
Db 517 AGACTGCCACCAACATCTACATTTTCAACTTGTCTGGGAGATGCTTGGCCACAGTA 576
Qy 332 CCATGCCCTTTCAGAGTACGGTCTACTTGAATTTCTGGCCCTTTTGGGATGTCGT 391
Db 577 CCGTCCCTTCCAGAGTGAATTTACCTAATGGGAACATGGCCATTGGAAACATCTTT 636
Qy 392 GCAAGATGTAATTTCCATTTGATTTACTACCAATGTTACCCAGATCTTCACTTGACA 451
Db 637 GCAAGATGATGATCTCCATGATTTACTATTAACATGTTACACAGCATATTCACCTTCGCA 696
Qy 452 TGATGAGCGGAGCCGCTACATCTGGGTGGCCACCCCGGAAGGCTTGGACTTCGCA 511
Db 697 CCATGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 756
Qy 512 CACCCCTGGAAGGCAAGATCATCAATATCTGATCTGGCTGCTGCTCACTGTTGGCA 571
Db 757 CTCCCGCAAAATGCCAAATTAATGATGTCTGCAACTGGATCTCTCTTCAAGCCATTGGTC 816
Qy 572 TCTTGCAATATGTCCTTGGAGGCAACCAAGTCAAGGAAAGCTCATGTCAATGATGCT 631
Db 817 TTCTGTAAATGTTTCATGCTTACCAACAAATAACAGGCAAGG-----TTCCATGATTTGTA 870
Qy 632 CCTTGAGTTCACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 691
Db 871 CACTTAACATTTCTTCATCCAACTGCTGATGAGGAAACCTGG--TGAAAGTCTGTGTTT 927
Qy 692 TCATCTTGGCTTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 751
Db 928 TCATCTTGGCTTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 987
Qy 752 TGCCTTCAAGAGGCTCCGCTCTTCTGCTGCTCCAGAGAAAGATCGCAACTGTGTA 811
Db 988 TGCCTTCAAGAGGCTCCGCTCTTCTGCTGCTCCAGAGAAAGATCGCAACTGTGTA 1047
Qy 812 GGATCACCAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 871
Db 1048 GGATCACCAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1107
Qy 872 ACATATTCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 931
Db 1108 ACATATTCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1167
Qy 932 GCTATTCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 991
Db 1168 CTTGGACCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1227
Qy 992 CTTTCTTGAATGAACCTTGAAGGGGTTTCCGGGACTTCTGCTTCCAGTAAGATGA 1051
Db 1228 CATTTCTGATGATGAACCTTGAAGGGGTTTCCGGGACTTCTGCTTCCAGTAAGATGA 1087
Qy 1052 GGATGAGCGGAGAGCATGAGCATGAGCATGAGCATGAGCATGAGCATGAGCATGAGCAT 1087
Db 1288 ACATGAGCAACAAACTCCATCGAATGTCAGA 1323

RESULT 45
AAV61993
ID AAV61993 standard; cDNA, 2162 BP.
XX
XX AAV61993;
AC
XX 11-JAN-1999 (first entry)
DE Human mu-opioid receptor cDNA variant 9.
XX
XX Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;
XX predisposition; addiction; analgesic; anaesthetic; anti-addictive;
XX psychopharmaceutical agent; diagnostic; side effect; drug; opiate;
XX cocaine; inherited alcoholism; human; ss.
```

XX	Homo sapiens.
OS	Synthetic.
XX	
FH	Key
FT	CDS
FT	Location/Qualifiers
FT	213..2040
FT	/tag= a
FT	/product= "mu-opioid receptor"
FT	502..503
FT	/tag= b
FT	/note= "Site of intron 1"
FT	855..856
FT	/tag= c
FT	/note= "Site of intron 2"
FT	1014
FT	/tag= e
FT	/note= "Wild type T is replaced by C"
FT	1376..1377
FT	/tag= d
FT	/note= "Site of intron 3"
PN	
XX	M09833937-A2.
PD	
XX	06-AUG-1998.
PR	
XX	02-FEB-1998; 98WO-DE000382.
PA	
XX	03-FEB-1997; 97DE-01003925.
PI	(DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
DR	
XX	Hoehne M, Wendel B;
PT	WPJ; 1998-437487/37.
PT	New genomic and cDNA sequences encoding human mu-opioid receptor - used,
PT	e.g. to predict pre-disposition to addiction and for development of
PT	analgesics, anaesthetics and anti-addiction agents.
XX	
PS	Claim 8; Page; 26pp; German.
XX	
CC	This sequence encodes a novel human mu-opioid receptor in which a T
CC	nucleotide at position 1014 of the wild-type sequence represented in
CC	AAV61984 is replaced by a C. The wild type receptor and its variants,
CC	polymorphisms and mutants are used in a method for detecting
CC	predisposition to disease, particularly addictive disease, by isolating
CC	cDNA from a sample, genotyping selected positions and comparing with a
CC	reference DNA. Such sequences are used to develop analgesic, anesthetic,
CC	anti-addictive and psychopharmaceutical agents, to construct genes and
CC	vectors, particularly for pharmaceutical development, to develop
CC	diagnostic kits for predicting risk of addiction, response to analgesics
CC	or anaesthetics, or development of side effects from a drug. Particular
CC	applications are to determine risk of addiction to opiates or cocaine, or
CC	of developing inherited alcoholism. Note: This sequence is not
CC	represented in the specification and has been constructed from the wild-
CC	-type sequence represented in AAV61984 in accordance with the
CC	specification
XX	
SO	Sequence 2162 BP; 562 A; 566 C; 458 G; 574 T; 0 U; 2 Other;
	Query Match 37.5%; Score 433.2; DB 2; Length 2162;
	Best Local Similarity 66.2%; Pred. No. 3.5e-96;
	Matches 659; Conservative 0; Mismatches 328; Indels 9; Gaps 2
OY	
Db	
	92 CCGGCTGGGGCGAGGCCGACACGAACGGAGCGGCCTCGGAGAGACCGGCAGCCTGAGC 151
	337 CGAGACCACGCGGTCCGAACCGCACCAACTGGGGCGGAGACAGCCTGTGCTCCCA 396
OY	
	152 CCGCGCACATCTCCCCGGGCGCATCGCGTTCATCATCAGCGCGGTCTACTCCGTAAGTTGG 211
Db	
	397 CCGGAGAGTCCCTTCATGATCAGAGGCGCATACGATCATGGCCCTCTACTCATTCTGTGTGG 456
OY	
	212 TCGTGGGCTTGTTGGGCAATCTGCTGTGTCATGTTGTGTATCTCCGATACACAAGAATCA 271

[illegible]

KW autonomous nervous system; peristalsis regulator; body weight;
 KW neuroendocrine disorder; MOR-1D; ss.
 OS Mus sp.
 XX Key Location/Qualifiers
 XX FT CDS 67..1245
 XX FT /*tag= a
 XX FT /product= "MOR-1D"
 XX FT /note= "no termination codon given"
 XX
 XX MO200004046-A2.
 XX PD 27-JAN-2000.
 XX PF 15-JUL-1999; 99MO-US015974.
 XX PR 16-JUL-1998; 98US-0092980P.
 XX PA (SLOK) SLOAN KETTERING INST CANCER RES.
 XX PI Paeternak G, Pan Y;
 XX DR WPI: 2000-182402/16.
 XX DR P-PSDB; AAY68879.
 XX PT New splice variants of the mu-opioid receptor, useful in screening for
 XX PT selective analgesics and for regulating morphine analgesia or body
 XX PT weight.
 XX PS Claim 32; Fig 2B; 83bp; English.
 XX
 CC The present sequence encodes a murine mu-opioid receptor (MOR-1) splice
 CC variant MOR-1D. The specification describes 11 new exons for the MOR-1
 CC gene, which combine to yield 15 novel splice variants of the MOR-1 gene.
 CC These splice variants are potential targets for modulating morphine
 CC analgesia and opioid-mediated ingestive responses. The MOR-1 polypeptide
 CC is used to screen compounds for opioid activity. Such compounds are
 CC potential analgesics or more generally agents that affect
 CC gastrointestinal motility, respiration or the immune, endocrine or
 CC autonomous nervous systems, e.g. regulators of peristalsis. Antagonists,
 CC agonists and ligands of MOR-1, as well as DNA vectors expressing MOR-1-
 CC encoding nucleic acids, or sequences antisense to MOR-1 nucleic acids,
 CC are used to regulate morphine analgesia and body weight. The level of MOR
 CC -1 or tissue distribution of MOR-1 can be measured to diagnose MOR-1
 CC related pharmacological abnormalities or neuroendocrine disorders,
 CC particularly inherited disorders. Transgenic animals with extra copies of
 CC the MOR-1 gene, or with endogenous alleles deleted, are used to study
 CC losses or gain of function phenotypes
 CC
 XX Sequence 1334 BP; 320 A; 397 C; 297 G; 320 T; 0 U; 0 Other;
 XX
 XX Query Match 37.5%; Score 432.4; DB 3; Length 1334;
 XX Best Local Similarity 65.8%; Pred. No. 4.6e-96;
 XX Matches 663; Conservative 0; Mismatches 336; Indels 9; Gaps 2;

Db 425 |||||CGCGCCCTTTCAAGAGTGTAACTACCGATGGGAAGTGCCCTTGGAAAACATCGCTCT 484
 Qy 392 GCAAGATAGTAATTTCCATTGATTAACAAATGTTCAACAGATCTTCACTTGACCA 451
 Db 485 GCAAGATGCTGATCTCAATAGACTAACAACATGTTCAACAGATCTTCACTTGACCA 544
 Qy 452 TGATGAGGCTGAGACCGGCTACATGCGCTGTCGCAACCCCGTGAAGCTTTGACCTTCCGA 511
 Db 545 CCAATGAGTGAACCGCTACATGCGCTGTCGCAACCCCGTGAAGCTTTGACCTTCCGA 604
 Qy 512 CACCCCTTGAAGCAAAAGATCAATATCTGCAATCTGAGCTGCTGCTGATCTTGAGCA 571
 Db 605 CCCCCGAAATGCCAAATGTCATATGTCGCAATGATCTCTCTTCTGCAATGAGTC 664
 Qy 572 TCTGTCAATAGTCTCTTGAGAGCAACAAAGTCAGAGGAAGAGTGAATGATCAATGAGTCT 631
 Db 665 TGCCCGTAATGTTATGAGCAACCAAAATACAGAGGAGGCTC-----CATGATATGCA 718
 Qy 632 CCTTGACGTTCCAGATGATGACTACTCTGCTGAGGACCTTCTCATGAAATCTGCGCT 691
 Db 719 CCTTCAGCTTCTCTCATATCCCATGATGTAAGGAACTGCTC---AAATCTGTGCTCT 775
 Qy 692 TCATCTTTCCTTGTGATGATCCCTGCTCTCATATCATCTGCTGATCAACCTGATGATCC 751
 Db 776 TCATCTTTCCTTGTGATGATCCCTGCTCTCATATCATCTGCTGATGATGATGATCT 835
 Qy 752 TGCCTCTCAAGAGGCTCGGCTCTTCTGCTCTCCAGAGAAAGATGCAACTGAGTGA 811
 Db 836 TACGACTCAAGAGGCTCGGCTCTTCTGCTCTCCAGAGAAAGATGCAACTGAGTGA 895
 Qy 812 GGATCAACAAGACTGCTGCTGCTGAGTGAAGTCTGCTGCTGATGATGATGATGATGATG 871
 Db 896 GGATCAACAAGACTGCTGCTGAGTGAAGTCTGCTGCTGATGATGATGATGATGATGATG 955
 Qy 872 ACATATTCATCTGCTGAGGCTTGGAGAGCACTTCCAGACAGCAGCTGCTCTGCA 931
 Db 956 ACATATTCATCTGCTGAGGCTTGGAGAGCACTTCCAGACAGCAGCTGCTCTGCA 1015
 Qy 932 GCTATTAATCTGATGATGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGA 991
 Db 1016 CTTGAGCACTTCTGATGATGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGA 1075
 Qy 992 CTTTCTGATGAAATCTTGAAGGCTTTCGAGGCTTCTGCTTCACTGAAGATGA 1051
 Db 1076 GCTTCTGATGAAATCTTGAAGGCTTTCGAGGCTTCTGCTTCACTGAAGATGA 1135
 Qy 1052 GGATGAGCGGACAGACATGACAGAGTCCGAATACATGTTCAAGATC 1099
 Db 1136 CAATCGAAGCAAAACTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 1183
 XX
 XX RESULT 47
 XX AAZ60737
 XX ID AAZ60737 standard; cDNA; 1346 BP.
 XX
 XX AC AAZ60737;
 XX
 XX DT 16-MAY-2000 (first entry)
 XX
 XX cDNA encoding murine mu-opioid receptor splice variant MOR-1B I.
 XX
 XX Mu-opioid receptor; MOR-1; splice variant; morphine analgesia;
 KW opioid-mediated ingestive response; opioid activity; analgesic;
 KW gastrointestinal motility; respiration; immune system; endocrine system;
 KW autonomous nervous system; peristalsis regulator; body weight;
 KW neuroendocrine disorder; MOR-1B I; ss.
 XX
 XX OS Mus sp.
 XX Key Location/Qualifiers
 XX FT CDS 67..1245
 XX FT /*tag= a

/product= "MOR-1B 1"

MO200004046-A2.

27-JAN-2000.

15-JUL-1999; 99WO-US015974.

16-JUL-1998; 98US-0092980P.

(SLOK) SLOAN KETTERING INST CANCER RES.

Pasternak G, Pan Y;

WPI, 2000-182402/16.

P-PSDB; AAV68886.

New splice variants of the mu-opioid receptor, useful in screening for selective analgesics and for regulating morphine analgesia or body weight.

Claim 46; Fig 2L-M; 83p; English.

The present sequence encodes a murine mu-opioid receptor (MOR-1) splice variant MOR-1B 1. The specification describes 11 new exons for the MOR-1 gene, which combine to yield 15 novel splice variants of the MOR-1 gene. These splice variants are potential targets for modulating morphine analgesia and opioid-mediated ingestive responses. The MOR-1 polypeptide is used to screen compounds for opioid activity. Such compounds are potential analgesics or more generally agents that affect gastrointestinal motility, respiration or the immune, endocrine or autonomic nervous systems, e.g. regulators of peristalsis. Antagonists, agonists and ligands of MOR-1, as well as DNA vectors expressing MOR-1-encoding nucleic acids, or sequences antisense to MOR-1 nucleic acids, are used to regulate morphine analgesia and body weight. The level of MOR-1 or tissue distribution of MOR-1 can be measured to diagnose MOR-1 related pharmacological abnormalities or neuroendocrine disorders, particularly inherited disorders. Transgenic animals with extra copies of the MOR-1 gene, or with endogenous alleles deleted, are used to study loss or gain of function phenotypes

Sequence 1346 BP; 338 A; 398 C; 282 G; 328 T; 0 U; 0 Other;

Query Match 37.5%; Score 432.4; DB 3; Length 1346;
Best Local Similarity 65.8%; Pred. No. 4.6e-96;
Matches 663; Conservative 0; Mismatches 336; Indels 9; Gaps 2;

QY 92 CCGGCTGGGCGAGCCGACGACGAGCGGCGGCTCGAGGACGCGAGCTGAGC 151
DB 185 CCGACCCATGCGGCTCTTAACCGGACGGGCTTGCGGAGGACGACCTGTGCTCAGA 244
QY 152 CCGGCGACATCTCCCGGCGATCCGGTCATCATGCGGCGGTCTACTCCGTAGTTCG 211
DB 245 CCGGACGCGCTTCATGTCACAGCCATCATGCGCTCTTATTTATTCGTGTGG 304
QY 212 TCGTGGGCTTGGTGGCACTGCTGTGTATGTTGTATCATCCGATACAAAGATGA 271
DB 305 TAGTGGGCTCTTTGAAACTTCCTGTCATATGATGATTAAGATATACAAATGA 364
QY 272 AGACAGCAACCAATTTATTTAACTTGCTTTGAGAGTGTAGTTACTACAA 331
DB 365 AGACTGCGACCAACATCTACATTTTCACTTGTGCTGTGCAATGCTTAGCCACTAGCA 424
QY 332 CGATGCGCTTTCAGAGTACGATCTACTGATGTAATTCCTGAGCTTTGGGAGTGTGCT 391
DB 425 CGCTGCGCTTTCAGAGTGTACTACTGATGGAACGAGGCGCTTTGGAACATCTCT 484
QY 392 GCAAGATAGTATTTTCACTTGTATTAACAATGTTCAACGACATCTTCACTTGACCA 451
DB 485 GCAAGATCGTATCTCAATAGACTACTACAAATGTTCAACGATCTTCACTTGACCA 544
QY 452 TGATGAGGTGAGCGCTCATTTGCGGTGCAACCGGTGAAGGTTGACCTTCGCA 511

DB 545 CCATGATGTAGACCGCTACATTTGCCGTCTGCCACCCCGGTGAAGCCCTGATTTCCGTA 604
QY 512 CACCTTGAAGCAAAATCATCAATATCTGATCTGCTGTGCTGATCTGTGCA 571
DB 605 CCCCCGAAATGCGCAAAATTTGTCATGTCTGCAATGATCTCTTCTGCAATGGC 664
QY 572 TCTTGCATATAGTCTTGGAGGACCAAAAGTCAGGAAGAGCTCGATCTGATGAGTCT 631
DB 665 TGCCGTAAATGTATTCAGGCACCAAAATACAGGACGAGGTC-----CATAGTTGCA 718
QY 632 CTTTGCAGTTCACAGATGATGATCTCTGCTGAGGACCTTTTCATGAAGATCTGCTCT 691
DB 719 CCGTCAGCTTCTCATCCCATGATGTAATGGAAGAACTGTCT--AAATCTGTCT 775
QY 692 TCATTTTGGCTTGTGATCCCTGTCTCATCATATGCTGTCTACACCTGATGATCC 751
DB 776 TCATCTTGGCTTTCATGACCGGCTCATCATCATCTGTGTATGAGACTGATGATCT 835
QY 752 TGCGTCTGAAGAGCGGCTCGGCTCTTTCTGCTCCGAGAGAAAGATGCAACTGCGTA 811
DB 836 TACGACTCAAGAGTCTCCGATGCTGTGCGGCTCCAAAGAAAGACAGAACTTGCGCA 895
QY 812 GGATCACCAGACTGTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 871
DB 896 GGATCACCAGGATGT 955
QY 872 ACATTTATCTGT 931
DB 956 ACATTTATGTATCTATCAACAGCATGATCAGATTCAGAAACCACTTCCAGACTGTT 1015
QY 932 GCTATTACTTTCGATGCTTGAAGCTTATGAGCTTATCAACAGTATGATCCATTTCTAG 991
DB 1016 CTTGCACTTCTTGTATGCTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1075
QY 992 CTTTCTTGTATGAATACTTCAAGCGGTGTTCGAGACTTGTCTTTCACCTGAAGATGA 1051
DB 1076 GCTTCTGATGAAATCTTCAAGAGATGTTTAAAGAGTGTGTGTGTGTGTGTGTGT 1135
QY 1052 GGATGAGCGGACAGCATGACAGATGCCAAATACAGTTCAAGATC 1099
DB 1136 CAATGAAACAGCAAACTGTCTGATCCGTCAAACACATGAGGAAAC 1183

RESULT 48
AAZ60736
ID AAZ60736 standard; cDNA, 1365 BP.
XX
XX AAZ60736;
DT 16-MAY-2000 (first entry)
XX
XX cDNA encoding murine mu-opioid receptor splice variant MOR-1A.
DB
XX Mu-opioid receptor; MOR-1; splice variant; morphine analgesia;
XX opioid-mediated ingestive response; opioid activity; analgesic;
XX gastrointestinal motility; respiration; immune system; endocrine system;
XX autonomic nervous system; peristalsis regulator; body weight;
XX neuroendocrine disorder; MOR-1A; ss.
XX
XX Mus sp.
OS
XX
XX
FH Key Location/Qualifiers
FT CDS 67..1239
FT /*tag= a
FT /product= "MOR-1A"
PN
XX
XX MO200004046-A2.
PD 27-JAN-2000.
PF 15-JUL-1999; 99WO-US015974.
PR 16-JUL-1998; 98US-0092980P.

XX
PA (SLOK) SLOAN KETTERING INST CANCER RES.

PI Pasternak G, Pan Y;

WPI; 2000-182402/16.

DR P-PSDB; AAY68885.

PT New splice variants of the mu-opioid receptor, useful in screening for
PT selective analgesics and for regulating morphine analgesia or body
PT weight.

Claim 44; Fig 2J; 83pp; English.

CC The present sequence encodes a murine mu-opioid receptor (MOR-1) splice
CC variant MOR-1A. The specification describes 11 new exons for the MOR-1
CC gene, which combine to yield 15 novel splice variants of the MOR-1 gene.
CC These splice variants are potential targets for modulating morphine
CC analgesia and opioid-mediated ingestive responses. The MOR-1 polypeptide
CC is used to screen compounds for opioid activity. Such compounds are
CC potential analgesics or more generally agents that affect
CC gastrointestinal motility, respiration or the immune, endocrine or
CC autonomic nervous systems, e.g. regulators of peristalsis. Antagonists,
CC agonists and ligands of MOR-1, as well as DNA vectors expressing MOR-1-
CC encoding nucleic acids, or sequences antisense to MOR-1 nucleic acids,
CC are used to regulate morphine analgesia and body weight. The level of MOR
CC -1 or tissue distribution of MOR-1 can be measured to diagnose MOR-1
CC related pharmacological abnormalities or neuroendocrine disorders,
CC particularly inherited disorders. Transgenic animals with extra copies of
CC the MOR-1 gene, or with endogenous alleles deleted, are used to study
CC loss or gain of function phenotypes

Sequence 1365 BP; 341 A; 399 C; 290 G; 335 T; 0 U; 0 Other;

Query Match 37.5%; Score 432.4; DB 3; Length 1365;

Best Local Similarity 65.8%; Pred. No. 4.7e-96;

Matches 663; Conservative 0; Mismatches 336; Indels 9; Gaps 2;

Qy	92	CGGGCTGGGGCCGAGCCCGGACACCAACGAGGCGCGCTCGGAGAGACGCGAGTGGAGC	151
Db	185	CCGACCCATGCGGTCTTAAACCGAGGGGCTTGGGGGAGCCACAGCCTGGCCCTCAGA	244
Qy	152	CCGGGACATCTTCCCGGGACATCCGGATCATCACGGCGGATCTACTCCGTAGTGTTCG	211
Db	245	CCGGCAGCCCTTCATGATGTCAGAGCCATCACCATATGAGCCCTCTATTCTATGATGTG	304
Qy	212	TGCTGGGCTTGGGGGCACTCGCTGTCATGTTGTGATCATCCGATACCAAAAGTGA	271
Db	305	TATGTGGCCCTCTTGGAAACTTCGTCGATGATATGATTTGTAAGATATACCAAAATGA	364
Qy	272	AGACACAAACCAATTTACATATTATTAACCTGGCTTGGCAGATGCTTATGTTACTCA	331
Db	365	AGACTGCAACCAACATCTACATTTTCAACCTTGCTGTGGAGATGCTTGGACATGCA	424
Qy	332	CCATGCCCTTTAGAGTACGCTCTACTTGATGAATCTCGCCTTTTGGGGATGTGCTGT	391
Db	425	CGCTGCCCTTTAGAGTGTAACTCTAGATGGGAAGCTGGCCCTTTGGAAAATCTCTCT	484
Qy	392	GCAAGATAGTAATTTTCATGTATCTCTCAACATGTTACACAGATCTTACCTTGACCA	451
Db	485	GCAAGATGTGATCTCAATAGACTCTCAACATGTTTACCAATGATCTTCAACCTCTGCA	544
Qy	452	TGATGAGCGTGACCGCTACATTTGCCGTGTGCAACCCCGTGAAGGCTTTGGACTTCGCA	511
Db	545	CCATGAGTGTAGACGCTACTATTCGCTGTGCAACCCGATCAAGGCCCTGGAATTTCCGTA	604
Qy	512	CAACCTTGAAGCAAAATCATCAATATCTGATCTGGCTGTCTGTCATCTGTGTGGCA	571
Db	605	CCCCCGAAATGCCAAATTTGCAATGTGTGCACTGGATCTCTCTTCTGCAATTTGTGTC	664
Qy	572	TCTCTGCAATAGTCTTTGAGGCAACAAAGTCAGGGAAGAGTCGATGTCAATTAAGTCT	631
Db	665	TGCGCCTAATGTTCAATGCAACCAAAATACAGGCAAGGGTCT-----CATGATTTGCA	718

OY	632	CCTTGCACTTCCAGATATAGACTACTCCTGGTGGAGACTCTTCACTGAAGATCTGCCTCT	691
Db	719	CCCTCACGTTCTCTCATCCACACATGATCTGGGAACCTGCTC-- -AAAATCTGTCT	775
OY	692	TCATCTTTCCTTGATGATCCCTGTCCCTCATCATCATGATGATGATGATGATCC	751
Db	776	TCATCTTTCGCTTATCATATGCCGGCTCTCATCATCATCTGTGTGTATGACCTGATGATCT	835
OY	752	TGCGTCTCAAGAGCGTCCGGCTCCTTTCTGCTCCGAGAGAAAGATGCAACTGGCTA	811
Db	836	TACGACTCMAAGTGTCCGCATGTCTGTGGGGCTCCAAAAGAAAGACAGGAACTCGCGCA	895
OY	812	GGATTACAGACTGGTCTCTGGAGGTGGGAGCTTGATGCTGTCTGCTGGAATCCCATTC	871
Db	896	GGATCACCCGGATGTGTGGTGTGTGTGTGTGTATTTATTTGTCTGTCTGGAACCCCATTC	955
OY	872	ACATAATTCATCCTGGTGGAGGCTCTGGGAGACCTCCACAGCACAGCTGCTCTCCCA	931
Db	956	ACATCTATGTATCATCAAGACACTGATCAAGATCCAGAAACCACTTCCAGACTGTTT	1015
OY	932	GCTATTAATTTCTGCATGCGCTTTAGGCTATACCAAGATAGCTGAAATCCCATTTCTTAG	991
Db	1016	CTGGCACTTCTGCAATGCTTGGGTACACAAAGAGCTGCTGAAACCACTGTTCTTTATG	1077
OY	992	CCTTCTCTGATGAAAACTTCAAGCGGATTTCCGGGACTTCTGCTTCCACTGAGAAATGA	1051
Db	1076	CGTTCCTGGATGAAAACTTCAACGATGTTTAAAGAAATTTCTGCATCCCAACTTCTCCCA	1133
OY	1052	GGATGAGCGGCAAGACCTAGCAGAGTCCGAAATACAGTTCCAGATC	1099
Db	1136	CAATCTGAACAGCAAAACTCTGCTGAAATCCGTCACAAACACTAGAGGAAAC	1183

RESULT 49

AAZ60726

ID AAZ60726

XX

AC AAZ60726;

XX

DT 16-M

XX 5

DE
CDNA

2000

KW M13-Q

KW opjg

KW	cast
KW	opto

KW gas

WV aulc
KW neily

neu
KW
YY

XX
09
Ms.9

US	MUS
VY	

XX
FEB 1961

FH Key

FT	CDS
10	10
20	20
30	30
40	40
50	50
60	60
70	70
80	80
90	90
100	100

ET

ET

XX

PT selective analgesic and for regulating morphine analgesia or body weight.

XX Claim 30; Fig 2A; 83bp; English.

CC The present sequence encodes a murine mu-opioid receptor (MOR-1) splice
CC variant MOR-1C. The specification describes 11 new exons for the MOR-1
CC gene, which combine to yield 15 novel splice variants of the MOR-1 gene.
CC These splice variants are potential targets for modulating morphine
CC analgesia and opioid-mediated ingestive responses. The MOR-1 polypeptide
CC is used to screen compounds for opioid activity. Such compounds are
CC potential analgesics or more generally agents that affect
CC gastrointestinal motility, respiration or the immune, endocrine or
CC autonomic nervous systems, e.g. regulators of peristalsis. Antagonists,
CC agonists and ligands of MOR-1, as well as DNA vectors expressing MOR-1-
CC encoding nucleic acids, or sequences antisense to MOR-1 nucleic acids,
CC are used to regulate morphine analgesia and body weight. The level of MOR
CC -1 or tissue distribution of MOR-1 can be measured to diagnose MOR-1
CC related pharmacological abnormalities or neuroendocrine disorders,
CC particularly inherited disorders. Transgenic animals with extra copies of
CC the MOR-1 gene, or with endogenous alleles deleted, are used to study
CC loss or gain of function phenotypes

XX Sequence 1423 BP; 343 A; 423 C; 317 G; 340 T; 0 U; 0 Other;

Query Match 37.5%; Score 432.4; DB 3; Length 1423;

Best Local Similarity 65.8%; Pred. No. 4.7e-96;

Matches 663; Conservative 0; Mismatches 336; Indels 9; Gaps 2;

QY 92 CCGGCTGGGCGGAGCCGAGCAGCAAGCGCGGCTGGAGAGCGCGAGCTGAGAC 151
DB 185 CCGAGCCATGCGGCTCTTAACCGCAGGGGCTTGGGGAGCCAGCCTGTGCTCCAGA 244
QY 152 CCGGCGACATCTCCCGGCGCATCCGGTATCATCAGCGCGGCTTACTCTCGTAGTTCG 211
DB 245 CCGGAGCGCTTCCATGATGACAGCAGCATCAGCATGAGCCCTTATCTATCGTGTG 304
QY 212 TCGTGGGCTGGTGGGCAATCGCTGTGTCATTTGTATATCCGATACCAAGATGA 271
DB 305 TAGTGGGCTCTTGGAAATCTCTGTGTATGTATGTATGTATGAATACCAAAATGA 364
QY 272 AGACAGCAACCAATTACATTTAATCTGCTTTGGAGATCTTTAGTTACTACAA 331
DB 365 AGACGCGCAACCAATCTACATTTTCAACCTTGTCTGGAGATGCTTTAGCAGTACGA 424
QY 332 CCATGCGCTTTGAGATGAGGTCTTACTTGATGATTTCTGGCTTTTGGGATGTGCT 391
DB 425 CGTGCCTTTGAGATGATGATCTACGATGGAACGTGGCCTTTGGAACATCTCT 484
QY 392 GCAAGATGTAATTTCCATTTGATTTACTACAACTGTTCAACGAGATCTTCACTTGACGA 451
DB 485 GCAAGATGTAATCTCAATGATGATCTACAACTGTTCAACGATCTTCAACCTCTGCA 544
QY 452 TGATGAGGTGAGCGGTACATTTGCGTGTGCAACCGGTGAAAGGCTTTGAGCTCCGCA 511
DB 545 CCATGAGGTGAGCGGTACATTTGCGTGTGCAACCGGTGAAAGGCTTTGAGCTCCGCA 604
QY 512 CACCTTGAAGCAAAATGATCATATATCTGATCTGCTGTGCTGATCTGTGCA 571
DB 605 CCCCCGAAATGCCAAATTTGTCATGTCTGCAATGTGATCTCTCTTCTGCAATGTGTC 664
QY 572 TCTCTGCAATAGTCTTGGAGGCAACCAAGTACAGGAAAGACGTGCATGATGAGTGTCT 631
DB 665 TGCCCGTATAGTCTTGGCAACCAAAATACAGGAGAGGCTC-----CATAGATTCCA 718
QY 632 CTTTCAGTTCACCATGATGATGATCTGCTGTGGAGCTCTTTCATGAAAGATCTGCTCT 691
DB 719 CCTTACGTTCTCTATCCCATGATGATGATGAGGAAAGCTGCTC---AAATCTGTGCT 775
QY 692 TCATCTTTCCTTGTGATTCCTGTCTCATCATCATGCTGTGCTACACCTGATGATCC 751
DB 776 TCATCTTTCCTTGTGATTCCTGTCTCATCATCATGCTGTGCTACACCTGATGATCT 835

QY 752 TGGCTCTCAAGAGCGTCCGGCTCTTTGTGCTCCCGAGAGAAAGATGCAACTGCGTA 811
DB 836 TACGACTCAAGAGTGTCCGATGCTGTGCGGCTCCAAAGAAAGACAGAACTGCGCA 895
QY 812 GGATCACCAGATGTGCTGTGGTGTGGAGAGTCTTGTGCTGTGCACTCCCATTC 871
DB 896 GGATCACCAGATGTGCTGTGGTGTGGAGAGTCTTGTGCTGTGCACTCCCATTC 955
QY 872 ACATTTATCTCTGTGAGGCTCTGGGAGACCTCCCAAGACAGCTGCTCTTCCA 931
DB 956 ACATCTATGATCATCAACACATGATCAGATTCAGAAACCATTTCCAGACTGTT 1015
QY 932 GCTATTTACTTTCGATGCGCTTGAAGCTTATACCAAGTGAAGTCCATTTCTTACG 991
DB 1016 CTTGCACTTTCTGATTTGCTTGGTTACAAACAGCTGCTGAACCAAGTTCTTTATG 1075
QY 992 CTTTCTTGATGAAATCTTCAAGCGGTGTTCCGGACTTGTCTTTCACATGAAGATGA 1051
DB 1076 GCTTCTTGATGAAATCTTCAAGCGGTGTTTGAAGAGTCTTGCATCCCACTTCTCCA 1135
QY 1052 GGATGAGCGGCAAGCATGACAGATGCCAATATACATTCAGATC 1099
DB 1136 CAATCGAACAGCAAAATCTCTGGAATCGTCAAAACACTAGGGAAC 1183

RESULT 50

AAZ60741
ID AAZ60741 standard; cDNA; 1610 BP.

AC AAZ60741;

DT 16-MAY-2000 (first entry)

DE cDNA encoding murine mu-opioid receptor splice variant MOR-1.

KW Mu-opioid receptor; MOR-1; splice variant; morphine analgesia;
KW opioid-mediated ingestive response; opioid activity; analgesic;
KW gastrointestinal motility; respiration; immune system; endocrine system;
KW autonomic nervous system; peristalsis regulator; body weight;
KW neuroendocrine disorder; MOR-1; ss.

OS Mus sp.

FH Key Location/Qualifiers

FT CDS 283..1479

FT /tag= a

FT /transl_except= (pos: 916..918, aa: G1y)

FT /product= "MOR-1"

PN WO200004046-A2.

PD 27-JAN-2000.

PF 15-JUL-1999; 99WO-US015974.

PR 16-JUL-1998; 98US-0092980P.

PA (SLOK) SLOAN KETTERING INST CANCER RES.

PI Pasternak G, Pan Y;

DR WPI; 2000-182402/16.

XX P-PSDB; AAY68889.

XX New splice variants of the mu-opioid receptor, useful in screening for

XX selective analgesics and for regulating morphine analgesia or body

XX weight.

XX Claim 29; Fig 2N; 83bp; English.

XX The present sequence encodes a murine mu-opioid receptor (MOR-1) splice

XX variant MOR-1. The specification describes 11 new exons for the MOR-1

XX gene, which combine to yield 15 novel splice variants of the MOR-1 gene.

CC These splice variants are potential targets for modulating morphine
 CC analgesia and opioid-mediated ingestive responses. The MOR-1 polypeptide
 CC is used to screen compounds for opioid activity. Such compounds are
 CC potential analgesics or more generally agents that affect
 CC gastrointestinal motility, respiration or the immune, endocrine or
 CC autonomic nervous systems, e.g. regulators of peristalsis. Antagonists,
 CC agonists and ligands of MOR-1, as well as DNA vectors expressing MOR-1-
 CC encoding nucleic acids, or sequences antisense to MOR-1 nucleic acids,
 CC are used to regulate morphine analgesia and body weight. The level of MOR
 CC -1 or tissue distribution of MOR-1 can be measured to diagnose MOR-1
 CC related pharmacological abnormalities or neuroendocrine disorders,
 CC particularly inherited disorders. Transgenic animals with extra copies of
 CC the MOR-1 gene, or with endogenous alleles deleted, are used to study
 CC loss or gain of function phenotypes

XX Sequence 1610 BP, 373 A, 476 C, 368 G, 393 T, 0 U, 0 Other;

Query Match 37.5%; Score 432.4; DB 3; Length 1610;

Best Local Similarity 65.8%; Pred. No. 5e-96;
 Matches 663; Conservative 0; Mismatches 336; Indels 9; Gaps 2;

QY 92 CCGGCTGGGCGGAGCCGACAGCAACGCGCGGCTCGAGAGACGCGAGCTGAGC 151
 DB 401 CCGACCCATGGGCTCTTAACCGACGCGGGCTTGGGAGACACAGCTGTGCCCTCAGA 460
 QY 152 CCGGACATCTCCCGGCGCANTCCGGTCATCATCAGCGCGGTCTCCGTAAGTTCG 211
 DB 461 CCGGAGCCCTTCCATGGTCAAGCATCACCATCATGCCCCCTATCTAATCGTGTG 520
 QY 212 TCGTGGGCTGTGGGCAACTCGTGTGATGTCGTATCATCGATACCAAGATGA 271
 DB 521 TAGTGGGCTCTTTGGAACTTCCGTGTGATGATGATGTAAGATATACAAATGA 580
 QY 272 AGACAGCAACCAATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 331
 DB 581 AGACTGCGACCAACATCTACATTTCAACTTGTGCTGAGAGCTTACGCACTAGCA 640
 QY 332 CCATGCCCTTTCAGAGCGTCACTTGAATTAATTCCTGCGCTTTGGGGATGTCGT 391
 DB 641 CGTGGCCCTTTCAGAGGTTTAACTTACCTGATGGGAACTGGCCCTTGGAAACATCTCT 700
 QY 392 GCAAGATAGTATTTCCATGATTACTTACCAATGTCACAGCATCTTCACTTGAACA 451
 DB 701 GCAAGATGATATCATAGTACATGATACCAATGTCACAGATCTTCACTTGAACA 760
 QY 452 TGATGAGCGTGGACCGCTACATTTGCGTGGCACCCCGTGAAGGCTTGGACTTCGCA 511
 DB 761 CCATGAGGTGAGACCGCTACATTTGCGTGGCACCCCGTGAAGGCTTGGACTTCGCA 820
 QY 512 CACGCTGGAAGCAAGATCATCAATATCTGATCTGCTGCTGCTGCTGCTGCTGCTGCA 571
 DB 821 CCCCCGAAATGCCAAATTTGTCAATGCTGCAATGATCTCTCTTCTGCTGCTGCTGCT 880
 QY 572 TCTGTGCAATAGTCTTGGAGGACCAAAAGTCAAGGGAAGAGTCAATGATGCT 631
 DB 881 TGCCCGTAATGTTATGAGCAACCAAAATACAGGAGGGGTC-----CATAGATTGCA 934
 QY 632 CTTGCAAGTCCGAGATGATCACTACTCTGCTGAGACCTTTCAATGAAGTCTGCGTCT 691
 DB 935 CCCCACGTTCTCATCTCCACATGATGATGAGGAACCTGCTC---AAATCTGTGCTCT 991
 QY 692 TCATCTTTGCTGCTGATCCCTGTCCTCATCATCATCATCATCATCATCATCATCATCAT 751
 DB 992 TCATCTTTGCTGCTGATCCCGGTCCTCATCATCATCATCATCATCATCATCATCATCAT 1051
 QY 752 TCGCTCTCAAGAGCGTCCGCTCTTCTGTGCTCCGAGAGAAAGATCGAACTGTGCTA 811
 DB 1052 TAGACTCAAGAGGTGCGGATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1111
 QY 812 GGATCACCAGCTGTCTGT 871
 DB 1112 GGATCACCAGCTGT 1171

QY 872 ACATATTCATCTGTGAGGCTGTGGGAGACCTCCACAGACAGCTGCTCTCCA 931
 DB 1172 ACATCTGTATATCAAGACATGATACAGATTCAGAAACCACTTCCAGACTGTTT 1231
 QY 932 GCTATTAATCTGTGATGCGCTTAGGCTATACCAAGATGCTGAATCCATTTCTTACG 991
 DB 1232 CTTGGACCTTGTGATGCTGCTTGGGTTACCAAAACAGCTGTGAACCCAGTTCTTATG 1291
 QY 992 CTTTCTTGAATGAACCTTCAAGCGGTGTTTCCGGGACTTGTGCTTTCCTGAAGATGA 1051
 DB 1292 CGTTCTCTGATGAAACCTTCAACGATGTTTATAGAGATTTCTGCATCCCACTTCTCCA 1351
 QY 1052 GGATGAGCGGCGACAGCATACAGAGTCCGAATATACGTTCAAGATC 1099
 DB 1352 CAATGAAACAGCAAACTTGTCTGAAATCCGTCAAAACACTAGGAAAC 1399

RESULT 51

AAZ60734
 ID AAZ60734 standard; cDNA; 1729 BP.

AAZ60734;

16-MAY-2000 (first entry)

cDNA encoding murine mu-opioid receptor splice variant MOR-1F.

Mu-opioid receptor; MOR-1; splice variant; morphine analgesia;
 KW opioid-mediated ingestive response; opioid activity; analgesic;
 KW gastrointestinal motility; respiration; immune system; endocrine system;
 KW autonomic nervous system; peristalsis regulator; body weight;
 KW neuroendocrine disorder; MOR-1F; ss.

XX Mus sp.

XX Key Location/Qualifiers

XX CDS 67..1401

XX FT /**tag= a

XX FT /product= "MOR-1F"

XX MO200004046-A2.

XX 27-JAN-2000.

XX 15-JUL-1999; 99MO-US015974.

XX 16-JUL-1998; 98US-0092980P.

XX (SLOAN) SLOAN KETTERING INST CANCER RES.

XX Pasternak G, Pan Y;

XX WPI; 2000-182402/16.

XX P-PSDB; AAY68888.

XX New splice variants of the mu-opioid receptor, useful in screening for

XX selective analgesics and for regulating morphine analgesia or body

XX weight.

XX Claim 36; Fig 2F; 83bp; English.

XX The present sequence encodes a murine mu-opioid receptor (MOR-1) splice
 CC variant MOR-1F. The specification describes 11 new exons for the MOR-1
 CC gene, which combine to yield 15 novel splice variants of the MOR-1 gene.
 CC These splice variants are potential targets for modulating morphine
 CC analgesia and opioid-mediated ingestive responses. The MOR-1 polypeptide
 CC is used to screen compounds for opioid activity. Such compounds are
 CC potential analgesics or more generally agents that affect
 CC gastrointestinal motility, respiration or the immune, endocrine or
 CC autonomic nervous systems, e.g. regulators of peristalsis. Antagonists,
 CC agonists and ligands of MOR-1, as well as DNA vectors expressing MOR-1-
 CC encoding nucleic acids, or sequences antisense to MOR-1 nucleic acids,
 CC are used to regulate morphine analgesia and body weight. The level of MOR


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Db 305 AGACTGCCACCAACATCTACATTTTCAACCTTGCTGTGGAGATGCTTAGCCACAGTA 364
Qy 332 CCATGCGCTTTCAGAGTACGGTCTACTTGATGAAATTCCTGGGCTTTTGGGATGCTGT 391
Db 365 CCGTCCCTTCAGAGTGTGAATTAATTAAGGAACATGGCAATTTGAAACCATCTTT 424
Qy 392 GCAAGATGTAATTTCTGATGATTTACTCAACATGTTACAGCATCTTCACTTGAACA 451
Db 425 GCAAGATGATCTCCATAGATTACTATACATTTTACAGCATATTCACCTCTGCA 484
Qy 452 TGATGAGGTGAGCGCTACATTTGCGGTGCGCACCCCGTGAAGGCTTTGACCTTCCGA 511
Db 485 CCATAGAGTGTGATGATACATTTGACATGCTGCACTGTCAGAGGCTTAGATTCCGTA 544
Qy 512 CACCTTGAAGGCAAGATCATCATATCTGATCTGCTGTGTCATCTGTGGCA 571
Db 545 CTCGCCGAATGCCAAATTAATCATGTCTGCACTGATCCTCTTCAGCATTTGCTC 604
Qy 572 TCTCTGCAATAGTCTTGGAGGACCAAAAGTCAGGGAAGACGTGATGCTTAGTGTCT 631
Db 605 TTCCTGTATGTTCTATGCTACACAAATACAGGCAAG-----TTCATAGATTGTA 658
Qy 632 CCTTGCACTTCCAGATGATGACTACTGCTGTGGACCTCTTCATGAAGATCTGCGTCT 691
Db 659 CACTAACATTTCTCTCATCCAACTGTGTACTGGGAAACCTCG--TGAAGATCTGTGTT 715
Qy 692 TCATTTTGGCTTGTGATCCCTGTCTCATCATATGTCGTCTACACCTGATGATCC 751
Db 716 TCATCTTGGCTTCAATTAAGCAAGTCTCATCATTAACCGTGTGCTATGAGACTGATGCT 775
Qy 752 TGGCTTCAAGAGCTCCGCGCTCTTTTGGCTCCGAGAGAAAGATGCAACCTGCGTA 811
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Qy 812 GGATCACAAGACTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 871
Db 836 GGATCACAAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 895
Qy 872 ACATTTTATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 931
Db 896 ACATTTTATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 955
Qy 932 GCTATTACTTCTGCACTGCTTGAAGCTATACCAACAGTAGCTGATCCCATCTCTAG 991
Db 956 CTTGGCACTTCTGCACTGCTTGAAGCTATACCAACAGTAGCTGATCCCATCTCTAG 1015
Qy 992 CTTTCTGTGATGAATCTTCAAGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1051
Db 1016 CATTTCTGATGAATGAATCTTCAAGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1075
Qy 1052 GGATGAGCGGCAAGCACTAGCAAGATCCGAAATA 1087
Db 1076 ACATTTGAGCAACAAATCTCACTGCAATTCGTGACA 1111

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RESULT 53
ABI98012
ID ABI98012 standard; cdna, 1203 BP.

ABI98012;
AC
XX
XX
18-FEB-2002 (first entry)
DT
XX
DE Non-endogenous human GPCR cdna, SEQ ID NO: 544.
XX
XX Human; G protein-coupled receptor; GPCR; non-endogenous; mutant;
KW constitutively activated GPCR; agonist; disease; ss.
XX
OS Homo sapiens.
XX Synthetic.
XX MO200177172-A2.

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PD 18-OCT-2001.
XX
PF 05-APR-2001; 2001WO-US011098.
XX
PR 07-APR-2000; 2000US-0195747P.
XX
PA (AREN-) ARENA PHARM INC.
XX
PI Lehmann-Brulisma K, Llaw CW, Lin I;
XX
DR WPI; 2001-648759/74.
XX
DR P-PSDB; ABB56376.
XX
PT Identifying agonists of G protein-coupled receptors (GPCRs) for use in
PT disease treatment, comprises contacting candidate compounds with versions
PT of GPCRs.
XX
PS Example 2; Page 345-346; 394pp; English.
XX
CC The invention relates to G protein-coupled receptors (GPCRs) for which
CC the endogenous ligand has been identified. Non-endogenous constitutively
CC activated versions of known GPCRs are used in the invention for the
CC direct identification of candidate compounds as receptor agonists,
CC inverse agonists or partial agonists. Such agonists are useful as
CC therapeutic agents for diseases or disorders associated with GPCRs. The
CC present sequence encodes a non-endogenous version of a known human GPCR
SQ
Sequence 1203 BP; 301 A; 348 C; 245 G; 309 T; 0 U; 0 Other;
Query Match 37.4%; Score 431.6; DB 5; Length 1203;
Best Local Similarity 66.1%; Pred. No. 7e-96;
Matches 658; Conservative 0; Mismatches 329; Indels 9; Gaps 2;
Qy 92 CCGGCTGGGCGGACCCGACAGCAACGGACCGCGCTGGAGAGACCGGACGTGAGC 151
Db 125 CCGACCCATGCGTCCGACACGACCAACTGGGCGGAGAGACAGCCTGTGCTCCGA 184
Qy 152 CCGGCAATCTCCCGGCGCATCCGGTCATCATCGAGGCGGTACTCCGTAGTGTG 211
Db 185 CCGGCAATCTCCCATATGATACGCGCATGACATGAGCCCTTATCTCCATCGTGTG 244
Qy 212 TCGTGGGCTTGGTGGGCAACTCGGTGATGTTGATGATCCGATACCAAGATGA 271
Db 245 TGTGTGGGCTTGTGGAACTTCTGTCATGATGATGATGATGATGATGATGATGATGAT 304
Qy 272 AGACAGCAACCAATTTATTAATTTAACTGCTTTGGAGATGCTTAACTTAA 331
Db 305 AGACTGCCACCAACATCTTCACTTTTCAACTTGTCTGGGAGATGCTTAGCCACAGTA 364
Qy 332 CCATGCCCTTCAAGATGATGATTTTCACTTGTGATGATTTTGGGATGCTGT 391
Db 365 CCGTCCCTTCAAGATGATGATTTTCACTTGTGATGATTTTGGGATGCTGT 424
Qy 392 GCAAGATGTAATTTCTGATGATTTACTCAACATGTTACAGCATCTTCACTTGAACA 451
Db 425 GCAAGATGATGATCTCCATAGATTACTATACATTTTACAGCATATTCACCTCTGCA 484
Qy 452 TGATGAGGTGAGCGCTACATTTGCGGTGCGCACCCCGTGAAGGCTTTGACCTTCCGA 511
Db 485 CCATAGAGTGTGATGATACATTTGCACTGCACTGTCAGAGGCTTAGATTCCGTA 544
Qy 512 CACCTTGAAGGCAAGATCATCATATCTGATCTGCTGTGTCATCTGTGGCA 571
Db 545 CTCGCCGAATGCCAAATTAATCATGTCTGCACTGATCCTCTTCAGCATTTGCTC 604
Qy 572 TCTCTGCAATAGTCTTGGAGGACCAAAAGTCAGGGAAGACGTGATGCTTAGTGTCT 631
Db 605 TTCCTGTATGTTCTATGCTACACAAATACAGGCAAG-----TTCATAGATTGTA 658
Qy 632 CTTTCTGTGATGAATCTTCAAGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 691
Db 659 CACTAACATTTCTCTCATCCAACTGTGTACTGGGAAACCTCG--TGAAGATCTGTGTT 715

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QY 812 GGATCACCGAGCTGGTCTGTGGTGGTGGAGAGCTGTGCTGTGAGCTCCCATTC 871
 DB 896 GGATCACCGAGCTGGTCTGTGGTGGTGGAGAGCTGTGCTGTGAGCTCCCATTC 955
 QY 872 ACATATTCATCTCTGTGGAGCTCTGGAGAGCACTCCACAGCAGACCTGCTCTTCCA 931
 DB 956 ACATCTATGTATCATCAAGAGCATGATCAGATTCAGAAACGACTTTCAGAGCTGTT 1015
 QY 932 GCTATTAATCTTGATGAGCTTAAAGGCTATPACCAAGTAGCTGATTCATTCATACG 991
 DB 1016 CTTGCACTTCTGCAATGCTCTGGGCTTACCAAAACAGCTGAAACCCAGTCTTTATG 1075
 QY 992 CTTTCTTGATGAACCTTCAAGGCTGTTTCCGGAGCTTCTGCTTTCACCTGAAGATGA 1051
 DB 1076 CTTTCTTGATGAACCTTCAAGGCTGTTTCCGGAGCTTCTGCTTTCACCTGAAGATGA 1135
 QY 1052 GGATGAGCGGAGAGCACTAGCAGAGTCCGAAATPACAGTTCAAGATC 1099
 DB 1136 CAATCGAAGCAGAAACCTGCTGAAATCCGTCAAAACACTAGGGAAC 1183
 RESULT 55
 ID AAV49252 standard; DNA; 2229 BP.
 AC AAV49252;
 DT 28-OCT-1998 (first entry)
 DE Mouse mu opiate receptor gene.
 XX Mouse; mu opiate receptor; transgenic animal; mammal; identification;
 KM exon; nervous tissue; pain; drug addiction; transplant rejection;
 KM immunosuppressant; analgesic; morphine; side effect; ds.
 OS Mus sp.
 FH Key location/Qualifiers
 FT CDS 256..1452
 FT /*tag= a
 FT /product= "mu opiate receptor"
 XX MO9802534-A2.
 XX 22-JAN-1998.
 XX 11-JUL-1997; 97WO-FR001282.
 XX 15-JUL-1996; 96FR-00008810.
 XX (CNRS) CENT NAT RECH SCI.
 XX Kieffer BL, Matthes HWD, Simonin F, Dierich A, Lemeur M;
 DR WPI; 1998-110582/10.
 DR P-PSDB; AAM44937.
 PT Transgenic animals defective in one type of opioid receptor - used to
 PT identify agents for treatment of pain, drug addiction and transplant
 PT rejection, lacking side effects of known opiate(s).
 XX Disclousure; Fig 11; 58pp; French.
 CC This sequence represents the gene encoding the mouse mu opiate receptor
 CC protein. The sequence is used to generate a transgenic non-human mammal
 CC for identifying agents for treating disorders associated with opiate
 CC receptors. In the mammal, the expression of the gene encoding the opiate
 CC receptor is modified, particularly by the deletion of an exon and/or
 CC insertion of a marker gene, e.g. the neomycin resistance gene, into the
 CC sequence. Especially the expression of the gene is altered in nervous
 CC tissue. The agents are potentially useful for treating severe pain
 CC (chronic or acute), drug addiction and/or prevention or treatment of
 CC transplant rejection (as immunosuppressants). The method may isolate and

CC identify powerful analgesics that lack morphine-like side effects
 XX Sequence 2229 BP; 562 A; 608 C; 489 G; 570 T; 0 U; 0 Other;
 SQ Query Match 37.3%; Score 430.8; DB 2; Length 2229;
 Best Local Similarity 65.7%; Pred. No. 1.4e-95;
 Matches 662; Conservative 0; Mismatches 337; Indels 9; Gaps 2;
 QY 92 CCGGCTGGGCGGAGCCCGAGCAGCAGCAGCGCCGCTGGAGAGACCGCAGCTGGAGC 151
 DB 374 CCGAGCCATGCGGCTTCTAACCGCAGCGGGCTTGGCGGAGCAGCGCTGGCCCTGAGA 433
 QY 152 CCGGAGCATATCCCGGAGCATCCCGGATCATCAGCGGGCTTACTCCGATGATGTTG 211
 DB 434 CCGGAGCCCTTCCATGATGATCAGAGCATCAGCATCAGCCCTTATTTATCTATGATG 493
 QY 212 TCGTGGCTGGTGGGAGCACTCGTGTGATGTTGATGATTCGATACCAAAAGATGA 271
 DB 494 TAGTGGGCTCTTGGAAACCTTCTGGTCAATGATGATGATGATGATGATGATGATGATG 553
 QY 272 AGACAGCAACCAATTTACATTTAACTGCGCTTTGGCAGATGCTTTAGTTACTACAA 331
 DB 554 AGACTGCGACCAACATCTACATTTTCAACCTTGTCTGGAGAGATGCTTGGCCACTGCA 613
 QY 332 CCATGCCCTTTCAAGATAGCGTCTACTGATGAATTCCTGGCCCTTTGGGGATGCTGT 391
 DB 614 CGTGGCCCTTTCAAGATAGTTTAACTGATGATGATGATGATGATGATGATGATGATG 673
 QY 392 GCAAGATGATTAATTTCCATTTACTTACAAATGTTTACCAAGATTTTCACTTGAACA 451
 DB 674 GCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 733
 QY 452 TGATGAGCGTGGAGCCGCTTACATGCGCTGGGCCACCCCGTGAAGCTTTGACCTCCGCA 511
 DB 734 CCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 793
 QY 512 CACCCCTTGAAGGCAAAAGATCATCAATATCTGATCTGATCTGATCTGATCTGATCTG 571
 DB 794 CCCCCGAAATGCAAAATTTGTCAATGTCTGCACTGATGATGATGATGATGATGATG 853
 QY 572 TCTTGTCAATAGTCTTGGAGGCAACCAAGTCAGGAAAGAGTGTGATGATGATGATG 631
 DB 854 TGCCGTAATGTTTATGAGCAACCAAAATPACAGGAGGCTC-----CATGATATGCA 907
 QY 632 CTTTGAAGTCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 691
 DB 908 CCCCACCTTCTCATCCCAATGATGATGATGATGATGATGATGATGATGATGATGATG 964
 QY 752 TGCATCTTGGCTTGGATCCCTGCTCATCATCATCATCATCATCATCATCATCATCAT 751
 DB 965 TCACTTTCGCTTCTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 1024
 QY 812 GGATCACAGACAGCTGCTGGTGGTGGTGGAGAGCTGTGCTGTGAGCTCCCATTC 871
 DB 1025 TACGACTCAAGAGTGTCCGATGCTGTGCGGCTTCAAAAGAAAGAGACAGGAACTCGGCA 1084
 QY 812 GGATCACAGACAGCTGCTGGTGGTGGTGGAGAGCTGTGCTGTGAGCTCCCATTC 871
 DB 1085 GGATCACAGACAGCTGCTGGTGGTGGTGGAGAGCTGTGCTGTGAGCTCCCATTC 1144
 QY 872 ACATATTCATCTCTGTGGAGCTCTGGAGAGCACTCCACAGCAGCAGCTGCTCTTCCA 931
 DB 1145 ACATCTATGTATCATCAAGAGCATGATCAGATTCAGAAACGACTTTCAGAGCTGTTT 1204
 QY 932 GCTATTAATCTTGATGAGCTTAAAGGCTATPACCAAGTAGCTGATTCATTCATACG 991
 DB 1205 CTTGCACTTCTGCAATGCTCTGGGCTTACCAAAACAGCTGTAACCCAGTTCTTTATG 1264
 QY 992 CTTTCTTGATGAACCTTCAAGGCTGTTTCCGGAGCTTCTGCTTTCACCTGAAGATGA 1051
 DB 1265 CTTTCTTGATGAACCTTCAAGGCTGTTTCCGGAGCTTCTGCTTTCACCTGAAGATGA 1324
 QY 1052 GGATGAGCGGAGAGCACTAGCAGAGTCCGAAATPACAGTTCAAGATC 1099

Db 1325 CAATCGACAGCAAACTCTGCTCGAATCCGTCAAAACACTAGGGAAC 1372

RESULT 56

ID ABX13057 standard; DNA; 1149 BP.

AC ABX13057;

DT 29-AUG-2003 (revised)

DT 28-MAY-2003 (First entry)

DE Human MOR-V2R DNA.

KM Human; G-protein coupled receptor; gene; ds; GPCR; palmitoylation site;
 KM phosphorylation cluster; arrestin; endosome; angina pectoris; rhinitis;
 KM atherosclerosis; asthma; emphysema; inflammatory disease; glaucoma; pain;
 KM rheumatoid arthritis; obesity; Parkinson's disease; MOR; VZR;
 KM vasopressin V2R receptor; mu opioid receptor.

05 Homo sapiens.
05 chimeric.

Chimeric.

FH	Key	Location/Qualifiers
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FT CDS

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/ product= "Human MOR-V2R"

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PN US2002106739-A1.

PD 08-AUG-2002.

PF 05-NOV-2001; 2001US-00993844.

PR 03-NOV-2000; 2000US-0245772P.

PR 08-JAN-2001; 2001US-0260363P.

PA (OAKL/) OAKLEY R H.

PA (BARA/) BARAK L. S.

PA (LAPD) LAPORTE S N

PA (CARO/) CARON M G.

PI Oakley RH, Barak LS, Laporte SA, Caron MG;

DR WPI; 2002-690758/74.

DR P-PSDB; ABG75675.

PT Modified G-protein coupled receptor useful for identifying an agonist
PT inverse agonist or antagonist of the receptor, comprises a carboxyl
PT terminal having one or more clusters of phosphorylation.

PS Disclosure; Fig 11; 57pp; English.

CC The invention relates to a modified G-protein coupled receptor (GPCR)
CC comprising an NPXXY motif, and a carboxyl terminal tail which comprises a
CC putative site of palmitoylation and clusters of phosphorylation, and a
CC retained portion of a carboxyl terminal region of a GPCR portion fused to
CC a portion of the carboxyl terminal from a second GPCR, that comprises
CC phosphorylation clusters and a putative palmitoylation site 10-25 amino
CC acid residues downstream of a second NPXXY motif. The modified GPCR is
CC useful for screening compounds for GPCR activity which comprises
CC providing a cell that expresses at least one modified GPCR, where the
CC cell further comprises arrestin conjugated to a detectable molecule,
CC exposing the cell to the compound, detecting the location of the arrestin
CC within the cell, comparing the location of the arrestin within the cell
CC in the presence of the compound to the location of the arrestin within
CC the cell in the absence of the compound and correlating a difference
CC between the location of arrestin within the cell in the presence of the
CC compound and the presence of the location of the arrestin within the cell
CC in the absence of the compound. Preferably, the arrestin is detected in
CC endosomes. The GPCR and a nucleic acid encoding the modified GPCR are
CC useful for preventing and/or treating a disease associated with GPCR in

QY	1010	TCAAGCGGTGTTTCCGGACTTCTGC	1035
Db	1028	TCAAGCATGCTTCAGAGACTTCTGC	1053

RESULT 57
AAZ60729
ID AAZ60729 standard; cDNA; 1542 BP.

AC AAZ60729;

DT 16-MAY-2000 (first entry)

DE cDNA encoding murine mu-opioid receptor splice variant MOR-1E.

KM Mu-opioid receptor; MOR-1; splice variant; morphine analgesia;
KM opioid-mediated ingestive response; opioid activity; analgesic;
KM gastrointestinal motility; respiration; immune system; endocrine system;
KM autonomic nervous system; morphine; peripheral
KM neuroendocrine disorder; MOR-1E; ss.
KM

OS Mus sp.

FH	Key	Location/Qualifiers
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3	3	3
4	4	4
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7	7	7
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100	100	100

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FT	/product= "MOR-1E"

PN WO200004046-A2.

PD 27-JAN-2000.

PF 15-JUL-1999; 99WO-US015974.

PR 16-JUL-1998; 98US-0092980P.

PA (SLOK) SLOAN KETTERING INST CANCER RES.

PI Pasternak G, Pan Y;

DR WPI; 2000-182402/16.

XX

PT New splice variants of the mu-opioid receptor, useful in screening for
PT selective analgesics and for regulating morphine analgesia or body
PT weight.

PS Claim 34; Fig 2C; 83pp; English.

CC The presen sequence encodes a murine mu-opioid receptor (MOR-1) splice
CC variant MOR-1E. The specification describes 11 new exons for the MOR-1
CC gene, which combine to yield 15 novel splice variants of the MOR-1 gene.
CC These splice variants are potential targets for modulating morphine
CC analgesia and opioid-mediated ingestive responses. The MOR-1 polypeptide
CC is used to screen compounds for opioid activity. Such compounds are
CC potential analgesics or more generally agents that affect
CC gastrointestinal motility, respiration or the immune, endocrine or
CC autonomic nervous systems, e.g. regulators of peristalsis. Antagonists,
CC agonists and ligands of MOR-1, as well as DNA vectors expressing MOR-1-
CC encoding nucleic acids, or sequences antisense to MOR-1 nucleic acid,
CC are used to regulate morphine analgesia and body weight. The level of MOR
CC -1 or tissue distribution of MOR-1 can be measured to diagnose MOR-1
CC related pharmacological abnormalities or neuroendocrine disorders,
CC particularly inherited disorders. Transgenic animals with extra copies of
CC the MOR-1 gene, or with endogenous alleles deleted, are used to study
CC loss or gain of function phenotypes

SQ Sequence 1542 BP; 369 A; 453 C; 346 G; 374 T; 0 U; 0 Other;

Query Match	37.2%	Score 429.2;	DB 3;	Length 1542;
Best Local Similarity	65.6%;	Pred. No. 3e-85;		
Matches 661; Conservative	0;	Mismatches 338;	Indels 9;	Gaps 2;

QY	92	CCGGCTGGGGCCGAGCCCGACAGCAACGGCAGCCGCCGCTCGAGAGACCCGCAAGCTGGAGC	151
Db	185	CCGACCCCATGCGAGTCTTAACCGCACGGGGGCTTGGCCGGAGGCACAAGCTCGGCCCTCAGA	244
QY	152	CCGGGCAATCTCCCGGGCCCATCCCGGCATCATCAAGCGGGGTCTACTCCGTAGTGTTCG	211
Db	245	CCGGGAGCCCTTCCATGGTCAACAGCCATCAACCATCAAGCCCTCTATTCTATCGTGTGTC	304
QY	212	TCTGGGGCTTGGTGGGCACTCGTGTGCATGTTCGTGATCATCCGATACCAAAAGATGA	271
Db	305	TAGTGGGGCTCTTTGGAAACTTCCGTGGCATGTATGTGATTGTAAAGATATACCAAAATGA	364
QY	272	AGACAGCAACCAACATTATTAACATTTCACCTGGCTTTGGCAGATGCTTTACTATCTACAA	331
Db	365	AGACTGCGACCAACATCTACATTTTCAACTTTCGCTTGGCAGATGCCCTTACCCACTAGCA	424
QY	332	CCATGCCCCCTTCAAGAGTACCGGTCTACTGTATGAATTCCTGTGACCTTTTGGGATGTGCTGT	391
Db	425	CGCTGCCCTTTCAGAGTGTTAATCTACTGATGGAAAGCTGGCCCTTTGGAAACATCCCTCT	484
QY	392	GCAAGATATGTAATTTCCATTGATTACTACAAACATGTTCCACGACATCTTCCACTTTGACCA	451
Db	485	GCAAGATGTGATCTCAATATAGACTACTACAAACATGTTCCACGACATCTTCCACTCTGCA	544
QY	452	TGATGAGGTGGACCGCTACCTTCCCGTGGGCCACCCCGTGAAGGCTTTGGACCTTCCGCA	511
Db	545	CCATGAGTGAAGCCGCTACATTTCCCGTCTGCGCACCCGGTGAAGGCCCTGTGATTTCCGTA	604
QY	512	CACCCCTTGAAGGCAAAAGTATCATCAATATCTGCATCTGGCTGCTGCATCTGTGGCA	571
Db	605	CCCCCGGAAATGCCAAATTTGTCAATGTCTGCGCACTGGATCTCTCTTCTGCGCATTTGGTC	664
QY	572	TCTCTGCATATGTCCTTGGAGGCAACAAAGTCAAGGGAAGACGTGGATGTCAATTGAGTCT	631
Db	665	TGCCGTATGTTCATGGCAACCAAAATTCAGGCAAGGGTCT-----CATTAATTTGCA	718
QY	632	CCTTGAGATGCCAGATGATGACATACCTCTGGTGGGACCTTTGATGAAATCTGCGCTCT	691
Db	719	CCCTCAGCTTCTTCATCTCCACATGTAATCTGGGAAACCTGCTC---AAATATCTGTTGCT	775
QY	692	TCATCTTTGACCTTGGTGTATCCCTGTCTCATCATCATCTGCTGTGTACACCTGTATGATCC	751
Db	776	TCATCTTGGCTTATCATATGCGGGTCTCATCATCACTGTGTATTGATGATGATGATCT	835
QY	752	TGCGTCTCAAGAGGCTCCGGCTCCTTTCTGGCTCCCGAGAGAAAGATCCGAACCTGGGTA	811
Db	836	TACACATCTMAAGTGTCCGATGTCTGTCGGGCTCTAAAGAAAGACAGGAACCTGGCGCA	895
QY	812	GGATCACCAAGCTGATCCCTGGTGTGTGGAGAGCTTCGTGCTGTGCTGCACTCCCATTC	871
Db	896	GGATCACCCCGATGT	955
QY	872	ACATATTCATCTGTGTGAGGCTCTGTGGGAGCACTTCCACAGACAGAGCTGCTCTTCCA	931
Db	956	ACATCTATGTATCATCAAAAGCACTGATACAGATTCCAGAAACCACTTTCAGACTGTCTT	1015
QY	932	GCTATTAATCTTGATGATGGCTTTAGGCTATACCAACATGAGCTGAATCCATTCCTACG	991
Db	1016	CTGTGGCACTTCTGATTTGCTTGGTTTACAAACACCTGTCTTAACCCCACTTCTTATG	1075
QY	992	CCTTTCTTGTAGAAAATTCAAGGGGTGTTCCGGGACTTCTGCTTTCACCTGAAGATGA	1051
Db	1076	CGTTCCTGTGATGAAAATTCAAAAGATGTTTAAAGAGTTCTGCATCCCAACTTCTCCA	1135
QY	1052	GGATGAGCGGCAAGCACTAGCAGAGTCCGAAATACAGTTCCAGATTC	1099
Db	1136	CAATCGAAACAGCAAACTGTGCTGAATCCGTCAAAAACATGAGGAAC	1183

RESULT 58	
AAD11041	
ID AAD11041	standard; cDNA; 1981 BP.

Query Match:	37.2%	Score 429.2	DB 6	Length 1981
Best Local Similarity	65.6%	Pred. No. 3.3e-95		
Matches 661	Conservative	0	Mismatches 338	Indels 9
			Gaps 2	
XX	(REGC) UNIV CALIFORNIA.			
PA				
XX				
PI	Evans CJ, Keith DE, Edwards RH, Kaufman D;			
XX				
DR	WPI, 2002-681194/73.			
XX				
PT	Mammalian DOR-1 opioid receptors, useful for screening for compounds			
XX	useful in the treatment of opioid addiction and poisoning.			
PS	Example 9; Fig 9; 61np; English.			
XX				
CC	This invention relates to the DNA and protein sequences of novel			
CC	mammalian opioid receptor (DOR-1) displayed at the surface of recombinant			
CC	host cells. The invention also comprises a method for screening a			
CC	candidate substance for opioid agonist activity and a method for			
CC	detecting the amount of activation of the opioid receptor in the presence			
CC	as compared to the absence of the candidate substance. The methods and			
CC	compounds of the invention may have anti-addictive agents and may be used			
CC	to modulate opioid receptor activity. The mammalian opioid receptor of			
CC	the invention may be used to screen for agonists and antagonists of it's			
CC	expression and activity which may be used to treat e.g. poisoning by, its			
CC	addiction to, opioids (such as morphine, codeine, and many semi-synthetic			
CC	congeners of morphine). The present sequence represents the DNA sequence			
CC	of the mouse mu opioid receptor DOR-2 of the invention			
CC				
XX				
SQ	Sequence 1981 BP; 499 A; 550 C; 436 G; 495 T; 0 U; 1 Other;			
Query Match:	37.2%	Score 429.2	DB 6	Length 1981
Best Local Similarity	65.6%	Pred. No. 3.3e-95		
Matches 661	Conservative	0	Mismatches 338	Indels 9
			Gaps 2	
OY	92 CCGGCTGGGCGCGAGCCGACAGCAACGGCAGCGCCGCTCGGAGAGACCGCAGCTGAGAC	151		
DB	374 CCGAACCCATGGCGTCTTAACCGAGGGCCCTTGGGGAGACAGCAGCTGCTCCACAGA	433		
OY	152 CCGGCGACATCTCCCGGCGCATCCGGTCATCATCAGCGGGGTCTACTCCGATGTTCCG	211		
DB	434 CCGGAGCGCTTCATGGTCAAGCAGCATCAACCATGAGCCCTTATCTATCGTGTGG	493		
OY	212 TCGTGGGCTTGGTGGGCACTCGCTGCTCATCTTGTGTATCATCCGATACACAAAGATGA	271		
DB	494 TAGTGGGCGCTCTTGTGGAACTTCCGTGCATGTATGTATGTAAAGATATACAAAAATGA	553		
OY	272 AGACGACAAACCAATTACATATTAACTGGCTTGGAGAGATCTTAAAGTATCAAA	331		
DB	554 AGACTGCCACCAACATCTACATTTTTCACACTTGTCTGTGAGATGCTTTAGCCACTAGCA	613		
OY	332 CCATGCGCTTCAAGATACGGTCTAATTGATGATTTCTGTGGCTTTTGGGAGTGTGCT	391		
DB	614 CGTGGCGCTTCAAGATGTTAACTACCTGATGGAAAGTGGCCCTTGGAAACATCTCT	673		
OY	392 GCAAGATATGTAATTTCCATTTGATTTACTACACATGTTTCAACGACATCTTACCTTGACCA	451		
DB	674 GCAAGATGATATCTCAATAGCACTACACACATGTTTCAACGATATCTTCAACCCCTGTGCA	733		
OY	452 TGATGAGCGTGAACCGCTACATTTGCGATGGCAACCGGTGAAGCTTTGGACCTTCGCGA	511		
DB	734 CCAATGATGTAGACCGCTACATTTGCGATGGCAACCGGTGAAGCTTTGGACCTTCGCGA	571		
OY	512 CACCTTGAAGGCAAAAGATCATATATCTGTGATCTGGCTGTGCTCATCTGTGTGGA	571		
DB	794 CCCCCGAAATATGCAAAATTTGTCAATGTCGTGAATGTGATCTCTCTCTGTGCAATTTGTC	853		
OY	572 TCTCTGCAATATGCTCTTGAAGGACCAAAATGTCAGGAAAGACGTGATGTCAATGAGTCT	631		
DB	854 TGCCCGTATATGTTCAATGCAACCAAAATATACAGGCAAGGGCTC-----CATAGATTGCA	907		
OY	632 CCTTGAGATTCACAGATGATGATGATCTCTGTGTGGAACCTCTTATGTAAGATTTGGCGCT	691		
DB	908 CCTTCAGATTTCTTCATCCACATGTATGTGGAGAAACCTTGCTC---AAATCTGTGTCT	964		
OY	692 TCATCTTGTGCTTGTGATTCCTGTGCTCATCATCATGATGCTGTGCTACACCTGATGATCC	751		

[illegible]

Query Match 37.1%; Score 427.6; DB 2; Length 1981;
 Best Local Similarity 65.5%; Pred. No. 8.1e-95;
 Matches 660; Conservative 0; Mismatches 339; Indels 9; Gaps 2;

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QY 92 CCGGCTGGGCGGACCCGACAGCAAGGAGCGCGGCTCGAGAGGACGGCGAGCTGGAGC 151
DB 374 CCGACCCATGCGGTCTTAACCCGACGGGCTTGGCGGGAACAGACCCGTGCCCCACAA 433
QY 152 CCGGACACATCTCCCGGCGCATCCGGTATCATCAAGCGGGTCACTCCGATGTTGG 211
DB 434 CCGGACCCCTTCCATGTCACAGCCATCAACATCACTGCCCCCTTAATTTATCGTGTG 493
QY 212 TCGTGGGCTTGGGCAACTCGCTGTCATGTTCTGATCATCCGATACAGAAAGTGA 271
DB 494 TAGTGGGCTCTTTGGAACTTCCTGGTATGATGATTTGAATATACCAAAATGA 553
QY 272 AGACGCAACCAACATTTACATTTTAACCTGGCTTTGGCAGATGCTTTAGTTACTACA 331
DB 554 AGACTGCCACCAACATCTACATTTTCAACCTTGCTCTGGCAGATGCTTGGCAGCTAGCA 613
QY 332 CCATGCCCTTTCAGATAGCTCTGATGAAATTCCTGGGCTTTGGGAGATGTCCT 391
DB 614 CGCTCCCTTTCAGAGTGTAACTACCTGATGGAACGTGGCCCTTTGGAAACATCTCT 673
QY 392 GCAAGATAGTATTTCCATTTGATTTACTACACATGTTCCAGACATCTTCACTTGACA 451
DB 674 GCAAGATGCTGATCTCAATAGACTACTACACATGTTCCAGATCTTCACTCTGCA 733
QY 452 TGATAGGCGTGAGCCGCTACATTTGCGTGGCCACCCCGTGAAGGCTTTGACCTTCCGA 511
DB 734 CATATAGTGTAGACCGCTACATTTGCGTGGCCACCCCGTGAAGGCTTGGATTTCCGTA 793
QY 512 CACCTTGAAGGCAAGATCATCATATCTGATCTGCTGTCGTATCTGTTGGA 571
DB 794 CCCCCGAATGTCGAAATGTCATGTCGCACTGATCTCTCTTTCGCAATGTC 853
QY 572 TCTCTGCAATAGCTCTTGGAGGACCAAGTACAGGAACGTCATGATGATGCT 631
DB 854 TGCCGCTATGTTTCATGCGACCAAAATACAGGAGGGTTC-----CATAGATTGCA 907
QY 632 CTTTCAGTTCACAGATGATGATCTCTCTGTTGGGACCTCTTTCATGAAATCTGCTCT 691
DB 908 CCCTCAGCTTCTCTATCCACATGATGATCTGGAAGAACTGCTC---AAATCTGTGCT 964
QY 692 TCATCTTGGCTTCTGATCTCTGTCCTATCATCATCTGTCGTCACCTGATGATCC 751
DB 965 TCATCTTGGCTTCTATCATGTCGCGGCTCTCATCATCTGTGTATGATGATGATCT 1024
QY 752 TGCGTCTCAAGAGCGCTCGGCTCTTTCGCTCCGAGAGAAAGTGGCAACTGCGCTA 811
DB 1025 TACAGCTCAAGAGTGTCCGATGCTGTGCGGCTCCAAAGAAAGACAGAAACCTGCGCA 1084
QY 812 GGATCAGCAGATGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 871
DB 1085 GGATCAGCAGATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1144
QY 872 ACAATATCATCTGCTGTGAGGCTCTGGGAGACCTCCCAAGCAAGCAAGCTGCTCTCTCA 931
DB 1145 ACATCTATGTCATCTCAAAAGCATGATCAGATTCAGAAACCACTTTCAGACATGTTT 1204
QY 932 GGTATTTACTTTCGATCGCTTGAAGTATACCAAGATGAGCTGATTCATTTCTTAG 991
DB 1205 CTTGCACTTCTGCAATGCTTGGGTTACAAACAGCTGTCTGAACCAAGTTCTTTTAG 1264
QY 992 CTTTCTTGTATGAAAACTTCAAGCGGTGTTCCGGGACTTCTGCTTTCACATGAAGATGA 1051
DB 1265 CGTTCTGTGATGAAAACTTCAACAGATGTTTATGAGAGTTCTGCACTCCAACTTCTCTCA 1324
QY 1052 GGATGAGCGGAGAGCACTAGCAAGTCCGAAATACAGTTCAAGATC 1099
DB 1325 CAATGGAACAGCAAAACTCTGCTCGAATCCGTCAAAAACACTAGGGAC 1372

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RESULT 61
 AAQ56700
 ID AAQ56700 standard; cDNA; 1821 BP.
 XX
 AC AAQ56700;
 XX
 DT 25-MAR-2003 (revised)
 DT 15-SEP-1994 (first entry)
 XX
 DE Sequence of murine delta opioid receptor in the DOR-1 cDNA clone.
 XX
 KW Opioid receptor; morphine; opiate; ss.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT CDS 29..1139
 FT /*tag= a
 XX
 PN M09404552-A1.
 XX
 PD 03-MAR-1994.
 XX
 PF 13-AUG-1993; 93WO-US007665.
 XX
 PR 13-AUG-1992; 92US-00929200.
 XX
 PA (REBC) UNIV CALIFORNIA.
 XX
 PI Evans CJ, Keith DE, Edwards RH, Kaufman D;
 DR MPI: 1994-081099/10.
 DR P-PSDB; AAR48629.
 XX
 PT DNA encoding opioid receptors and antibodies against this receptor - used
 PT to express and locate these receptors, and screen cpds. for opioid
 PT (ant)agonist activity.
 XX
 PS Claim 1; Fig 5; 74pp; English.
 XX
 CC A cDNA library was constructed using mRNA isolated from the NG109-15 cell
 CC line. A single clone, named the DOR-1 clone was isolated. Comparisons
 CC with known sequences in GenBank showed highest homology between DOR-1 and
 CC the G-protein-coupled somatostatin receptor. Other features of the DOR-1
 CC clone AA sequence deduced from the cDNA sequence include 3 consensus
 CC glycosylation sites at residues 18 and 33 (predicted to be in the C-
 CC extracellular N-terminal domain), and at residue 310 (close to the C-
 CC terminus and predicted to be intracellular). Phosphokinase C consensus
 CC sites are present within predicted intracellular domains, at residues
 CC 242,255, 344 & 352. Seven putative membrane-spanning regions were
 CC identified. The DOR-1 clone produces a delta receptor with a predicted
 CC mol. wt. of 40,558 kDa prior to post-translational modifications.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 1821 BP; 339 A; 559 C; 541 G; 382 T; 0 U; 0 Other;

Query Match 36.6%; Score 422.6; DB 2; Length 1821;
 Best Local Similarity 67.1%; Pred. No. 1.3e-93;
 Matches 634; Conservative 0; Mismatches 299; Indels 12; Gaps 2;

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QY 93 CCGGCTGGGCGGACCCGACAGCAAGGAGCGCGGCTCGAGAGGACGGCGAGCTGGAGC 152
DB 91 CGCCTTTCACAGCGGCTTTCACAGGCGGCGCCCAATGCTGTGGGCTCCCGGAGCCCG 150
QY 153 CCGGACACATCTCCCGGCGCATCCGGTATCATCAAGCGGTCTACTCCGATGTTTCT 212
DB 151 TAGTGGGCTCTTTGGAACTTCCTGGTATGATGATTTGAATATACCAAAATGA 210
QY 212 CTTTCTTGTATGAAAACTTCAAGCGGTGTTCCGGGACTTCTGCTTTCACATGAAGATGA 272
DB 211 AGTGGGCTTCTGAGCAAGTGTCTGTATGTTTGGATCGTCCGATACCAAAATTTGAA 270
QY 272 GACAGCAACCAACATTTACATTTTAACCTGCTTGGCAAGTGTCTTATGATGATGATC 332

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[illegible]

XX	PD	24-JUL-2001.
XX	XX	
PF	PF	13-FEB-1995; 95US-00387707.
XX	XX	
PR	XX	13-AUG-1992; 92US-00929200.
XX	XX	
PA	PA	(REGC) UNIV CALIFORNIA.
PI	PI	Evans CJ, Keith DE, Edwards RH, Kaufman D;
XX	XX	
DR	DR	WPI; 2001-463944/50.
XX	XX	P-PEDB; AAE05742.
PT	PT	Nucleic acids encoding mammalian kappa and mu opioid receptors, useful
PR	PR	e.g. to identify substances for treating opioid addiction and/or useful
XX	XX	as analgesics.
XX	XX	
PS	PS	Example 5; Fig 5; 46pp; English.
XX	XX	
CC	CC	The invention relates to recombinant nucleic acid molecules which encode
CC	CC	the murine delta opioid receptor, as well as recombinant nucleic acid
CC	CC	molecules which can be retrieved using low-stringency hybridisation to
CC	CC	this disclosed DNA. The invention provides genes encoding delta, kappa,
CC	CC	and mu receptors of any species containing genes encoding such receptors
CC	CC	sufficiently homologous to hybridise under low-stringency conditions. The
CC	CC	nucleic acids may be used to recombinantly express kappa and mu opioid
CC	CC	receptors in host cells. These cells may then be used in assays to
CC	CC	identify modulators of the receptors activity that may be used, for
CC	CC	example as analgesics or to combat the effects of opioid addiction. The
CC	CC	nucleic acids and their complements may also be used as probe sequences
CC	CC	to identify and characterise opioid receptor nucleic acids. The present
CC	CC	sequence is murine delta opioid receptor (DOR-1) cDNA
XX	XX	
SQ	SQ	Sequence 1829 BP; 340 A; 562 C; 543 G; 384 T; 0 U; 0 Other;
		Query Match 36.6%; Score 422.6; DB 5; Length 1829;
		Best Local Similarity 67.1%; Pred. No. 1.3e-93;
		Matches 634; Conservative 0; Mismatches 299; Indels 12; Gaps 2
QY	93	CGGCTGGGCCGAGCCCGACAGCAACGAGCGCGCGCTTCGAGAGACGCGCAGCTGGAGCC 152
DB	91	CGCCTTCCACAGCGCTTCCCACAGCGGGGCGCAATGCATGCGGGATCGCGGAGACC 150
QY	153	CGCGCACATCTCCCGGCCCATCCGGGTATATACAACGGCGCTACTCCGTAGTGTTGCT 212
DB	151	TAGTGCCTCGGCTCCCTCGGCCCTTAGCCATGCATCAACCGGCTCTACTCGCTGTGGCC 210
QY	213	CGTGGGCTTGTGGGCAACTCGCTGTGATGTTCTGTATCATCCGATACACAAAGATGA 272
DB	211	AGTGGGGCTTCTGGGCAACTGTCTGTATGTTGGCATCGTCCGGTACACCAATTGAA 270
QY	273	GACAGCAACCAACATTATCATTTTAACCTGGCTTTGGCAGATGCTTTAAGTATCTAAC 332
DB	271	GACCCGCAACCAACATCTACATCTTCAACTGGCTTTGGTATGATGCGTGGCCACACGAC 330
QY	333	CATGGCCCTTTAGAGTAAGGTCTACTTTGTATGAATTCCTGGCTTTTGGGAGATGTGTC 392
DB	331	GCTGCGCTTCCAGAGCGCAAGTACTTATGAGAACGTGGCCGCTTTGGGAGACTGTGTG 390
QY	393	CAAGATAGTAATTTTCATTTGATTACTAGAACATGTTCAACAGCATCTTCACTTGACAT 452
DB	391	CAAGGCTGTGCTCTCATTTGACTTAAACAATGTTTCACTACATCTTCAACCTTCACAT 450
QY	453	GATGAGCGTGAACCGCTACTATTCGCGTGTCCACCCCGTGAAGGGCTTTGGACCTCCGAC 512
DB	451	GATGAGCGTGAACCGCTACTATTCGCTGTCTGTCATCTGTCCAAGCCCTGGACTTCCGAC 510
QY	513	AACCTTGAAGGCAAGATCATCAATCTGCATCTGGCTGTCTGTGCTCATCTGTTGGCAT 572
DB	511	ACGACCCAAAGGCAAGGATGATTAATATATGATCTGGGGCTTGGCTTACAGGTGTGGGGGT 570
QY	573	CTCTGCAATTAATCTTTGGAGGACCAAAAGTCAGGGAAGAAGTCATGATCTAATGAGTCTC 632

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Db      571 CCCCATCATGTCATGAGGAGTACCCCAACCCCGGAGTGTGACAGTGTATGATGCTCA 630
Qy      633 CTTCGAGTTCCCAATGATGACTACTCTCTGTGGAGACCTTCTTCAAGAGATCTGGCTTT 692
Db      631 GTTCCCAAGTCC-----CAGCTGGTACTGGGACACTGTGACCAGATCTGCGCTGTT 681
Qy      693 CATCTTTGCTTGTGATCCCTGCTCTCATCATCATCGTCTGTACACCTGATATGCTT 752
Db      692 CCTCTTTGCTTGTGATCCCAATCTCATCATCAGGTGTCTATGGCTCATGCTACT 741
Qy      753 GCGTCTCAAGAGCGTCCGCGCTCTTCTGTGGCTCCGAGAGAAAGATCGCAACTGGCTAG 812
Db      742 GCGCTCGGCAAGCGTGTGCTGTCTGTCCGGTTCAGAGAGAAAGACCGAGCTGGGGG 801
Qy      813 GATCACAGACTGTGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 872
Db      802 CATCACGCGCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 861
Qy      873 CATATTCAATCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 929
Db      862 CATCTTCGTCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 921
Qy      930 CAGCTATTACTTCTGTGATCGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 989
Db      922 CGCACTGCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 981
Qy      990 CGCCTTTCTTGTATGAAAACTTCAAGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1034
Db      982 CGCCTTCTGTGAGAGAACTTCAAGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1026

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RESULT 63

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ABS53439 ID ABS53439 standard; cDNA; 1829 BP.
XX AC ABS53439;
XX DT 19-NOV-2002 (first entry)
XX DE cDNA encoding human delta opioid receptor protein (DOR-1).
XX KW Enkephalin; opioid receptor; poisoning; addiction; morphine; codeine; ss;
XX gene; DOR-1; human.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX CDS 29..1147
XX FT /*tag=a
FT /product="Human DOR-1 protein"

XX US6432652-B1.
XX PD 13-AUG-2002.
XX PF 14-MAR-1995; 95US-00405271.
XX PR 13-AUG-1992; 92US-00929200.
XX PR 13-AUG-1993; 93WO-US007665.
XX PR 13-FEB-1995; 95US-00387707.
XX PR 13-MAR-1995; 95US-00403260.
XX PA (REGC ) UNIV CALIFORNIA.
XX PI Evans CJ, Keith DE, Edwards RH, Kaufman D;
XX WPI; 2002-681194/73.
XX DR P-PSDB; ABG33029.
XX PT Mammalian DOR-1 opioid receptors, useful for screening for compounds
XX useful in the treatment of opioid addiction and poisoning.

```

PS Claim 3; Fig 5; 61pp; English.

CC This invention relates to the DNA and protein sequences of novel
 CC mammalian opioid receptor (DOR-1) displayed at the surface of recombinant
 CC host cells. The invention also comprises a method for screening a
 CC candidate substance for opioid agonist activity and a method for
 CC detecting the amount of activation of the opioid receptor in the presence
 CC as compared to the absence of the candidate substance. The methods and
 CC compounds of the invention may have anti-addictive agents and may be used
 CC to modulate opioid receptor activity. The mammalian opioid receptor of
 CC the invention may be used to screen for agonists and antagonists of it's
 CC expression and activity which may be used to treat e.g. poisoning by, and
 CC addiction to, opioid (such as morphine, codeine, and many semi-synthetic
 CC congeners of morphine). The present sequence represents the cDNA sequence
 CC encoding the human delta opioid receptor (DOR-1) protein of the invention
 XX SQ Sequence 1829 BP; 340 A; 562 C; 543 G; 384 T; 0 U; 0 Other;

Query Match 36.6%; Score 422.6; DB 6; Length 1829;

Best Local Similarity 67.1%; Pred. No. 1.3e-93;

Matches 634; Conservative 0; Mismatches 299; Indels 12; Gaps 2;

```

Qy      93 CGGCTGGGCGGACCGGACGAGCAAGCGGACCGCGCTGTGAGAGACGCGCACTGGAGCC 152
Db      91 CGCCTTCCCAAGCGCTTCCCAAGCGGCGGCGCAATGTGTGGGTGTGCGCGGAGCCCG 150
Qy      153 CGGCAATCTTCCCGGCCATCCGGTCAATCAACGCGGTCTACTCCGTAGTGTGCT 212
Db      151 TAGTGTCTGTCTCTGCGCTGAGCCATGCGCATCAACGCGGCTCTACTCGGCTGTGGCC 210
Qy      213 CGTGGGCTTGTGGGCACTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 272
Db      211 AGTGGAGCTTCTGGGCAACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 270
Qy      273 GACAGCAACCAATTTATCATATTTAATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 332
Db      271 GACGCGCAACCAATCTATCATTTTCAATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 330
Qy      333 CATGCCCTTTCAGAGTACGCTTACTTGTATGTAATTCCTGTGTGTGTGTGTGTGTGTGTGT 392
Db      331 GCTGCCCTTCCAGACGCGCAAGTACTGTATGAAAGTGTGCGGCTGTGTGTGTGTGTGTGT 390
Qy      393 CAAGATAGAAATTCATGATTACTATCAACAAGTTCACAGATCTTACCTGACAT 452
Db      391 CAAGCTGTGCTCTCATTTGACTATCAACAAGTTCATGATCTTACCTGACAT 450
Qy      453 GATGACGCTGACCGCTACATTGCGGTGTGCCACCCCGTGAAGGCTTTGGAATTCGCGAC 512
Db      451 GATGACGCTGACCGCTACATTGCTGTGTCATCTGTGCAAGCCCTGTGACTTCCGGAC 510
Qy      513 ACCCTTGAAGGCAAGATCATCATATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 572
Db      511 ACCAGCCAAAGGCAAGTGTATGATCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 570
Qy      573 CTCTGCATATGCTCTTGAAGGACCAAGTCAAGGAAAGCTGTGATGTATGAGTGTCTC 632
Db      571 CCCCATCATGTCATGAGGAGTACCCCAACCCCGGAGTGTGACAGTGTATGATGCTCA 630
Qy      633 CTTCGAGTTCCCAATGATGACTACTCTCTGTGGAGACCTTCTTCAAGAGATCTGGCTTT 692
Db      631 GTTCCCAAGTCC-----CAGCTGGTACTGGGACACTGTGACCAGATCTGCGCTGTT 681
Qy      693 CATCTTTGCTTGTGATCCCTGCTCTCATCATCATCGTCTGTACACCTGATATGCTT 752
Db      692 CCTCTTTGCTTGTGATCCCAATCTCATCATCAGGTGTCTATGGCTCATGCTACT 741
Qy      753 GCGTCTCAAGAGCGTCCGCGCTCTTCTGTGGCTCCGAGAGAAAGATCGCAACTGGCTAG 812
Db      742 GCGCTCGGCAAGCGTGTGCTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 801
Qy      813 GATCACAGACTGTGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 872
Db      802 CATCACGCGCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 861

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Query Match	36.6%	Score 422.6	DB 2	Length 2218
Beet Local Similarity	67.1%	Fred. No. 1.4e-93		
Matches 634; Conservative	0	Mismatches 299	Indels 12	Gaps 2

QY	93	CGGCTGGGCGAGGCGCGAAGACAACGAGCGGCGCTCGGAGGACGCGACGTGAGACC	152
Db	120	CGCCTTTCGACGGCGCTTCCCGACGGGGGCGCAATGCGTGGGGTGGCGGGAGCCG	179
QY	153	CGCGACATCTCCCGGACATCCGGTCATCATCAGCGCGGTCTACTCCGTAGTGTCT	212
Db	180	TAGTGGCTCGTCCCTCGCGCTTAGCGATCGCATCAGCGCGCTCTACTGCGTGTGGCG	239
QY	213	CGTGGGCTTGGTGGGCACTCGCTGGTCACTTGTGTATCATCTCGATACAAAGATGA	272
Db	240	AGTGGGGCTTGGGCAACGTGCTGTATGTTTGGCATGTCGTGGGTACACCAATTGA	299
QY	273	GACAGCAACCAATTTATATATTAACTGGCTTTGGCAGATGCTTTAGTTACTACAC	332
Db	300	GACGGCCACCAACATCTACATCTTCAATCTGGCTTTGGCTGATGGCGTGGCAACAAGC	359
QY	333	CATCGCCCTTTCAGAGTACGGTCTACTGTGATGATTTCTGCGCTTTTGGGGATGTGCTGT	392
Db	360	GCTGGCCCTTCAGAGCGCCAAAGTCTTGATGGAACGGTGGCGCTTTGGCGAGCTGCTGT	419
QY	393	CAAGATAGTAATTTCCATTTGATTAATTAATTAATGTTCAACGACATCTTCACTTGAACAT	452
Db	420	CAAGCTGTGTCTTCACATTAATGACTACTCAACATGTCTCATAGACATCTTACCTTCAACAT	479
QY	453	GATGAGCGTGAACGCTACATTTGCGCGATGCGCACCCCGTGAAGGCTTTGACCTTCCGAC	512
Db	480	GATGAGCTGGAACCGCTACATTTGCTGTGTGCACTCTGTCAAAAGCCCTGACCTTCCGAC	539
QY	513	ACCCTTGAAGCAAAATCATCAATATCTGCATCTGCTGCTGTGTCTATCTGTTGGCAT	572
Db	540	ACCAGCCAAAGCCAAAGCTGATCAATATATGATCTGGGTCTTGGCTTCAAGGTGTGCGGGT	599
QY	573	CTTGCATATAGTCCCTGAGGACCAAAAGTCAGGGAAGAAGTCATGATCATTTAGTGTCT	632
Db	600	CCCATCATGATGATGCGAGTGAACCAACCCGGGATGTGTCAATGTGATGTGATGATGCTCA	659
QY	633	CTTGCAGTTCACAGATGATGACTACTCTCGTGTGGAACTCTTTCATGAAGATCTGCTT	692
Db	660	GTTCCCAAGTCC-----CAGCTGTACTGGGAACGTGTGACCAAGATCTGGTGT	710
QY	693	CATCTTTGCTTGTGATTCCTGTTCCTGTCTCATCATCATGTCTGTGTCACACCTGATGATCT	752
Db	711	CCTCTTTGCTTGTGATGTCGATCTCATCATCATCAGGTGTGCTATAGGCTTCATGTACT	770
QY	753	GCGTCTAAAGCGCGCGGCTCTTTTCGCGCTCCGAGAGAAAGTGCSCAATCTGCGTAG	812
Db	771	GCGCTTGGCGACGCTGCTGTGTGTCTGTCCGGTTCCAAAGAGAAAGAACGCACTTGGCG	830
QY	813	GATCACCAAGCTGTGCTGT	872
Db	831	CATACCGGAGATGATGCTGT	890
QY	873	CATATTAATCTGTGTGAAGGCTCTGGGG--AGACCTTCCACAGACACAGTGTCTCTCT	929
Db	891	CATCTTCTCATCTGTGTGAAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	950
QY	929	CAGCATTAATCTTGCATCGCTTGAAGGCTTATACCAACAGTAGCTGTAATCCATTTCTTA	989
Db	951	CGCACTGACCTGTGTGATTTGGCTGTGGCTTACGCCAACAGACCTTCAACCCGGTTCTTA	1010
QY	990	CGCCTTCTTGATGAAAACTTCAAGCGGTGTCTTCCGGGACTTCTG	1034
Db	1011	CGCCTCTGTGACGGAACCTTCAAGCGGTGTCTTCCGCGACGCTCTG	1055
RESULT 65			
ABV75085			
ID	ABV75085 standard; DNA; 2219 BP.		
XX			
AC	ABV75085;		
DT	19-FEB-2003 (first entry)		

XX XX Murine delta-opioid receptor encoding DNA.
XX XX Delta-opioid receptor; transgenic; anticonvulsant; epilepsy; mouse; gene;
XX KM ds.
XX OS Mus sp.
XX XX Key Location/Qualifiers
XX FH /tag= a
XX FT CDS /product= "delta-opioid receptor"
XX PN WO200279423-A2.
XX PD 10-OCT-2002.
XX PF 29-MAR-2002; 2002WO-US009715.
XX PR 29-MAR-2001; 2001US-0280513P.
XX XX (DELT-) DELTAGEN INC.
XX PA Allen KD;
XX PI WPI: 2003-067441/06.
XX DR P-P8DB; ABB82650.
XX XX
XX PT New transgenic mouse comprising a disruption in a delta-opioid receptor
XX PT gene, useful for preparing a pharmaceutical composition for treating
XX PT epilepsy.
XX PS Disclosure; Fig 1, 61pp; English.
XX CC The invention relates to a transgenic mouse comprising a disruption in a
XX CC delta-opioid receptor gene. There is no native expression of endogenous
XX CC delta-opioid receptor gene. The transgenic mouse comprising a disruption
XX CC in a delta-opioid receptor gene is useful for preparing a pharmaceutical
XX CC composition for treating epilepsy. The present sequence represents a
XX CC mouse delta-opioid receptor encoding DNA
XX SQ Sequence 2219 BP; 460 A; 649 C; 650 G; 460 T; 0 U; 0 Other;
Query Match 36.6%; Score 422.6; DB 7; Length 2219;
Best Local Similarity 67.1%; Pred. No. 1.4e-93;
Matches 634; Conservative 0; Mismatches 299; Indels 12; Gaps 2;
QY 93 CGGCTGGGCGGAGCCGAGCAGCAGCGGCGGCTGGAGAGCAGCGCAGCTGGAGCC 152
DB 121 CGCCTTCCGACGCGCTTCCGAGCGGCGGCGCAATGCGTGGGCTGCCGGAGCCGG 180
QY 153 CGCGCATCTCCCGGCGCATCCCGTCAATCAACGCGGCTCTACTCCGTAAGTTCGT 212
DB 181 TAGTCCCTGCTCCGCGCTAGCCATCGCATCAACGCGCTCTACTCCGCTGTGCGC 240
QY 213 CGTGGCTTGGTGGGGAATCGCTGTATGTTTCGATCAACCAATACAAAGTGA 272
DB 241 AGTGGGCTTGGGGAAGCTGCTGATGTTTGGCATGTCGCGTACACCAAAATTGA 300
QY 273 GACAGCAACCAATTTATATATTTAACTGGCTTGGAGATGCTTAGTACTACAC 332
DB 301 GACCGGCAACCAATCTATATCTTCAATGCTTGGCTGATGCGCTGGCAGCAGC 360
QY 333 CATGCCCTTTCAGAGTACGCTTACTTGAATGATTCCTGGCTTTGGAGATGTGCTG 392
DB 361 GCTGCCCTTTCAGAGGCGCAAGTACTTGTATGAAAGTGGCGTGTGGAGCTGCTG 420
QY 393 CAAGATAGTAATTTCCATGATTAATCAAAAGTTCACACAGATTTTACCTGACCT 452
DB 421 CAAGGCTGTGCTCTCATTAATGACTACAAAGTTCACATACCTTACCTCAACAT 480
QY 453 GATGAGCGTGAACGCTATACGCTGTGACACCCCGTAAGGCTTTGACTTCGAC 512
|||||

DB 481 GATGAGCGTGAACCGCTATACCTGCTGTGCCATCTCTCAAAAGCCGTGAGCTCCGAC 540
QY 513 ACCCTTGAAGGAAGAT 572
DB 541 ACCAGCAAGGCGCAAGCTGAT 600
QY 573 CTCTGCAATAGTCTTGGAGGACCAAGTCAAGGAGAGAGTCAATGATTAAGTCTC 632
DB 601 CCCCATCATGATGATGAGGATGACCAACCCCGGATGATGAGTATGATGATGATGATGAT 660
QY 633 CTTCGAGTTCACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 692
DB 661 GTTCCCAAGTCC-----CAGCTGTATCTGGGACACTGTGACCAAGATCTGCGTGT 711
QY 693 CATCTTGGCTTGTGATATCCCTGCTCTATATATATATATATATATATATATATATATAT 752
DB 712 CCTCTTGGCTTGTGATATCCCTGCTCTATATATATATATATATATATATATATATATAT 771
QY 753 GCGCTCAAGAGCGGCTCCCTTCTGCTCCGAGAGAAAGATCGCAACCTGCGTAG 812
DB 772 GCGCTGCGGAGCGTCCCTGCTCTGCTCCGAGAGAAAGATCGCAACCTGCGTAG 831
QY 813 GATCAACCAAGTGTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 872
DB 832 CATCAAGCGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 891
QY 873 CATATTCATCTGTGTGAGAGCTGTGGG---AGCATCTCCACAGACAGCTGTCTCTC 929
DB 892 CATCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 951
QY 930 CAGTATTACTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 989
DB 952 CGCATGCACTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1011
QY 990 CGCCTTCTTGTATGAAGAACTTCAAGCGGTGTTTCGGGACTTCTG 1034
DB 1012 CGCCTTCTGAGCAGAACTTCAAGCGGTGTTTCGGGACTTCTG 1056
RESULT 66
AAQ75927
ID AAQ75927 strand; DNA; 2272 BP.
XX AC AAQ75927;
XX XX 25-MAR-2003 (revised)
DT 17-AUG-1995 (first entry)
DE Mouse delta opioid receptor MOR1 cDNA.
XX XX
XX KM Mouse; kappa; delta; mu; opioid receptor; brain; primer; PCR; amplify;
XX KM transmembrane domain; somatostatin; receptor; human; expression vector;
XX KM truncate; chimaeric; assay; probe; ss.
OS Mus musculus.
XX XX
XX FH Key Location/Qualifiers
XX FH CDS 12..1130
XX FT /tag= a
XX FT /product= "mouse delta opioid receptor"
XX PN WO9428132-A2.
XX XX
XX PD 08-DEC-1994.
XX PF 20-MAY-1994; 94WO-US005747.
XX XX
XX PR 20-MAY-1993; 93US-00066296.
XX PR 30-JUL-1993; 93US-00100694.
XX PR 05-NOV-1993; 93US-00147592.
XX XX
XX PA (ARCH-) ARCH DEV CORP.
XX XX

PI Bell GI, Reisine T, Yasuda K;
 XX WPI; 1995-022804/03.
 DR P-PSDB; AAR67670.
 XX Polynucleotides and peptides derived from opioid receptor polypeptides -
 PT for use in therapeutic compositions and in screening assays for useful
 XX drug substances.
 XX
 XX Claim 6; Page 215-221; 300pp; English.
 CC The nucleotide sequence of the novel mouse delta opioid receptor gene
 CC MOR1. The gene was isolated from a mouse brain cDNA library using a
 CC fragment (amplified from the cDNA library with primers AAQ7529-30) as a
 CC probe. The primers are based on the conserved sequences present in the
 CC second and third transmembrane domains of somatostatin (SRI) receptor
 CC subtypes SSTR1, SSTR2 and SSTR3. The 1.3 kb EcoRI-SacI fragment from the
 CC mouse delta opioid receptor clone, lambda ms1-2, was subcloned into the
 CC CMV promoter-based expression vector pCMV-6c. The resultant construct
 CC pCMV-ms1-2 was transfected into COS-1 cells for protein production. The
 CC gene encoding the opioid receptor can be used to produce complete,
 CC truncated or chimeric opioid receptor proteins. The opioid receptors
 CC thus produced are useful for the development of novel assays designed to
 CC select or improve substances, capable of interacting with the opioid
 CC receptor proteins, for use in diagnosis, drug design and therapeutic
 CC applications. (Updated on 25-MAR-2003 to correct PN field.)
 CC
 XX Sequence 2272 BP; 485 A; 665 C; 650 G; 472 T; 0 U; 0 Other;
 SQ
 Query Match 36.6%; Score 422.6; DB 2; Length 2272;
 Best Local Similarity 67.1%; Pred. No. 1.4e-93;
 Matches 634; Conservative 0; Mismatches 299; Indels 12; Gaps 2;
 QY 93 CGGCTGGGCGGAGCCGAGCAGCAACGCGCGGCTTGAGAGACGCGACCTGAGCC 152
 DB 74 CGCCTTCCAGAGGCTTCCAGAGCGGGCGCAATGCGTGGGGTCCGCGAGCCG 133
 QY 153 CGCGACATCTCCCGGCGCATCCGGTCAATCATCAGGGGGTCTACTCCGTAGTTCCT 212
 DB 134 TAGTGCTCTGCTCCCTCGCCCTTGCATCCGCAATCAGCGGCTCTACTCGAGTGTGCGC 193
 QY 213 CGTGGGCTTGATGGGCACTCGGTGTCATGTTGATCATCCGATACCAAAAGATGA 272
 DB 194 AGTGGGCTTCTGGGCAAGCTGCTGTCATGTTTGGCATGTCGGTACCAAAATGA 253
 QY 273 GACAGCAACCAATTATTAATTTAACTGGCTTTGGAGATGCTTATTAACAAC 332
 DB 254 GACCGCACCAACATCTACATCTTCAATCTGGCTTTGGCTGATGCGCTGGCACAC 313
 QY 333 CATGCCCTTTCAGAGTACGCTACTGATGAATTCCTGGCCCTTTGGGAGATGCTG 392
 DB 314 GGTGCCCTTTCAGAGGCGCAAGTACTGATGAAAGTGCGCGCTTGGGAGCTGTG 373
 QY 393 CAAGATAGTAATTTTCATGATTACTACAAAGTTCACACAGCATCTTACCTTGACAT 452
 DB 374 CAAGGCTGTGCTCTCATGATGACTACAAAGTTCATGATGATTTACCTTACCAT 433
 QY 453 GATGACGTGAGACCGGTACATGCGGTGTCACCCCGTGAAGGCTTTGACTTCGAC 512
 DB 434 GATGACGTGAGACCGGTACATGCTGTGTCATCTGTCACAAAGCCTGGAATTCGAC 493
 QY 513 ACCCTTGAAGGCAAGATATCATATTCGATCTTGGCTGCTGCTCATCTTTGGCAT 572
 DB 494 ACCAGCAAGGCGCAAGCTATCAATATATGATCTGGCTTGGCTTCAAGGTTCGGGGT 553
 QY 573 CTCTGCAATAGTCTCTTGAGAGCCAAAGTCAAGAGAAAGCTGATGATGAGTCTC 632
 DB 554 CCCCATCATGCTATGAGTACCCAAAGCCCGGAGTGTGAGAGTATGATGCTCCA 613
 QY 633 CTTCGAGTCCAGATGATGACTACTCTGTGGTGAACCTTTGATGAAGATCTGCGTCTT 692
 DB 614 GTTCCCAAGTCC-----CAGCTGTACTGGAGCACTGTGACCAAGATCTGCGTGT 664

QY 693 CATCTTGCTTCGATGCCGTCCTCATCATCATGCTGCTTACACCTGATGATCCT 752
 DB 665 CCTCTTTCCTTCGATGTCGATCCGATCTCATATCAGGTCGTCATGAGCTTATCTACT 724
 QY 753 GCGTCTCAAGAGCGCTCCGAGCTCTTCTGAGCTCCGAGAGAAAGATCCGACCTGAG 812
 DB 725 GCGCTTGCGAGCGTCGCTGCTGTCCGGTTCCAAAGAGAAAGACCGAGCTTCGGGG 784
 QY 813 GATCAACGACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 872
 DB 785 CATCAAGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 844
 QY 873 CATATTCATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 929
 DB 845 CATCTTTCGATCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 904
 QY 930 CAGCTATTAATCTTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 989
 DB 905 CGCAGTGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 964
 QY 990 CGCCTTCTTGATGAAGAACTTCAAGCGGTCTTTCCGGGACTTCTG 1034
 DB 965 CGCCTTCTTGAGAGAACTTCAAGCGGTCTTCCGCAAGCTCTG 1009
 RESULT 67
 AAD50856
 ID AAD50856 standard; DNA, 1176 BP.
 XX
 XX AAD50856;
 AC 27-OCT-2003 (revised)
 XX
 DT 02-APR-2003 (first entry)
 XX
 DE Human modified mu opioid receptor DNA #1.
 XX
 KW Human; membrane-spanning signal-transducing protein; MSST protein;
 OS mu opioid receptor; receptor; gene; mutant; mutein; de.
 OS Homo sapiens.
 OS Tobacco etch virus.
 OS Chimeric.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1176
 FT /*tag= a
 FT /product= "Mu opioid receptor modified protein"
 FT /note= "No stop codon"
 FT /partial
 FT misc_feature 529..549
 FT /*tag= b
 FT /note= "TEV protease cleavage site"
 FT
 XX
 XX MO200286507-A1.
 PN
 XX
 PD 31-OCT-2002.
 XX
 PF 24-APR-2002; 2002MO-US013250.
 XX
 PR 24-APR-2001; 2001US-0286250P.
 PR 21-AUG-2001; 2001US-0093506P.
 XX
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 XX
 PI Kobilka BK, Ghanouni P, Lee TW;
 XX
 DR WPI; 2003-103418/09.
 DR P-PSDB; AAE33276.
 XX
 PT Identifying an agent that modulates activity of a membrane-spanning,
 PT signal-transducing (MSST) protein, by detecting a conformational change
 PT in a MSST protein upon interaction with a ligand.
 XX

PS Example 12; Page 96-98; 104pp; English.

CC The present invention relates to methods and compositions for identifying
 CC agents that modulate activity of a membrane-spanning, signal-transducing
 CC (MSST) protein. The method involves detecting a conformational change in
 CC a MSST protein upon interaction with a ligand. The method is useful for
 CC identifying agents that modulate (e.g. agonists or antagonists) activity
 CC of MSST protein. The present sequence is human modified mu opioid
 CC receptor DNA. This sequence is modified to contain a tobacco etch virus
 CC (TEV) protease cleavage site in the second intracellular loop. This
 CC sequence is used to illustrate the method of the invention. (Updated on
 CC 27-OCT-2003 to standardise OS field)

XX Sequence 1176 BP; 292 A; 342 C; 241 G; 301 T; 0 U; 0 Other;

Query Match 36.0%; Score 415.6; DB 7; Length 1176;
 Best Local Similarity 65.1%; Pred. No. 5,99-92;
 Matches 648; Conservative 0; Mismatches 339; Indels 9; Gaps 2;

QY 92 CCGGCTGGGCGAGCCGACAGCAACGGAGCGCGCTCGGAGAGCGGCGAGCTGGAGC 151
 DB 125 CCGACCCATCGGCTCGAAACCGACCGACCTGGCGGAGAGACGCTGTGCTCCAA 184
 QY 152 CCGCGACATCTCCCGGCGCATCCGCTCATCATCAGCGCGGTCTACTCCGATGTTGG 211
 DB 185 CCGGAGATCCCTCCATGATCAGGCGCATCAGCATATGCGCTCTATCTCATCGTGTGG 244
 QY 212 TGTGGGCTTGTGGCAACTGCTGTGTATGTTCTGTATCATCCGATACAAAGATGA 271
 DB 245 TGGTGGGCTCTTCGGAACCTTCGTGTATGTGATTCATGATACACCAAGATGA 304
 QY 272 AGACAGCAACCAATTTACATTTTACCTGGCTTGGCAGATGTTAGTTACTACAA 331
 DB 305 AATCTGCCACCAACATCTACATTTTACCTGTGCTGGCAGATGCTTACCAAGATGA 364
 QY 332 CCATGCGCTTTCAGAGTACGATCTACTGATGAATTCCTGGCTTTGGGAGATGTCGT 391
 DB 365 CCGTCCCTTCAGAGTGTGAATTAATCTATGGAACATGGCATTTGGAAACATCTTT 424
 QY 392 GCAAGATGATTAATTTCCATTGATTAACAACATGTTCAACAGCATCTTCACTTGACA 451
 DB 425 GCAAGATGATTAATTTCCATTGATTAACAACATGTTCAACAGCATCTTCACTTGACA 484
 QY 452 TGATAGGCTGAGCGCTACATTCGCGTGGCAACCGCGTGAAGCTTGGACTTCGGA 511
 DB 485 CCATAGGTGTATGATACATTCAGTGTGCCACCTGTCAAGGAAACCTCTACTTCC 544
 QY 512 CACCTTGAAGCAAAATCATCATATATGCTGCTGCTGTGCTATCTGTTGCA 571
 DB 545 AGGGGGAATGCCAAATTAATCAATGTCTGCAACTGATCTCTCTTCAAGCATTTGTC 604
 QY 572 TCTTGCAATGATCTTGGAGGCAACCAAGTCAAGGAGACGTGATCAATGATGCT 631
 DB 605 TTCCTGATATGTTATAGCTACAAACAAATACAGGCAAG-----TTCATATGATTGA 658
 QY 632 CTTTGAGTTCCCAATGATGACTACTCTGTGTGGGAACTCTTCAATGAAGATGTGGTCT 691
 DB 659 CACTAATCTCTCTCACTCAACCTGTGTAGGAAAACTGCG--TGAAGATCTGTGTT 715
 QY 692 TCATCTTTGCTTGGATCCCTGTGCTCATCATCATCTGCTGCTACCCGTGATGTC 751
 DB 716 TCAATCTGCTTCAATATGACAGTCTCATATTAACGTGTGCTATGACATGATATCT 775
 QY 752 TCGCTCTCAAGAGCGTCCGCTCTTCTTGTGCTCCGAGAGAAAGATCCGACCTGCTGA 811
 DB 776 TCGGCTCTCAAGAGTCCGACATGCTCTGTGCTCCAAAGAAAGACAGAAATCTTGA 835
 QY 812 GGATACCAAGATGCTGCTGT 871
 DB 836 GGATACCAAGATGCTGCTGT 895
 QY 872 ACATATTTCTCTGT 931

DB 896 ACATTTACGTCATCTTAAAGCCTGGTTACATCCAGAAATCACTGTCAGACTGTT 955
 QY 932 GCTATTAATCTTGCATGCGCTTAGGCTATACCAACAGTAGCTGATCCATTTCTAGC 991
 DB 956 CTGGCACTTCTGCAATTTGCTCTTAGGTTACAAACAGCTGCTCAACCAAGTCTTAG 1015
 QY 992 CTTTTCTTGATGAAAACTTCAAGCGGTGTTTCCGGGACTTGTCTTTCATGAAATGA 1051
 DB 1016 CATTTCTGATGAAAACTTCAACAGATGCTTCAAGAGATGTTGTAATCCCACTTTCA 1075
 QY 1052 GGATGAGCGGAGAGCACTACAGATCCGAAAT 1087
 DB 1076 ACATTTAGCAACAAATCTCACTCGAATTCGACAG 1111

RESULT 68

AA06656
 ID AA06656 standard; cDNA; 2216 BP.

AC AA06656;

DT 25-MAR-2003 (revised)

DT 19-JAN-1995 (first entry)

DE Murine delta opioid receptor coding sequence.

XX delta opioid; enkephalin; receptor; mouse; murine; analgesic; pain;

KW drug addiction; neurological disorder; psychiatric; disorder;

XX cardiovascular disorder; de.

OS Mus musculus.

FH Key Location/Qualifiers

FT CDS 59..1174

FT FT /*tag= a /product= "opioid_receptor"

PN FR2697850-A1.

PD 13-MAY-1994.

PF 10-NOV-1992; 92FR-00013526.

PR 10-NOV-1992; 92FR-00013526.

PA (U957-) UNIT PASTEUR STRASBOURG LOUIS.

PI Kieffer B;

DR WPI: 1994-178255/22.

DR P-PSDB; AAR6503.

PT New nucleic acid encoding opioid receptor - and related polypeptide,

PT antisense nucleic acid, probes, recombinant cells and ligands, useful in

PT diagnosis and treatment of e.g. neurological disorders.

PS Claim 3; Page 16-18; 29pp; French.

XX A cDNA bank constructed from hybridoma NG108-15, was used to transfect
 CC COS-1 cells. The cells were tested for ability to bind tritium-labelled
 CC Tyr-D-Thr-Gly-Phe-Leu-Thr, in the presence or absence of the opioid
 CC antagonist naloxone. Clone K56 was isolated from a positive colony and
 CC found to contain a 2216bp insert. This cDNA encodes a delta opioid
 CC (enkephalin) receptor with apparent dissociation constant 1.4nM and Bmax
 CC 3.9-6.4 pmole/mg protein. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 2216 BP; 460 A; 647 C; 649 G; 460 T; 0 U; 0 Other;

Query Match 35.6%; Score 411.4; DB 2; Length 2216;

Best Local Similarity 67.1%; Pred. No. 8,1e-91;

Matches 634; Conservative 0; Mismatches 296; Indels 15; Gaps 3;

QY 93 CCGTGGGCGAGCCGACAGCAACGGAGCGCGCTCGAGAGACGCGACGCTGAGCC 152

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Db      121 |C|C|C|T|T|C|C|C|A|G|C|G|C|T|T|C|C|C|A|G|C|G|C|G|C|C|C|A|T|G|C|T|G|G|G|T|G|C|C|G|G|A|G|C|C|G|C| 180
Qy      153 |G|C|G|G|C|A|C|T|T|C|C|C|G|G|C|C|A|T|C|C|G|G|T|C|A|T|C|A|C|G|G|G|G|T|C|T|A|T|C|T|G|A|G|T|T|G|T| 212
Db      181 |T|A|G|T|G|C|T|G|T|C|C|T|G|C|C|C|T|A|G|C|C|A|T|G|C|C|A|T|C|A|C|G|G|G|T|C|T|A|C|T|G|G|T|G|G|C|G|C| 240
Qy      213 |C|G|T|G|G|C|T|G|T|G|G|G|C|A|C|T|G|C|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T| 272
Db      241 |A|G|T|G|G|G|C|T|T|G|G|G|C|A|A|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T| 300
Qy      273 |G|A|C|A|G|C|A|C|A|C|A|T|T|A|C|A|T|T|T|A|C|T|G|C|T|T|G|G|A|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T| 332
Db      301 |G|A|C|G|G|C|A|C|A|C|A|T|T|A|C|A|T|T|T|A|C|A|T|T|G|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T| 360
Qy      333 |C|A|T|G|C|C|T|T|C|C|A|G|A|G|G|C|C|A|G|T|A|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T| 392
Db      361 |G|C|T|G|C|C|T|T|C|C|A|G|A|G|G|C|C|A|G|T|A|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T| 420
Qy      393 |C|A|G|A|T|A|T|T|T|C|A|T|T|G|T|A|T|T|A|C|A|C|A|T|T|T|A|C|A|C|A|T|T|T|A|C|A|C|A|T|T|T|A|C|A|C|A|T| 452
Db      421 |C|A|A|G|G|C|T|G|C|T|C|C|A|T|T|G|A|C|T|A|C|A|A|C|A|T|T|G|A|C|T|A|C|A|C|T|T|G|A|C|C|T|C|A|C|A|T| 480
Qy      453 |G|A|T|G|A|G|G|G|A|G|C|G|T|A|C|A|T|T|G|C|G|T|G|G|C|C|C|G|G|A|G|G|C|T|T|G|A|C|T|T|G|A|C|C|G|C|A|C| 512
Db      481 |G|A|T|G|A|G|G|G|A|G|C|G|T|A|C|A|T|T|G|C|G|T|G|G|C|C|C|G|G|A|G|G|C|T|T|G|A|C|T|T|G|A|C|C|G|C|A|C| 540
Qy      513 |A|C|C|T|T|G|A|A|G|G|C|A|A|G|A|T|C|A|T|A|T|C|T|G|A|C|T|T|G|C|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T| 572
Db      541 |A|C|C|A|G|C|A|A|G|G|C|A|A|G|C|A|T|C|A|T|A|T|A|T|A|G|C|A|T|T|G|G|G|T|C|T|T|G|G|T|C|A|G|G|T|G|G|G|G|T| 600
Qy      573 |C|T|T|G|C|A|T|A|G|T|C|T|T|G|A|G|G|A|C|C|A|A|G|T|C|A|G|G|A|A|G|C|G|C|A|T|G|T|A|T|G|A|G|T|C| 632
Db      601 |C|C|C|A|T|C|A|T|G|C|A|T|G|A|G|G|A|C|C|C|C|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G| 653
Qy      633 |C|T|T|G|A|G|T|T|C|C|C|A|G|A|T|G|A|C|T|C|C|G|T|G|G|G|A|G|C|C|T|T|C|A|T|G|A|A|G|A|T|G|G|G|T|T| 692
Db      654 |G|C|T|C|A|G|T|T|C|C|C|A|T|G|C|C|G|C|G|T|G|T|A|C|T|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G| 708
Qy      693 |C|A|T|T|T|G|C|T|T|G|T|G|A|T|C|C|T|G|T|C|T|C|T|C|A|T|C|A|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T| 752
Db      709 |C|C|T|T|T|G|C|T|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T| 768
Qy      753 |G|G|T|T|C|A|A|A|G|G|T|C|C|G|C|T|C|T|T|G|G|G|T|C|C|G|A|G|A|A|A|G|A|T|G|G|A|C|C|T|G|G|T|G| 812
Db      769 |G|G|G|C|T|G|G|C|A|G|G|T|G|C|T|G|T|C|G|G|T|T|C|C|A|G|A|G|A|G|A|G|A|C|C|G|A|G|C|T|G|G|G|G| 828
Qy      813 |G|A|T|C|A|C|A|G|A|C|T|G|T|C|T|G|T|G|T|G|G|G|A|G|T|C|T|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G| 872
Db      829 |C|A|T|C|A|G|G|G|C|A|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T|G|T| 888
Qy      873 |C|A|T|A|T|T|C|A|T|C|T|G|T|G|A|G|G|C|T|T|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G|G| 929
Db      889 |C|A|T|T|T|G|C|A|T|G|T|G|A|C|G|T|G|G|T|G|G|A|C|A|T|C|A|T|C|G|G|C|C|G|A|C|C|C|A|C|T|T|G|T|G|T|G|G| 948
Qy      930 |C|A|G|A|T|A|T|A|C|T|T|G|C|A|T|G|C|T|T|A|G|G|C|T|A|T|A|C|A|A|C|A|G|A|T|G|C|T|T|G|A|T|T|C|A|T|T|C|T|A| 989
Db      949 |G|C|G|A|C|T|G|A|C|C|T|G|T|G|A|T|T|G|C|T|G|G|G|C|T|A|C|G|C|A|A|C|A|G|A|C|A|C|C|T|C|A|C|C|G|G|T|T|C|T|A| 1008
Qy      990 |G|C|C|T|T|T|C|T|T|G|A|T|G|A|A|A|C|T|T|C|A|A|G|G|G|T|G|T|T|C|C|G|G|A|C|T|T|C|T|G| 1034
Db      1009 |G|C|C|T|T|C|C|T|G|A|C|G|A|A|C|T|T|C|A|A|G|G|C|T|G|C|T|T|C|C|G|C|A|G|C|T|C|T|G| 1053

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XX      XX Human; probe; ss; array element; Parkinson's disease;
XX      KW Signalling pathway population; cancer; adenocarcinoma; leukaemia;
XX      KW Immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.
XX      OS Homo sapiens.
XX      PN US6500938-B1.
XX      PD 31-DEC-2002.
XX      PF 30-JAN-1998; 98US-00016434.
XX      PR 30-JAN-1998; 98US-00016434.
XX      PA (INCY-) INCYTE GENOMICS INC.
XX      PI Au-Young J, Seilhamer JJ;
XX      DR WPI; 2003-352189/33.
XX      PT Combination of polynucleotide probes, useful as array elements in a
XX      PT microarray for monitoring the expression of a number of target
XX      PT polynucleotides.
XX      PS Claim 1; SEQ ID NO 1405; 65bp; English.

The invention relates to a combination which, comprises a number of
CC polynucleotide probes comprising a sequence selected from one of the 1490
CC sequences mentioned in the specification. The combination is useful as an
CC array element in a microarray for monitoring the expression of a number
CC of target polynucleotides. The microarray is particularly useful in the
CC diagnosis and treatment of cancer and immunopathology and neuropathology.
CC The microarray is useful in diagnostics and treatment regimens, drug
CC discovery and development, toxicological and carcinogenicity studies,
CC for forensic and pharmacogenomics. The microarray is also useful for
CC monitoring progression of diseases and for developing sophisticated
CC profiles for the effects of currently available therapeutic drugs. The
CC combination is also useful for purifying a subpopulation of mRNAs. CDNs
CC and genomic fragments and in research and diagnostic applications. The
CC array can detect changes in expression in a large number of genes coding
CC for different signalling pathway populations which can be used to diagnose
CC various diseases including cancer e.g. adenocarcinoma and leukaemia,
CC immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease
CC and Parkinson's disease. The present sequence represents a polynucleotide
CC probe of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format directly from USPTO at
CC segdata.uspto.gov/sequence.html?docID=06500938B1
XX
SQ      Sequence 1773 BP; 263 A; 602 C; 591 G; 317 T; 0 U; 0 Other;
Query Match      35.4%; Score 408.6; DB 7; Length 1773;
Best Local Similarity 64.7%; Pred. No. 3; 6e-90;
Matches 644; Conservative 0; Mismatches 339; Indels 12; Gaps 2;

Qy      44 |C|T|T|G|C|C|C|C|A|G|C|G|C|T|G|C|C|C|C|C|C|A|C|A|G|A|G|G|C|T|T|T|C|C|G|G|C|T|G|G|C|G|C| 103
Db      247 |C|T|T|G|C|C|C|G|G|C|C|A|G|T|G|A|G|C|C|C|C|C|T|T|T|G|C|C|A|A|C|C|C|T|T|G|A|C|G|C|T|A|C|C|T|A| 306
Qy      104 |A|G|C|C|G|A|G|C|A|G|C|G|C|G|C|G|C|G|C|G|A|G|A|C|G|C|C|A|G|T|G|A|G|C|C|G|C|C|A|C|A|T|T| 163
Db      307 |G|G|G|C|T|T|C|C|A|G|C|C|T|G|G|C|C|C|A|T|G|T|G|G|G|G|C|C|C|C|A|G|A|C|C|G|G|A|G|C|G|C|T|G|T| 366
Qy      164 |C|C|C|G|G|C|A|T|C|C|G|G|T|C|A|T|C|A|C|A|G|G|G|G|T|T|A|C|T|C|C|T|G|T|G|T|T|G|T|G|G|C|T|T|G| 223
Db      367 |C|C|T|G|C|C|T|G|C|A|T|C|C|A|T|C|A|C|C|G|C|T|T|A|C|T|C|G|G|C|C|G|T|G|G|C|C|G|G|G|G|C|T|G|C| 426
Qy      224 |T|G|G|C|A|C|T|G|T|G|T|C|A|T|T|T|G|T|G|A|T|C|C|C|A|T|A|C|A|A|A|G|T|G|A|A|G|A|G|A|C|A|C|A| 283
Db      427 |T|G|G|C|A|G|T|G|T|T|C|A|T|G|T|T|G|G|C|A|T|G|T|C|C|G|G|T|A|C|T|A|A|G|A|T|G|A|A|G|G|G|C|A|C|A| 486
Qy      284 |A|C|A|T|T|A|C|A|T|T|T|A|C|T|G|G|C|T|T|G|G|A|G|A|T|G|T|T|A|G|T|A|C|T|A|C|A|C|A|T|G|C|C|T|T|C| 343

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RESULT 69
 ACAS6807
 ID ACAS6807 standard; cDNA; 1773 BP.
 AC ACAS6807;
 XX
 XX 06-JUN-2003 (first entry)
 DT
 XX Human signalling pathway polynucleotide probe SEQ ID NO 1405.

```
DB 487 ACATCTACATCTTCAACCTGGCTTACCGGATGCGGTGGCCACGACGAGCTGCTTCC 546
QY 344 AGAGTACCGGTCTACTTATGATGAATTCCTGGCCCTTTGGGGATGCTGTGCAAGATGTA 403
DB 547 AGAGTGCCAGTACGATGATGAGACGTGGCCCTTGGCGAGCTGTCTTCAAGGCTGTGC 606
QY 404 TTTCCATTGATTATACAAATGTTTCAACGACATCTTTCCTTGAACCAATGAGAGTGG 463
DB 607 TCTCATGACTACTACAAATATGTTTACACGACATCTTTCACGCTACCAATGATGAGTGG 666
QY 464 ACCGCTACATTCCTGGTSCCAACCCGCTGAAGGCTTTGACTTCGCAACACCTTGAAG 523
DB 667 ACCGCTACATTCCTGGTSCCAACCCGCTGAAGGCTTTGACTTCGCAACACCTTGAAG 726
QY 524 CAAAGATCAATATCTGATCTGGCTGTCTGTCTGATCTGTGGCATCTCTGCAATAG 583
DB 727 CCAAGCTGATCAACATCTGATCTGGGTCTGGCCCTCAGGCGTGGCGTGCATCATGG 786
QY 584 TCCTTGAGAGGACCAAAAGTCAGGGAAGAGCTGATGTCATTGAGTCTCTTGCACTTC 643
DB 787 TCATGGCTGTGACCCGCTCCCGGAGCGTGCAGTGTGTGTCATGCTTCCAGTCCCAAGC 846
QY 644 CAGATGATGACTACTCTGTGGTGGACCTCTTCAATGAAGATCTGCTTCTTGTGCT 703
DB 847 C-----CAGCTGTACTGTGGACACGCTGACCAAGATCTGCTGTTCTCTTGTGCT 897
QY 704 TCGATGATCCCTGTCTCATCATCATGCTGTGTGTCACACCTGATGATCTGCGCTCAAG 763
DB 898 TGTGTGTGCTCCATCTCATCATCATGCTGTGTGTCACACCTGATGATCTGCGCTCAAG 957
QY 764 GCGTCCGCTCTCTTCTGTGCTCCGAGAGAAAGATGCAACTGCTGAGATCAACGAC 823
DB 958 GTGTGGCTGTGTGTGCTGCGCTCCAGAGAAAGACCGGCGCTGCGGCTCATCAACGCA 1017
QY 824 TGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 883
DB 1018 TGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1077
QY 884 TGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 940
DB 1078 TGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1137
QY 941 TGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1000
DB 1138 TGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1197
QY 1001 ATGAAACTTCAAGCGGTGTTCCGGGACTTCTGC 1035
DB 1198 ACGAGAACTTCAAGCGGTGTTCCGGGACTTCTGC 1232

RESULT 70
ABT34217
ID ABT34217 standard; DNA; 1773 BP.
XX
XX ABT34217;
AC
XX
XX
XX
XX 12-JUN-2003 (first entry)
DT
XX
DE Human delta-opioid receptor gene SEQ ID No 3.
XX
XX Ealing disorder; polymorphism; dataset; allele; HGBASE identification;
XX serotonin receptor 1D; delta-opioid receptor; dopamine receptor D2;
XX anorexia nervosa; bulimia nervosa; human; ds.
OS
XX Homo sapiens.
XX
XX WO2003012143-A1.
XX
XX 13-FEB-2003.
PD
XX
PF 16-JUL-2002; 2002WO-US022555.
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XX
PR 16-JUL-2001; 2001US-0305153P.
PR 20-JUL-2001; 2001US-0306440P.
PR 13-NOV-2001; 2001US-0331285P.
PR 19-DEC-2001; 2001US-0340843P.
PR 19-DEC-2001; 2001US-0340844P.
XX
PA (PRIC-) PRICE FOUND LTD.
XX
XX Bergen AW, Yeager M;
PI
XX
XX WPI; 2003-268122/26.
XX
XX New nucleic acid molecule having polymorphisms in the serotonin receptor
PT ID, delta-opioid receptor, or dopamine receptor D2, useful in diagnostic
PT and prognostic assays for eating disorders, such as anorexia and bulimia
PT nervosa.
XX
XX Disclosure; Page 126-127; 149pp; English.
XX
XX The invention relates to a novel isolated nucleic acid molecule
XX comprising a variant gene associated with an eating disorder and selected
XX from any of 119 polymorphisms with their corresponding genotyping in
XX dataset, alleles and HGBASE identification, given in the specification.
XX The novel nucleic acid molecule has polymorphisms in the serotonin
XX receptor 1D, delta-opioid receptor, or dopamine receptor D2, which is
XX useful in diagnostic and prognostic assays for eating disorders, in
XX particular anorexia nervosa and bulimia nervosa. This polynucleotide
XX sequence represents a human delta-opioid receptor gene of the invention
XX
XX Sequence 1773 BP; 263 A; 602 C; 591 G; 317 T; 0 U; 0 Other;
XX
XX Query Match 35.4%; Score 408.6; DB 7; Length 1773;
XX Best Local Similarity 64.7%; Pred. No. 3.6e-90;
XX Matches 644; Conservative 0; Mismatches 339; Indels 12; Gaps 2;
QY 44 CCGTGGCCCGGAGCGCGCTGCGCCCGCAAGAGCGCGCTGTTCCGGCTGGGCGG 103
DB 247 CCGTGGCCCGGAGCGCGCTGCGCCCGCAAGAGCGCGCTGTTCCGGCTGGGCGG 306
QY 104 AGCCGACAGCAACGCGAGCGCGCTGCGAGAGAGCGCGAGCTGAGCCGCGACATCT 163
DB 307 GGGCTTCCCGAGCGCGTGGCGCAATGCGTGGGGGCGCGAGAGCGGGAGGCGCTCGT 366
QY 164 CCGCGGCGATCCCGGCTCATCATCAGCGGCTTCTCCGTAGTGTCTGTGGCTTGG 223
DB 367 CCGTGGCGCGTGGCAATCGCCATCACCGCGCTTACTCGCGCGCTGTGGCGGCTGC 426
QY 224 TGGGGAATCGCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 283
DB 427 TGGGGAATCGCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 486
QY 284 ACATTTACATATTTAACTGCTTGGAGATGCTTTAGTACTTACCAACATGCTTTC 343
DB 487 ACATCTACATCTTCAACCTGGCTTACCGGATGCGGTGGCCACGACGAGCTGCTTCC 546
QY 344 AGAGTACCGGTCTACTTATGATGAATTCCTGGCCCTTTGGGGATGCTGTGCAAGATGTA 403
DB 547 AGAGTGCCAGTACGATGATGAGACGTGGCCCTTGGCGAGCTGTCTTCAAGGCTGTGC 606
QY 404 TTTCCATTGATTATACAAATGTTTCAACGACATCTTTCCTTGAACCAATGAGAGTGG 463
DB 607 TCTCATGACTACTACAAATATGTTTACACGACATCTTTCACGCTACCAATGATGAGTGG 666
QY 464 ACCGCTACATTCCTGGTSCCAACCCGCTGAAGGCTTTGACTTCGCAACACCTTGAAG 523
DB 667 ACCGCTACATTCCTGGTSCCAACCCGCTGAAGGCTTTGACTTCGCAACACCTTGAAG 726
QY 524 CAAAGATCAATATCTGATCTGGCTGTCTGTCTGATCTGTGGCATCTCTGCAATAG 583
DB 727 CCAAGCTGATCAACATCTGATCTGGGTCTGGCCCTCAGGCGTGGCGTGCATCATGG 786
QY 584 TCCTTGAGAGGACCAAAAGTCAGGGAAGAGCTGATGTCATTGAGTCTCTTGCACTTC 643
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```

OS Chimeric.
XX
XX Key Location/Qualifiers
XX CDS 1..1197
XX FT /*tag= a
XX FT /product= "Mu oploid receptor modified protein"
XX FT /note= "No stop codon"
XX FT /partial
XX FT 823..843
XX FT misc_feature
XX FT /tag= b
XX FT /note= "TEV protease cleavage site"
XX
XX MO200286507-A1.
XX
XX 31-OCT-2002.
XX
XX 24-APR-2002; 2002WO-US013250.
XX
XX 24-APR-2001; 2001US-0286250P.
XX 21-AUG-2001; 2001US-00935061.
XX
XX (STRD ) UNIV LELAND STANFORD JUNIOR.
XX
XX Kobilka BK, Ghanouni P, Lee TW;
XX
XX WPI, 2003-103418/09.
XX P-PSDB; AAE33277.
XX
XX Identifying an agent that modulates activity of a membrane-spanning,
XX signal-transducing (MSTR) protein, by detecting a conformational change
XX in a MSTR protein upon interaction with a ligand.
XX
XX Example 12; Page 99-101; 104pp; English.
XX
XX The present invention relates to methods and compositions for identifying
XX agents that modulate activity of a membrane-spanning, signal-transducing
XX (MSTR) protein. The method involves detecting a conformational change in
XX a MSTR protein upon interaction with a ligand. The method is useful for
XX identifying agents that modulate (e.g. agonists or antagonists) activity
XX of MSTR protein. The present sequence is human modified mu oploid
XX receptor DNA. This sequence is modified to contain a Tobacco etch virus
XX (TEV) protease cleavage site in the third intracellular loop. This
XX sequence is used to illustrate the method of the invention. (Updated on
XX 27-OCT-2003 to standardise OS field)
XX
XX Sequence 1197 BP; 295 A; 350 C; 244 G; 308 T; 0 U; 0 Other;
XX
Query Match 34.9%; Score 402.2; DB 7; Length 1197;
Best Local Similarity 64.8%; Pred. No. 1.2e-88;
Matches 659; Conservative 0; Mismatches 328; Indels 30; Gaps 3;

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Db 425 GCAGATGATGATCTCCATGATGATTAATAATGATGTCACGACATATTCAACCTCTGCA 484
Qy 452 TCATGAGCGTGGACCGCTTACATTTGCCGTGTGGCACCCTGGAAAGTTTGACTCCGA 511
Db 485 CCATGAGTGTGATGATGATCATTTGACATGTCGACCCCTGTCAAGGCTTAGATTCCGA 544
Qy 512 CACCTTGAAAGGCAAGATCATATATCTGATCTGGCTGTGTGTCATCTGTGGCA 571
Db 545 CTCGCCGAATGCCAAATTAATTAATGTCGAATGGAATCCTCTCTTTCAGCATTTGGTC 604
Qy 572 TCTCTGATATAGTCTCTGGAGGACCAAAAGTCAGGGAAGACGTGATCATTTAGTGTCT 631
Db 605 TTCCTGTAATGTTTACATAGCTACACAAAATACAGGCA-----GGTTCATGATTTGA 658
Qy 632 CCTTGCAAGTCCCAATGATGATCTCTGTGTGGACCTTTTCATGAAGATCTGCTCT 691
Db 659 CACTAACATCTCTCATCCMACCTGTACTGGGAAAACCTGCT--GAAGATCTGTGTTT 715
Qy 692 TCATCTTTGCGCTTCCGATCCCTGTCTGATCATGTCATGCTACACCTGATGATCC 751
Db 716 TCATCTTCCCTTTCATTTATGCAAGTCTCATTTACGCTGTGCTATGGAATGATGATCT 775
Qy 752 TCGCTCTCAAGACGTCGCGCTCTTTCTGAGCTCCCGAGAGAAAG-----797
Db 776 TCGGCTCAAGAGTGTCCGATGCTCTGGCTCCAAAAGAACGAAACCTTACT 835
Qy 798 -----TCGCACTGCGCTAGATCACCAACTGCTCTGTGTGTGTGGCACTTTG 850
Db 836 TCAGGGAGAGATCTTCAGAGATCACAGATGTGTGTGTGTGTGTGTGTGTGTGTGT 895
Qy 851 TCGTCTGCGAGCTCCCATTCATATTCATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGT 910
Db 896 TCGTCTGCGAGCTCCCATTCATATTCATTCATTAACCTGTGTGTGTGTGTGTGTGTGTGT 955
Qy 911 ACAGACAGAGCTCTCTCTCACTTATTTACTTGTGATCTGCTTGTAGGCTATACCAAGTA 970
Db 956 AAACATAGTTCAGAGCTGTTTCTTGCACTTCTGATTTGCTGATTCACAAACAGCT 1015
Qy 971 GCGTGAATCCATTTCTTACGCTTTTGTATGAAGAACTTCAAGCGGTGTTTCCGGACT 1030
Db 1016 GCCTCAACCAAGCTCTTTATGATTTGTGAAGAACTTCAAGCGATGCTTCAGAGAGT 1075
Qy 1031 TCTGCTTTCAGTAAGATGAGATGAGGACGACGACTGACAGTCCGAATA 1087
Db 1076 TCTGATCCCACTCTTCCAACTTGAAGCAAAAATCCACTCGAATTCGACGA 1132

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RESULT 75
ABX94262
ID ABX94262 standard; DNA; 1829 BP.

ABX94262;
12-JUN-2003 (first entry)

Human orphanin FQ/nociceptin receptor gene, coding sequence #2.

Human; single nucleotide polymorphism; SNP; C510T; A804G;
orphanin FQ/nociceptin receptor; loci mapping; C1026T; C1126G;
addictive disease; pain; analgesic response; physiological response;
anxiety; stress; endogenous opiod system; neurotransmitter release;
learning; memory; cognition; alcohol self-administration;
behavioural sensitisation; cocaine; drug addiction; opiate withdrawal;
immune function; cardiovascular function; renal function;
gastrointestinal function; motor function; coding region; ds.

Homo sapiens.

Key Location/Qualifiers
variation replace(510..T)
/*tag= a
/standard name= "SNP"
/note= "C510T SNP specifically claimed in Claim 1"

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FT variation replace(804,A)
FT /tag= b
FT /standard_name= "SNP"
FT /note= "A804G SNP specifically claimed in Claim 1"
FT variation replace(1026,T)
FT /tag= c
FT /standard_name= "SNP"
FT /note= "C1026T SNP specifically claimed in Claim 1"
FT variation replace(1126,G)
FT /tag= d
FT /standard_name= "SNP"
FT /note= "C1126G SNP specifically claimed in Claim 1"
PN US2003008289-A1.
XX 09-JAN-2003.
XX 09-OCT-2001; 2001US-00905186.
XX 14-JUL-2000; 2000US-0218205P.
XX (KREB/) KREEK M J.
XX (LAFO/) LAFORGE K S.
XX Kreek MJ, Laforge KS;
XX MPI; 2003-353089/33.
XX
XX New variant allele of a human orphanin FQ/nociceptin receptor gene,
XX useful for determining a subject's susceptibility to addictive diseases
XX or to pain, comprises at least one variation (e.g. G-46A, A804G or C510T)
XX in its DNA sequence.
XX
XX Example; Fig 9; 29pp; English.
XX
XX The present invention relates to the identification of novel single
XX nucleotide polymorphisms (SNPs) within the human orphanin FQ/nociceptin
XX receptor gene. The polymorphisms disclosed are G-46A (located in the 5'-
XX untranslated region), GIVS I 135C (located in intron 1), GIVS I 250A
XX (located in intron 1), GIVS I 251A (located in intron 1), C510T (a silent
XX mutation located in the coding region), GIVS III 67T (located in intron
XX 3), A804G (a silent mutation located in the coding region), C1026T (a
XX silent mutation in the coding region), and C1126G (located in the 3'-
XX untranslated region). The SNPs and variant alleles of human orphanin
XX FQ/nociceptin receptor DNA are useful in mapping the locus of the human
XX orphanin FQ/nociceptin receptor gene, determining a subject's increased
XX or decreased susceptibility to addictive diseases, susceptibility to pain
XX and response to analgesics, physiological responses related to the
XX endogenous opioid system or neurotransmitter release, anxiety and stress,
XX learning, memory and cognition, alcohol self-administration, behavioural
XX sensitisation to cocaine, drug addiction, opiate withdrawal and
XX tolerance, food intake, immune function, cardiovascular function, renal
XX function, gastrointestinal function, and motor function. The present
XX sequence represents the coding region of the human orphanin FQ/nociceptin
XX receptor gene
XX
XX Sequence 1829 BP; 296 A; 602 C; 542 G; 389 T; 0 U; 0 Other;
SQ
Query Match 34.2%; Score 395; DB 7; Length 1829;
Best Local Similarity 65.2%; Pred. No. 8.1e-87;
Matches 616; Conservative 0; Mismatches 320; Indels 9; Gaps 2;
QY 153 CGCGACATCTCCCGGCATCCGCGATCATCAACGGGCGTCTCTCGTAGTGTGT 212
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 213 CGTGGCTTGTGGGCAACTCGCTGTCATGTTCTGTATCATCCGATCACAAAGATGA 272
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 222 CGGAGGGCTCTCGGGAACTGCTGTATGATGATCTTCAAGACACCAAAATGA 281
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 273 GACGAGCAACAACTTTATCATTTTAACCTGGCTTTGGAGATGCTTTAGTTACTACAAC 332
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 282 GACAGCCACCAATATTATCTTAACTTGAACCTGGCCGACACTGTGTCCTGTGAC 341
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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QY 333 CATGCCCTTTCAGAGTACGCTCTACTGTATGTAATTCCTGGCTTTTGGGATGTCGTG 392
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 342 GCTGCCCTTCCAGGGACGAGACATCTCTGGGCTTTCGGCCGTTTGGAAATGCGCTGG 401
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 393 CAAGATAGTAATTTTCCATTTGATTTACTACAACATGTTCCACGACATCTTCACTTACCAT 452
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 402 CAAGACATGATTTGCACTTGTACTACTACAAATGTTCAACGACCTTCACTTAACTGCG 461
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 453 GATGAGCGTGAACCGCTACATTTGCCGTGTGCCACCCCGTGAAGGCTTTGGAATTCCGAC 512
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 452 CATGAGTGTGATCGCTATGTAGCATCTGCACCCCATCCGTCCTCGACATCGCGAC 521
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 513 ACCCTTGAAGCAAAATCATCAATATCTGATCTGCTGTCTGTCTGATCTGTTGGCAT 572
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 522 GTCCAGCAAGCCCAAGCTGTCAATGTGACCATTGGGCCCTTGCTGTGTTCGTGT 581
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 573 CTCTGCAATAGTCTTGGAGGCAACCAAGTCAAGGAAAGCTGATGTCAATTGAGTGTG 632
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 582 TCCCGTTGCCATCATGGGCTCGGACAGTCTG-----GAGATGAAGATCGAGTGTCT 635
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 633 CTTCGAGTTCCCAATGATGATGACTACTCTGTGGGACTCTTTCATGAAGATCTGCTTT 692
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 636 GGTGAGATCCCTACCCCTCAGATTAAC---TGGGGCCGGGTGTTGCCATCTGCATCTT 692
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 693 CATCTTGGCTTTCGATCCGCTGTCCTGATCATCATGCTGCTACACCTGATGATCT 752
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 693 CCTCTTCTCTTCATCGTCCCGCTGCTGTGATCTCTGTCTACAGCTCATGATCTCG 752
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 753 GCGTCTCAAGAGCGTCCGCTCTTCTGTGCTCCGAGAGAAAGTCCAACTGCTGTAG 812
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 753 GCGGCTCGTGAAGTCCGCTCTGTCTGTGCGGTCCGAGAGAAAGACCGGAACCTGCGCG 812
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 813 GATCACCAAGTCTGCTGTGTGTGTGTGTGCACTTCTGTCTGTCTGGAATCCCATTTCA 872
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 813 CATCACTCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTCA 872
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 873 CATATTCAATCCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 932
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 873 GGTCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 932
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 933 CTATTACTTGTGATCGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 992
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 933 TGTGCGTTTGTGCAAGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 992
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 993 CTTTCTTGTATGAATTTTCAAGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1052
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 993 CTTCTGTGATGAAGAACTTCAAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1052
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1053 GATGAGCGGAGAGCACTACAGAGTCCGAATTAAGTTGAGA 1097
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1053 CCGGAGCTGTGAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1097
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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RESULT 76
ABS53446
ID ABS53446 standard; cDNA; 1805 BP.
XX
XX ABS53446;
XX
XX 19-NOV-2002 (first entry)
XX
XX cDNA encoding human opioid receptor ORL-1.
XX
XX Enkephalin; opioid receptor; poisoning; addiction; morphine; codeine; ss;
XX gene; human; ORL-1.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 10..1176
XX FT /tag= a
XX FT /product= "Human opioid receptor ORL-1"
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XX US6432652-B1.
 XX 13-AUG-2002.
 PD 14-MAR-1995; 95US-00405271.
 XX 13-AUG-1992; 92US-00929200.
 PR 13-AUG-1993; 93WO-US007665.
 PR 13-FEB-1995; 95US-00387707.
 PR 13-MAR-1995; 95US-00403260.
 XX (REGC) UNIV CALIFORNIA.
 PA Evans CJ, Keith DE, Edwards RH, Kaufman D;
 PI WPI, 2002-681194/73.
 DR P-PSDB; ABG33031.
 XX Mammalian DOR-1 opioid receptors, useful for screening for compounds
 PT useful in the treatment of opioid addiction and poisoning.
 XX Disclosure; Fig 11; 61pp; English.
 PS This invention relates to the DNA and protein sequences of novel
 CC mammalian opioid receptor (DOR-1) displayed at the surface of recombinant
 CC host cells. The invention also comprises a method for screening a
 CC candidate substance for opioid agonist activity and a method for
 CC detecting the amount of activation of the opioid receptor in the presence
 CC as compared to the absence of the candidate substance. The methods and
 CC compounds of the invention may have anti-addictive agents and may be used
 CC to modulate opioid receptor activity. The mammalian opioid receptor of
 CC the invention may be used to screen for agonists and antagonists of its
 CC expression and activity which may be used to treat e.g. poisoning by, and
 CC addiction to, opioids (such as morphine, codeine, and many semi-synthetic
 CC congeners of morphine). The present sequence represents the cDNA encoding
 CC the human opioid receptor ORL-1 protein shown in the specification
 XX
 SQ Sequence 1805 BP; 291 A; 598 C; 533 G; 383 T; 0 U; 0 Other;

Query Match 34.1%; Score 393.4; DB 6; Length 1805;
 Best Local Similarity 65.1%; Pred. No. 2e-86;
 Matches 615; Conservative 0; Mismatches 321; Indels 9; Gaps 2;

QY 153 CCGGCACATCTCCCGGCATCCCGTCAATCATCAGCGGGCTCTACTCCGTAGTGTCT 212
 Db 138 CCCCTTCCCTCCCGCTCGGCTCAAGGTCAATCGGGGCTCTACTCCGTAGTGTCT 197
 QY 213 CGTGGGCTTGGTGGGCACTCGGTGTCATGTTCCGATCATCCGATACAAAGATGAA 272
 Db 198 CGAAGGGCTCTGGGGAACCTGCTGTCAATGATCGTCAAGGACACCAAAATGAA 257
 QY 273 GACAGCAACCAATTATTAATTTAACTGGCTTGGAGATGCTTTAGTTACTACAAC 332
 Db 258 GACAGCAACCAATTATTAATTTAACTGGCTTGGAGATGCTTTAGTTACTACAAC 317
 QY 333 CATGCCCTTCAAGATGAGTCTACTGTATGTAATTCCTGGCTTTGGGAGATGCTGTG 392
 Db 318 GCTGCCCTTCCAGGGGACGAGATCTCTCGGGCTTCTGGCGTTGGAAATGCGCTGG 377
 QY 393 CAAGATAGTAATTTCCATGATTAATTAACCAAGTTCACACAGATCTTCACTTGAACCT 452
 Db 378 CAAGACAGTCAATTCATTAATTAATTAACCAAGTTCACACAGATCTTCACTTGAACCT 437
 QY 453 GATGAGCTGAGCCGCTACATTCGCTGTGCAACCCCGTGAAGAGCTTTGAGATTCGAC 512
 Db 438 CATGAGTGTGATTCGCTATGTAGCATCTGCCACCCCATCCGCTCGAGCTCGGAC 497
 QY 513 ACCCTTGAAGCAAGATCATCAATATCTGCATCTGGCTGTGCTGTCTCTGTGGCAT 572
 Db 498 GTTCAGCAAGCCCGAGGCTGTCAATGTGGCATCTGGGCTCTGTGTGTGCTGTGT 557
 QY 573 CTCTCAATATGCTTTGGAGGACCAAAATCAAGGAAAGCTGATGTGATTTGAGTCTC 632

Db 558 TCCCGTGCATCATGAGGCTCGGACAGATC-----GAGATGAAGATGAGTGCCT 611
 QY 633 CTTCAGATTTCCAGATGATGACTACTCTCGTGGGACCTCTTCATGAAGATCTGGCTT 692
 Db 612 GGTGAGATCTTACCCCTCAGAAATTAAC--TGGGCTCCGGTGTGTCATGCAATCTT 668
 QY 693 CATCTTGGCTTCTGATATCCCTGTCTCATATCATATGCTGTCTACACCTGATGATCT 752
 Db 669 CCTCTTCTCTTCAATGCTCCCGTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 728
 QY 753 GCGTCTCAAGAGCGTCCGCTCTCTTTCTGGCTCCGAGAGAAAGATCGCACTGCTGAG 812
 Db 729 GCGGCTCGGTGAGATCCGCTGCTCTCGGAGCTCCGAGAGAGACCGGAACCTGGGAG 788
 QY 813 CATCAACAGATCTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 872
 Db 789 CATCACTCGGCTGT 848
 QY 873 CATATTCATCTCGTGTGAGGCTCTGGGAGACCTCCGACAGACAGCTGTCTCTCCAG 932
 Db 849 GGTCTTCTGCTGTGCCCCAGAGGCTGGGCTTACGCCAGACAGACAGCTGTGCTGCT 908
 QY 933 CTATTACTTCTGATCGCTTGTAGGCTATACCAAGATGACCTGAATCCCATTTCTACGC 992
 Db 909 TCTGGGCTTCTGACAGGCTGCTGGGCTAAGTCAAGAGCTGCTCAACCCCATCTCTAGC 968
 QY 993 CTTTCTTGATGAACCTTCAGCGGCTGTTCCGGAATCTTCTGCTTCTCACTGAAGTGA 1052
 Db 969 CTTCCTGTGATGAACCTTCAGCGGCTGCTTCCGGAATCTTCTGCTGCTGCTGCTG 1028
 QY 1053 GATGAGCGGCGAGACCATAGAGAGTCCGAATACAGTTCAAGGA 1097
 Db 1029 CCGGACGTGACAGTGTCTGACCGGTGCGACATTCGACAGGA 1073

RESULT 77
 ABX94264
 ID ABX94264 standard; DNA; 1829 BP.
 XX
 AC ABX94264;
 XX
 XX 12-JUN-2003 (first entry)
 XX
 DE Human orphanin FQ/nociceptin receptor gene, 3'-untranslated region.
 XX
 KW Human; single nucleotide polymorphism; SNP; C1126G;
 KW orphanin FQ/nociceptin receptor; local mapping; motor function;
 KW addictive disease; pain; analgesic response; physiological response;
 KW anxiety; stress; endogenous opioid system; neurotransmitter release;
 KW learning; memory; cognition; alcohol self-administration;
 KW behavioral sensitization; cocaine; drug addiction; opiate withdrawal;
 KW immune function; cardiovascular function; renal function;
 KW gastrointestinal function; ds.
 KW
 OS Homo sapiens.
 XX
 XX
 XX Key Location/Qualifiers
 FH variation replace(1126, C)
 FT /tag= a
 FT /standard_name= "SNP"
 FT /note= "C1126G SNP specifically claimed in claim 1"
 XX
 PN US2003008289-A1.
 XX
 PD 09-JAN-2003.
 XX
 PF 09-OCT-2001; 2001US-00905186.
 XX
 XX 14-JUL-2000; 2000US-0218205P.
 PR
 XX (KREB/) KREK M J.
 PA (LAFO/) LAFORE K S.

XX Kreek MJ, LaForge KS;
 XX WPI, 2003-353089/33.
 XX
 XX New variant allele of a human orphanin FQ/nociceptin receptor gene,
 PT useful for determining a subject's susceptibility to addictive diseases
 PT or to pain, comprises at least one variation (e.g. G-46A, A804G or C510T)
 PT in its DNA sequence.
 XX
 XX Example: Fig 11; 29p; English.
 XX
 CC The present invention relates to the identification of novel single
 CC nucleotide polymorphisms (SNPs) within the human orphanin FQ/nociceptin
 CC receptor gene. The polymorphisms disclosed are G-46A (located in the 5'-
 CC untranslated region), GIVS I 135C (located in intron 1), GIVS I 250A
 CC (located in intron 1), GIVS I 251A (located in intron 1), C510T (a silent
 CC mutation located in the coding region), GIVS III 67T (located in intron
 CC 3), A804G (a silent mutation located in the coding region), C1026T (a
 CC silent mutation in the coding region), and C1126G (located in the 3'-
 CC untranslated region). The SNPs and variant alleles of human orphanin
 CC FQ/nociceptin receptor DNA are useful in mapping the locus of the human
 CC orphanin FQ/nociceptin receptor gene, determining a subject's increased
 CC or decreased susceptibility to addictive diseases, susceptibility to pain
 CC and response to analgesics, physiological responses related to the
 CC endogenous opioid system or neurotransmitter release, anxiety and stress,
 CC learning, memory and cognition, alcohol self-administration, behavioural
 CC sensitisation to cocaine, drug addiction, opiate withdrawal and
 CC tolerance, food intake, immune function, cardiovascular function, renal
 CC function, gastrointestinal function, and motor function. The present
 CC sequence represents the 3'-untranslated region of the human orphanin
 CC FQ/nociceptin receptor gene
 XX
 XX Sequence 1829 BP; 297 A; 601 C; 542 G; 389 T; 0 U; 0 Other;

Query Match 34.1%; Score 393.4; DB 7; Length 1829;
 Best Local Similarity 65.1%; Pred. No. 2e-86;
 Matches 615; Conservative 0; Mismatches 321; Indels 9; Gaps 2;

153 CGCGGACATCTCCCGGCAATCCGGTCAATCAGCGGGCTTACTCCGATGTTCT 212
 162 CGCTTCTCGCCCTCGGGCTCAAGGTACATCGGGGCTCTACTGGCGTGTGT 221
 213 CGTGGCTTGTGGGCACTCGTGTGATGTTCCGATCATCCGATACAAAGTGA 272
 222 CGAGGGCTCTGGGGAATGCTGTGATGATCGATCTCAGGCAACCAAAATGA 281
 273 GACAGCAACCAATTTATATATTTAACTGGCTTGGAGATGCTTACTACTAAC 332
 282 GACAGCCACCAATTTATATCTTTAACTGGCCCTGGCCGACACTGTGCTGTAC 341
 333 CATGCCCTTCAAGATGCGTCTACTGTATGTAATTCCTGAGCTTTGGGATGTGCTG 392
 342 GCTGCCCTTCCAGGGCAAGCAATCTCTCGGCTTCTGGCGCTTGGAAATGCGCTG 401
 393 CAAGATGTAATTTCCATGATTTACTCAAAATGTTCAACAGATTTTACCTTGACAT 452
 402 CAAGACAGTCATTCATGATGATCACTAACAAATGTTCAACAGATTTTACCTTGAC 461
 453 GATGACGCTGGAACGGTATACATTCGATGAGCCACCCCGTGAAGGCTTTGAACTTCGGCAC 512
 462 CATGATGTGATCGCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 521
 513 ACCCTTGAAGGCAAGATCATCATATCTGATCTGCTGCTGCTGCTGCTGCTGCTGCT 572
 522 GTCCAGCAAGCCCAAGCTGTGATGATGATGATGATGATGATGATGATGATGATGAT 581
 573 CTCTGCAATAGTCTTGGAGGACCAAAATGCAAGGAGAGCTGATGATGATGATGATGAT 632
 582 TCCCGTTGCAATCATGCTGCGACAGGTC-----GAGGATGAAGAGATGCAAGGCT 635
 633 CTTCGAGTTCCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 692

DB 636 GGTGAGATCCCTACCCCTCAGATTAAC---TG66GCCCGGNGTTGGCATCTGATCTT 692
 QY CATCTTGGCTTTCGATATCCCTGTCATCATATGCTGTGCTACACCTGATGATCTT 752
 DB 693 CCTCTTCCCTTCAACGCGCCCGGTGCTGATCTCTGTGCTACAGCTTCATGATCCG 752
 QY GCGTTCGAAGACCGCGGCTCTCTTGTGCTCCGAGAGAAAGATTCGCAACCTGCTAG 812
 DB 753 GCGGCTCCGTGAGATCCCGCTGCTCTGCGGCTCCGAGAGAGACCCGAACTCGGGCG 812
 QY GATCACAGACTGTGCTGT 872
 DB 813 CATCACTGGCTGT 872
 QY CATATTCATCTGT 932
 DB 873 GGTCTTGT 932
 QY CTATTACTTGT 992
 DB 993 TGTGCGCTTGT 992
 QY CTCTTGT 1052
 DB 993 CTCTTGT 1052
 QY 1053 CATGAGGCGGCAAGACATTAAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1097
 DB 1053 CGGAGCGGTGAGGT 1097
 RESULT 78
 ABX94263
 ID ABX94263 standard; DNA; 1829 BP.
 XX
 XX ABX94263;
 AC 12-JUN-2003 (first entry)
 XX
 XX
 DT 12-JUN-2003 (first entry)
 XX
 DE Human orphanin FQ/nociceptin receptor gene, coding sequence #3.
 XX
 XX Human; single nucleotide polymorphism; SNP; C510T; A804G;
 KW orphanin FQ/nociceptin receptor; local mapping; C1026T; C1126G;
 KW addictive disease; pain; analgesic response; physiological response;
 KW anxiety; stress; endogenous opioid system; neurotransmitter release;
 KW learning; memory; cognition; alcohol self-administration;
 KW behavioural sensitisation; cocaine; drug addiction; opiate withdrawal;
 KW immune function; cardiovascular function; renal function;
 KW gastrointestinal function; motor function; coding region; ds.
 XX
 OS Homo sapiens.
 XX
 XX Key
 FH location/Qualifiers
 FT replace(510,T)
 FT
 FT variation
 FT /tag= a
 FT /standard name= "SNP"
 FT /note= "C510T SNP specifically claimed in Claim 1"
 FT
 FT variation
 FT /tag= b
 FT /standard name= "SNP"
 FT /note= "A804G SNP specifically claimed in Claim 1"
 FT
 FT variation
 FT /tag= c
 FT /standard name= "SNP"
 FT /note= "C1026T SNP specifically claimed in Claim 1"
 FT
 FT variation
 FT /tag= d
 FT /standard name= "SNP"
 FT /note= "C1126G SNP specifically claimed in Claim 1"
 XX
 XX US2003008289-A1.
 PN 09-JAN-2003.

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XX 09-OCT-2001; 2001US-00905186.
XX
XX
XX 14-JUL-2000; 2000US-0218205P.
XX
XX (KREEK/) KREEK M J.
XX PA
XX (LAFO/) LAFORGE K S.
XX
XX Kreek MJ, LaForge KS;
XX
XX MPI; 2003-353089/33.
XX
XX New variant allele of a human orphanin FQ/nociceptin receptor gene,
XX useful for determining a subject's susceptibility to addictive diseases
XX or to pain, comprises at least one variation (e.g. G-46A, A804G or C510T)
XX in its DNA sequence.
XX
XX Example; Fig 10; 299p; English.
XX
XX The present invention relates to the identification of novel single
XX nucleotide polymorphisms (SNPs) within the human orphanin FQ/nociceptin
XX receptor gene. The polymorphisms disclosed are G-46A (located in the 5'-
XX untranslated region), GIVS I 135C (located in intron 1), GIVS I 250A
XX (located in intron 1), GIVS I 251A (located in intron 1), C510T (a silent
XX mutation located in the coding region), GIVS III 677 (located in intron
XX 3), A804G (a silent mutation located in the coding region), C1026T (a
XX silent mutation in the coding region), and C1126G (located in the 3'-
XX untranslated region). The SNPs and variant alleles of human orphanin
XX FQ/nociceptin receptor DNA are useful in mapping the locus of the human
XX orphanin FQ/nociceptin receptor gene, determining a subject's increased
XX or decreased susceptibility to addictive diseases, susceptibility to pain
XX and response to analgesics, physiological responses related to the
XX endogenous opioid system or neurotransmitter release, anxiety and stress,
XX learning, memory and cognition, alcohol self-administration, behavioural
XX sensitisation to cocaine, drug addiction, opiate withdrawal and
XX tolerance, food intake, immune function, cardiovascular function, renal
XX function, gastrointestinal function, and motor function. The present
XX sequence represents the coding region of the human orphanin FQ/nociceptin
XX receptor gene
XX
XX
XX Sequence 1829 BP; 297 A; 601 C; 541 G; 390 T; 0 U; 0 Other;
XX
XX Query Match 34.1%; Score 393.4; DB 7; Length 1829;
XX
XX Best Local Similarity 65.1%; Pred. No. 2e-86;
XX
XX Matches 615; Conservative 0; Mismatches 321; Indels 9; Gaps 2;
XX
QY 153 CCGCGACATCTCCCGGCCATCCGGTCATCATCAGCGCGTCTACTCCGTAGTGTCT 212
XX
DB 162 CGCCTTCCGCCCTCGGGCTCAAGGTACCATCGGGGGCTCTACCTGGCGGTGTGT 221
XX
QY 213 CGTGGCTTGGTGGGCACTCGGTGTCTATGTTCTGATCATCCGATACAAAGATGAA 272
XX
DB 222 CGAGGGCTCTCGGGGACCTGCTGTCACTACGTCATCCAGGACACCAAAATGAA 281
XX
QY 273 GACAGAACCAACATTTATTAATTAACCTGGCTTGGAGATGCTTTAGTACTACAAAC 332
XX
DB 282 GACAGCACCAATATTACATCTTTAACCCTGGCCCTGGCGACACTCTGCTCTGTGAC 341
XX
QY 333 CATGCCCTTTCAAGATCCGTCTACTTGTATGAAATTCCTGGCCCTTTGGAGATGTGCTG 392
XX
DB 342 GCTGCCCTTCAAGGGAGGACATCTCTGCGGCTTCTGGCGTTTGGAAATGCGGTG 401
XX
QY 393 CAAGATAGTAAATTTTCATTGATTACTACAAACATGTTACACAGACATTTCACTTGACAT 452
XX
DB 402 CAAGACAGTCATTTGACATTAACACTACAAACATGTTACACAGACCTTCACTTAATCTGC 461
XX
QY 453 GATGACGCGGACCGGCTATATGCGGTGACACCCCGGAGGAGCTTTGAGATTCGCGAC 512
XX
DB 462 CATGAGTGTGATCGCTATGATGACATCTGCAACCCCACTCCGCTTGAGAGTCCGAC 521
XX
QY 513 ACCCTTGAAGGCAAGATCATCAATATCTGATCTGGCTGTCTGTCTGATCTGTTGGCAT 572
XX
DB 522 GTTCAGCAAGCCGACGCTGTCAATGTGCGCATCTGGGCCCTGCTCTGTTGTGTGTGT 581
XX

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```

QY 573 CTCTGCAATAGTCCTTGGAGGACCAAGATCAGGGAGACGTGATGATTTAGTGTCTC 632
XX
DB 582 TCCCGTGCATCATAGGCGCTCGGACAGGTCTC-----GAGATGAAGATGAGTGCCT 635
XX
QY 633 CTTCGAGTTCCAGATGATGACTACTCTGTGTGGAGACTTTTCATGAAGATGTGGCTTT 692
XX
DB 636 GGTGAGATCCCTACCCCTCAGGATTTAC---TGGGGCCCGGTGTGTTCATCTGCATCTT 692
XX
QY 693 CATCTTGGCTTTCGATATCCCTGTCTCTATCATCATTCGTCTGTACACCTGATATCTCT 752
XX
DB 693 CCTCTTCTCTTCATCGATCGCCGCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 752
XX
QY 753 GCGTCTCAAGACGCGCGGCTCTTTCTGGGCTCCGAGAGAAAGATTCGACCTGGGTAG 812
XX
DB 753 GCGGCTCCGTGAGATCGCTGTCTCGGCTCTCGGATCCGAGAGAAAGACCGAATCTGGGCG 812
XX
QY 813 GATCACAGACTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 872
XX
DB 813 CATCATCTGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 872
XX
QY 873 CATATTATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 932
XX
DB 873 GGTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 932
XX
QY 933 CATATTATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 992
XX
DB 933 TCTGCGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 992
XX
QY 993 CTTCCTGTGATGAAGATTTCAAGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1052
XX
DB 993 CTTCCTGTGATGAAGATTTCAAGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1052
XX
QY 1053 GATGAGCGGCGAGACCATAGCAGAGTCCGAATACAGTTACGGA 1097
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DB 1053 CCGGATGTGCGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1097
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XX
XX RESULT 79
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XX ACAS6793
XX ID ACAS6793 standard; cDNA; 1973 BP.
XX
XX ACAS6793;
XX
XX 06-JUN-2003 (first entry)
XX
XX Human signalling pathway polynucleotide probe SEQ ID NO 1391.
XX
XX Human; probe; ss; array element; Parkinson's disease;
XX signalling pathway population; cancer; adenocarcinoma; leukaemia;
XX immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.
XX
XX Homo sapiens.
XX
XX US6500938-B1.
XX
XX 31-DEC-2002.
XX
XX 30-JAN-1998; 98US-00016434.
XX
XX 30-JAN-1998; 98US-00016434.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX
XX Au-Young J, Seilhamer JJ;
XX
XX MPI; 2003-352189/33.
XX
XX Combination of polynucleotide probes, useful as array elements in a
XX PT microarray for monitoring the expression of a number of target
XX PT polynucleotides.
XX
XX Claim 1, SEQ ID NO 1391; 65pp; English.
XX

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XX Sequence 1973 BP; 315 A; 650 C; 587 G; 421 T; 0 U; 0 Other;
 SQ

Query Match 34.1%; Score 393.4; DB 9; Length 1973;
 Best Local Similarity 65.1%; Pred. No. 2.1e-86;

Matches 615; Conservative 0; Mismatches 321; Indels 9; Gaps 2;

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153 CGCGCATCTCCCGGCGCATCCGGTCATCATCAGGGGCTACTCCGTAGTGTCT 212
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Db CGCCTTCTGCCCCCTCGGGCTCAAGGTCAACATCGTGGGGCTTACTGGCGGTGTGT 365
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Qy CCGTGGGCTTGTGGGCACTCGCTGTGTCATGTTCTGATCATCCGATACAAAGATGA 272
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db CGAGGGCTCTCGGGAACTGCTTGTCTATGATGATCTCTCAGGACACCAAAATGA 425
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Qy GACAGCAACCAATTTAATTTAAGCTTGGGAGATGCTTTAGTTACTACAAC 332
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Qy CATGCCCTTTGAGATAGGTCTACTGATGAAATCTCTGGCCTTTGGGAGTGTGTG 392
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Db GCGTCCCTTTCAGGGGACGAGACATCTCGGGCTTCTGGCCTTTGGGAGTGTGTG 545
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Qy CAAGATAGTAATTTCCATGATTAATAACAAGATTTACACAGCATCTTACCTTGACAT 452
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db CAAGACATGATTCATGATTAATAACAAGATTTACACAGCATCTTACCTTGACAT 605
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy GATGAGCGTGACCGGTACATGCGGTGTGCCACCCCGTGAAGCTTTGGACTTCGGAC 512
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db CATGAGTGTGATCGCTATGATGACCATGTGCCACCCCATCCGCTCGACGTCCGAC 665
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy ACCCTTGAAGCAAGATATCATATCTGCATCTGTGGCTGTGTCTCATCTGTGGCAT 572
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db GTTCAGCAAGCCAGAGCTGTCAATGTGGCAATCTGGCCCTGTGTGTGTGTGTGT 725
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy CTCTGCAATAGTCTCTTGAGAGCACCAAGTCAAGGAGAGAGTGTATGATGAGTCTC 632
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db TCCCGTTCATCATGAGGCTCGGACAGATC-----GAGGATGAAGATGAGTGTCT 779
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy CTTCGATTTCCAGATGATGATGATCTCTCTGTGGAGACTTTCATGAGATGTGCTTT 692
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db GGTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 836
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy CATCTTGTGCTTCTGTATCTCTGTCTCTCATCATCTGTGTGTGTGTGTGTGTGT 752
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db CCTCTTCTCTCATCTGTCTCTGTCTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 896
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy GCGTCTCAAGAGGCTCGGCTCTCTGTGAGCTCCGAGAGAAAGATCGCACTGTGAG 812
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db GCGGCTCGGTGAGTCCGCTGTCTGTGAGCTCCGAGAGAAAGATCGGAGCTGTGAG 956
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy GATCAGCAGACTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 872
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db CATCAGTGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1016
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy CATTTATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 932
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db GGTCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1076
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy CATTTATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 992
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db TCTGCGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1136
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy CTTTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1052
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db CTTTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1196
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy GATGAGCGGACAGACATGACAGAGTCCGAAATACAGTTTCAGGA 1097
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db GATGAGCGGACAGACATGACAGAGTCCGAAATACAGTTTCAGGA 1197
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    1197 CGGAGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1241
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
  
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RESULT 81

ABX94045
 ID ABX94045 strand; cDNA; 2534 BP.

AC ABX94045;

DT 12-JUN-2003 (first entry)

DE cDNA encoding human orphanin FQ receptor (OPQR).

KW Human; orphanin FQ receptor; OPQ; orphanin FQ; psychotropic drug;
 KW nociceptin; gastrointestinal motility; diarrhoea; nausea; fever; pain;
 KW inflammation; learning disorder; memory disorder; drug dependence;
 KW stress-related neuronal dysfunction;
 KW orphanin FR receptor-mediated disease; gene; ss.

OS Homo sapiens.

PN US2003045696-A1.

PD 06-MAR-2003.

PF 01-MAR-2002; 2002US-00087345.

PR 01-MAR-2001; 2001US-0272429P.

PA (UNM1) UNIV MICHIGAN.

PI Owyang C;

DR WPI; 2003-371474/35.

PT New compositions, useful for identifying pharmaceutical agents for
 PT treating diseases mediated by orphanin FQ signaling, e.g. learning and
 PT memory disorders, comprises orphanin FQ receptor splice variants or
 PT encoding nucleic acids.

PS Disclosure; Fig 19; 65pp; English.

CC The invention describes a new composition comprising: (a) an isolated
 CC nucleic acid having one of 9 fully defined sequences with 439-1566 base
 CC pairs (bp); (b) an isolated nucleic acid 85% identical to (a) and
 CC encoding a polypeptide that binds to Orphanin FQ; or (c) an isolated
 CC polypeptide that is at least 95% identical to one of 5 fully defined
 CC sequences with 99-367 amino acids, where the polypeptide binds to
 CC Orphanin FQ. The polypeptide or nucleic acid is useful for screening or
 CC identifying pharmaceutical agents, particularly psychotropic drugs, for
 CC the treatment of a variety of disease states mediated by orphanin FQ
 CC (also called nociceptin) signalling. These disease states include
 CC gastrointestinal motility (e.g. diarrhoea), nausea, fever, pain,
 CC inflammation, learning and memory disorders, drug dependence, stress-
 CC related neuronal dysfunctions, etc. The polypeptide or nucleic acid is
 CC also useful for generating animal models of orphanin FR receptor-mediated
 CC disease state. This is the cDNA sequence of human orphanin FQ receptor
 CC (OPQR).

XX Sequence 2534 BP; 416 A; 809 C; 769 G; 540 T; 0 U; 0 Other;

SQ Query Match 34.1%; Score 393.4; DB 7; Length 2534;

Best Local Similarity 65.1%; Pred. No. 2.3e-86;
 Matches 615; Conservative 0; Mismatches 321; Indels 9; Gaps 2;

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153 CGCGCATCTCCCGGCGCATCCGGTCATCATCAGGGGCTACTCCGTAGTGTCT 212
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db CGCCTTCTGCCCCCTCGGGCTCAAGGTCAACATCGTGGGGCTTACTGGCGGTGTGT 305
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy CCGTGGGCTTGTGGGCACTCGCTGTGTCATGTTCTGATCATCCGATACAAAGATGA 272
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db CGAGGGCTCTCGGGAACTGCTTGTCTATGATGATCTCTCAGGACACCAAAATGA 365
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy GACAGCAACCAATTTAATTTAAGCTTGGGAGATGCTTTAGTTACTACAAC 332
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db GACAGCAACCAATTTAATTTAATTTAAGCTTGGGAGATGCTTTAGTTACTACAAC 425
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
  
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QY 333 CATGCCCTTTGAGATGAGTCACTTGAATTCCTGACCTTTTGGGATGATGCTG 392
   |||||
DB 426 GCTGCCCTTCCAGGCGACGGAATCTCTCGGGCTTCTGCGCTTTGGAAATGCGCTG 485
   |||||
QY 393 CAAGATAGTAATTTCCATTGATTACTACAACATGTTACACAGCATCTTCACTTGAACAT 452
   |||||
DB 486 CAAGACAGTATGACATGACTACTACAACATGTTACACAGCATCTTCACTTGAACAT 545
   |||||
QY 453 GATGAGCGTGAACCGCTACATTCGCGTGGCCACCCCGGAAGGCTTTGACTTCCGAC 512
   |||||
DB 546 CATGAGTGTGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 605
   |||||
QY 513 ACCCTTGAAGCAAGATCATATATGATGATGATGATGATGATGATGATGATGATGAT 572
   |||||
DB 606 GTCCAGCAAGGCGGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 665
   |||||
QY 573 CTCTGCAATGATCTCTTGAAGGACCAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAG 632
   |||||
DB 666 TCCCGTGGCATCATGAGGCTCGGACAGGTC-----GAGGATGAAGAGATGAGAGTGCCT 719
   |||||
QY 633 CTTCGATTTCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 692
   |||||
DB 720 GGTGAGATGATCTTACCCCTCAGAGATTAC---TGAGGCGCGGATGATGATGATGATGAT 776
   |||||
QY 693 CATCTTGGCTTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 752
   |||||
DB 777 CCTCTTCTCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 836
   |||||
QY 753 GCGTCTCAAGAGCGTCCGCTCTCTTCTGAGCTCCGAGAGAAAGATGCAACCTGCTGAG 812
   |||||
DB 837 GCGGCTCGGAGAGTCCGCTCTCTCTGAGGCTCCGAGAGAGAGAGAGAGAGAGAGAGAG 896
   |||||
QY 813 GATGACGAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 872
   |||||
DB 897 CATCTGAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 956
   |||||
QY 873 CATATTCATCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 932
   |||||
DB 957 GGTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1016
   |||||
QY 933 CTATTATCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 992
   |||||
DB 1017 TCTGCGCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1076
   |||||
QY 993 CTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1052
   |||||
DB 1077 CTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1136
   |||||
QY 1053 GATGAGCGGCGACAGCATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 1097
   |||||
DB 1137 CCGGAGCGTGAAGTGTCTGACCGGCTGAGCATGAGATGAGATGAGATGAGATGAGAT 1181
   |||||

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KW Ulcer; gene; ds.
XX
OS Homo sapiens.
XX
PN WO200261087-A2.
XX
PD 08-AUG-2002.
XX
PF 19-DEC-2001; 2001WO-US050107.
XX
PR 19-DEC-2000; 2000US-0257144P.
XX
PI (LIFE-) LIFESPAN BIOSCIENCES INC.
XX
PI Burner GC, Roush CL, Brown JP;
XX
DR WPI; 2003-046718/04.
XX
DR P-PsDB; ABP81862.
XX
PT New isolated antigenic peptides e.g., for G protein-coupled receptors
PT (GPCR), useful for diagnosing and designing drugs for treating conditions
PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
PT autoimmune diseases.
XX
PS Disclosure; Fig 1; 523pp; English.
XX
CC The present invention describes antigenic peptides (i) comprising: (a)
CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC acids. Also described: (1) an assay for the detection of a particular G
CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
CC and (2) an isolated antibody having high specificity and high affinity or
CC avidity for a particular GPCR. (1) can be used as GPCR modulators and in
CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an
CC antibody against a particular GPCR, and in the production of specific
CC antibodies. The peptides and antibodies are also useful for detecting the
CC presence or absence of corresponding GPCRs. The antigenic peptides for
CC GPCRs and antibodies are useful for diagnosing and designing drugs for
CC treating immune-related diseases, growth-related diseases, cell
CC regeneration-related diseases, immunological-related cell proliferative
CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC any other disorder in which GPCRs are involved. The antibodies may be
CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC exemplification of the present invention.
XX
SQ Sequence 2534 BP; 416 A; 809 C; 769 G; 540 T; 0 U; 0 Other;

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Query Match 34.1%; Score 393.4; DB 7; Length 2534;
 Best Local Similarity 65.1%; Pred. No. 2.3e-86;
 Matches 615; Conservative 0; Mismatches 321; Indels 9; Gaps 2;

```

QY 153 CGCGCATCTTCCCGGCGCATCCGGTATCATACAGCGGCTCTACTCCGATGTTTCT 212
   |||||
DB 246 GCGCTTCTCTGCGCTCGGGCTCAAGGTCAACATGATGAGGCTCTTACCTGCGCGTGTGT 305
   |||||
QY 213 CGTGGGCTTGTGTGAGCACTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 272
   |||||
DB 306 CGAGAGGCTCTCTGAGAACTGCTTGTATATGATGATGATGATGATGATGATGATGATGAT 365
   |||||
QY 273 GACAGCAACCAATTTATCATATTTAACTGCTTGTGAGCATGCTTTAGTTACTACAAC 332
   |||||
DB 366 GACAGCAACCAATTTATCATATTTAACTGCTTGTGAGCATGCTTTAGTTACTACAAC 425
   |||||
QY 333 CATGCCCTTTGAGATGAGTCACTTGAATTCCTGACCTTTTGGGATGATGCTG 392
   |||||
DB 426 GCTGCCCTTCCAGGCGACGGAATCTCTCGGGCTTCTGCGCTTTGGAAATGCGCTG 485
   |||||

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QY 393 CAAGATAGTAATTTCTGATGATTAACAAGATGTTACACAGATCTGCCTGACAT 452
DB 486 CAAGACAGTCATTTGCTGATTAACAAGATGTTACACAGATCTGCCTGACAT 545
QY 453 GATGACCGTGAACCGGTACATGTCCTGTGACACCCCGTGAAGCTTTGAGCTTCGAC 512
DB 546 CATGAGTGTGATCGGTATGTAGCCATCTGCCACCCCATCCGAGCCCTGAGAGTCCGAC 605
QY 513 ACCCTTGAAGCAAGATCATATATCTGATCTGCTGCTGTCTCATCTGTTGGCAT 572
DB 606 GTCCAGCAAGCCCAAGCTGTGATGTGCGCATCTGAGGCTGAGCTGTGTCGTGT 665
QY 573 CTCTGCAATATGCTTTGAGAGCAACAAGTCAAGGAGGAGAGCTGATGATGAGCTC 632
DB 666 TCCCGTTCATCATGAGCTCGGACAGGTC-----GAGATGAAGATGAGTGCCT 719
QY 633 CTTCGAGTTCCAGATGATGACTACTCTGTGTGAGCACTTTATGAAGATCTGCTCT 692
DB 720 GGTGAGATCCCTACCCCTCAGGATTAC---TGGGCCCCGGTGTGGCATCTGCATCT 776
QY 693 CATCTTTGCTTGTGATCTCTGTCTCTCATCATCATCTGTCTGTACACCTGATCTCT 752
DB 777 CCTCTTCTCTCATCTGTCCTCGCTCGTCACTCTGTCTGTCTACAGCCTCATGATCTCG 836
QY 753 GGGTCTCAAGAGCGTCCGGCTCTTTCTGCTCCGAGAGAAAGATCGGACCTGTGAG 812
DB 837 GGGGCTCCGTGAGTCCGCTCTCTCGGAGCTCCGAGAGAAAGACCGGAACTGTGAGCG 896
QY 813 GATCACAGACTGTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 872
DB 897 CATCATCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 956
QY 873 CATATTCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 932
DB 957 GGTCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1016
QY 933 CATATTCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 992
DB 1017 TCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1076
QY 993 CTTCCTGTGATGAAGCTTCAAGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1052
DB 1077 CTTCCTGTGATGAAGCTTCAAGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1136
QY 1053 GATGAGCGGCAAGACCTAGACAGATCGGAATATACAGTTCAAGGA 1097
DB 1137 CCGGAGCGTGAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1181

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RESULT 83

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ABI98010
ID ABI98010 standard; cDNA; 1113 BP.
XX
XX AC ABI98010;
XX
XX DT 18-FEB-2002 (first entry)
XX
XX DE Non-endogenous human GPCR cDNA, SEQ ID NO: 540.
XX
XX KW Human; G protein-coupled receptor; GPCR; non-endogenous; mutant;
XX constitutively activated GPCR; agonist; disease; ss.
XX
XX OS Homo sapiens.
XX
XX PN Synthetic.
XX
XX PN WO20017172-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 05-APR-2001; 2001WO-US011098.
XX
XX PR 07-APR-2000; 2000US-0195747P.

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XX (AREN-) ARENA PHARM INC.
XX PA
XX PI Lehmann-Brunnema K, Llaw CM, Lin I;
XX DR WPI; 2001-648759/74.
XX DR P-PSDB; ABB56374.
XX
XX PT Identifying agonists of G protein-coupled receptors (GPCRs) for use in
XX PT disease treatment, comprises contacting candidate compounds with versions
XX PT of GPCRs.
XX
XX PS Example 2; Page 342; 394pp; English.
XX
XX CC The invention relates to G protein-coupled receptors (GPCRs) for which
XX CC the endogenous ligand has been identified. Non-endogenous constitutively
XX CC activated versions of known GPCRs are used in the invention for the
XX CC direct identification of candidate compounds as receptor agonists,
XX CC inverse agonists or partial agonists. Such agonists are useful as
XX CC therapeutic agents for diseases or disorders associated with GPCRs. The
XX CC present sequence encodes a non-endogenous version of a known human GPCR
SQ Sequence 1113 BP; 176 A; 378 C; 309 G; 250 T; 0 U; 0 Other;
Query Match 34.0%; Score 391.8; DB 5; Length 1113;
Best Local Similarity 65.0%; Pred. No. 4,1e-86;
Matches 614; Conservative 0; Mismatches 322; Indels 9; Gaps 2;
QY 153 CGCGACATCTTCCCGGCGATCCCGATCATCAACGCGGATCTACTCGGATGTCTGT 212
DB 129 CGCTTCTCGCTCCCTCGGAGCTCAAGTCAATCGTGGGCTCTACCTGCGGTGTGT 188
QY 213 CGTGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 272
DB 189 CGAGGCTCTCGGAGAACTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 248
QY 273 GACAGCAACCAATTTATATTTTAACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 332
DB 249 GACAGCAACCAATTTATATTTTAACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 308
QY 333 CATGCCCTTTCAGATGAGTCTACTGTATGAAATCTGTGCTTTTGGGATGTGTGT 392
DB 309 GCTGCCCTTTCAGAGGACAGGACATCTCTGTGGCTTTGTGGGATGTGTGTGT 368
QY 393 CAAGATAGTAATTTCTGATGATTAACAAGATGTTACACAGATCTGCCTGACAT 452
DB 369 CAAGACAGTCATTTGCTGATTAACAAGATGTTACACAGATCTGCCTGACAT 428
QY 453 GATGACCGTGAACCGGTACATGTCCTGTGACACCCCGTGAAGCTTTGAGCTTCGAC 512
DB 429 CATGAGTGTGATCGGTATGTAGCCATCTGCCACCCCATCCGAGCCCTGAGCTCCGAC 488
QY 513 ACCCTTGAAGCAAGATCATATATCTGATCTGCTGTGTGTGTGTGTGTGTGTGTGT 572
DB 489 GTCCAGCAAGCCCAAGCTGTGATGTGCGCATCTGAGGCTGTGTGTGTGTGTGTGT 548
QY 573 CTCTGCAATATGCTTTGAGAGCAACAAGTCAAGGAGAGCTGATGATGATGATGAT 632
DB 549 TCCCGTTCATCATGAGGCTCGGACAGGTC-----GAGATGAAGATGAGATGAGTGCCT 602
QY 633 CTTCGAGTTCCAGATGATGACTACTCTGTGTGAGGAGCTTTATGAAGATCTGAGCTCT 692
DB 603 GGTGAGATCCCTTACCCCTCAGGATTAC---TGGGCCCCGGTGTGGCATCTGCATCTCT 659
QY 693 CATCTTTGCTTGTGATCTCTGTCTCTCATCATCATCTGTCTGTACACCTGATGATCT 752
DB 660 CCTCTTCTCTCATCTGTCTCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 719
QY 753 GCGTCTCAAGAGCGTCCGCTCTTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 812
DB 720 GCGGCTCCGTGAGTCCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 779
QY 813 GATCACAGACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 872

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D6		CCTGTTTCCTTCAATCGACGCCGGAGTGCTGCATCCTGTCTGACTAAGCCATTGATCCG	752
Oy	693	GCGTCTCAAGAAGCGCTCGGGCTCTCTTCTGCTCCCCGAAGAAGATCGCAAACCTGCGTAG	812
D6	753	GCGGCTCCGTGGAGATCCCGCTGCTCTCGGGGCTCCC GAAGAAGAACCGGAACCCTGCGGCG	812
Oy	813	GATCACGACA CTGGGCTGGTGGTGGTGGAGAGCTGTTGGTGGCTGGAGCTCCCATTC A	872
D6	813	CATCACTTGGCTGGTGCTGGTGGTAAGTAACTGTGTGTTGTTGGAGGCTGTGAAGCCTGTCCA	872
Oy	873	CATAATTCATCTGCTGGTGGAGGCTCTGSGGAGACCTCCCA CAGACAGCTGCTCTCCAG	932
D6	873	GGCTTCGTGGTGGTGCGCCCAAGGGCTGGGGGGTTCA GCGCAGACGACGAGATGGCGGTGC AT	932
Oy	933	CTATTACTTCTTG CATCGCTGCTTAAGCTTAACCAACAGTAGCTGAATCCCATTTCTAC GC	992
D6	933	TCTGGCTTCTGCA CGGCGCTGGGCTA AGTCAACAGCTGCTCA ACCCATCTCTACGC	992
Oy	993	CTTCTCTGATGAAA CTC CAAGCGGTGTTTTCCGGGAC TTTCTGCTTCCACTGGAAGTAG	1052
D6	993	CTTCTGATAGAACTTCAAGG CCTGCTTCCGCAAGTTCT GTGTGCATCTGCCCTCG	1052
Oy	1053	GATGAGCGCGCAGACAGACTAGACAGAGTCCGAATACAG TTCAAGGA	1097
D6	1053	CCGGAGCTGCAGGTGTCTGACCGGCTGCGCAGCATTTGCCAAG A	1097
RESULT 85			
AZ60727	ID	AZ60727 standard; cDNA; 1238 BP.	
XX AC	AZ60727;		
XX DT	16-MAY-2000 (first entry)		
XX DE	cDNA encoding murine mu-opioid receptor splice variant MOR-1G.		
KW KW	Mu-opioid receptor; MOR-1; splice variant; morphine analgesia; opioid-mediated ingestive response; opioid activity; analgesic; gastrointestinal motility; respiration; immune system; endocrine system; autonomous nervous system; peristalsis regulator; body weight; neuroendocrine disorder; MOR-1G; ss.		
XX OS	Mus sp.		
XX FH	Key	Location/Qualifiers	
FT FT	CDS	18..1097 /*tag= a /product= "MOR-1G"	
XX MO	MO200004046-A2.		
XX PD	27-JAN-2000.		
XX PF	15-JUN-1999;	99WO-US015974.	
XX PR	16-JUL-1998;	98US-0092980P.	
XX PA	(SLOC) SLOAN KETTERING INST CANCER RES. Paeternak G, Pan Y;		
XX DR	WIPI; 2000-182402/16. P-PsDB; AA V68878.		
PT PT	New splice variants of the mu-opioid receptor, useful in screening for selective analgesics and for regulating morphine analgesia or body weight.		
XX PS	Claim 38; Fig 2b; 83pp; English.		
CC CC	The present sequence encodes a murine mu-opioid receptor (MOR-1) splice variant MOR-1G. The specification describes 11 new exons for the MOR-1		

CC	gene, which combine to yield 15 novel splice variants of the MOR-1 gene.
CC	These splice variants are potential targets for modulating morphine
CC	analgesia and opioid-mediated ingestive responses. The MOR-1 polypeptide
CC	is used to screen compounds for opioid activity. Such compounds are
CC	potential analgesics or more generally agents that affect
CC	gastrointestinal motility, respiration or the immune, endocrine or
CC	autonomous nervous systems, e.g. regulators of peristalsis. Antagonists,
CC	agonists and ligands of MOR-1, as well as DNA vectors expressing MOR-1-
CC	encoding nucleic acids, or sequences antisense to MOR-1 nucleic acids,
CC	are used to regulate morphine analgesia and body weight. The level of MOR
CC	-1 or tissue distribution of MOR-1 can be measured to diagnose MOR-1
CC	related pharmacological abnormalities or neuroendocrine disorders,
CC	particularly inherited disorders. Transgenic animals with extra copies of
CC	the MOR-1 gene, or with endogenous alleles deleted, are used to study
CC	loss or gain of function phenotypes
XX	
SQ	Sequence 1238 BP; 319 A; 343 C; 266 G; 310 T; 0 U; 0 Other;
Query Match	33.6%; Score 387.6; DB 3; Length 1238;
Best Local Similarity	67.8%; Pred. No. 4.6e-85;
Matches 575; Conservative	0; Mismatches 264; Indels 9; Gaps 2;
QY	252 CATCCGATTACCAAAAGATGAAGAAGAGCAAGACCAATTTACATATTTAACTGCTTGCGC 311
DB	179 CCTCAGATTATCCAAATGAAGACTGCCACACATCTTACATTTTCAACCTGCTCGGC 238
QY	312 AGATGCTTTAGTTACTACCAACATGCCCTTTACAGAGTACGAGTCTTATGTAATTCCTG 371
DB	239 AGATGCTTTAGCCACTAGACAGCGTCCCTTTACAGAGTTTAACTACTGATGGGAACGTG 298
QY	372 GCCTTTGGGGATGATGCTGTCGAAGATATGTAATTTCCATGTATTACTACAAACATGTTAC 431
DB	299 GCCCTTTGGAAACATCTCTGCAAGATCGATCTCAATGACTACTACACCAATGTTTAC 358
QY	432 CAGCATCTTACACCTTGAACATGATGAGCGTGAACCGCTACATTTGCCGTGCCACCCCGT 491
DB	359 CAGATATTACACCTCTGCAACATGATGATGAGCCGTTACATTTGCCGTGCCACCCCGT 418
QY	492 GAAGGCTTTGGAATTCGCAACACCCCTTGAAGGCAAGATCATATATTCGATCTGACT 551
DB	419 CAAGGCCCTGGATTTCGTAACCCCGCAAAATGTCATATGTCATGCAACTGGAT 478
QY	552 GCTGTGCTCATCTGTGGCATCTTCGAAATATGTCCTTGGAGGACCAAAATCAGGGAAGA 611
DB	479 CCTCTCTTTCGCCATATGATGCTGCCCGGTAATGTTATATGCAACCAAAATACAGGCA--- 535
QY	612 CGTGAATGATTAAGAGCTCCCTTGAAGTTCCAGATGATGATGACTACTCCGTGGGAGCT 671
DB	536 ---GGGATCCATATATGCAACCTCAGCTTCTCATGCCACATGATGATGAGGAACCT 592
QY	672 CTTTCATGAAATATGAGCTCTTTCATCTTTGGCTTCGTATCCATCATCATCGT 731
DB	593 GCTC---AAATATGATGCTTTCATCTTCCGCTTCATCATATGCGGATCATCATCACTGT 649
QY	732 CTGCTACACCTGATGATCTCTGGCTCTCAAGAGCGTCCGCGCTCTTTCTGGCTCCGAGA 791
DB	650 GTGTTATGAGCTATGATCTTACAGACTCAAGAGTGTCCGATGCTGTCCGAGCTCAAGA 709
QY	792 GAAGAATTCGAACCTGGGTATGATCAACAGACATCGTCTGTGGTGGTGCAGCTTCGT 851
DB	710 AAAGAGACAGGAACCTGGGAGAGATCACCCGAGATGATCTGTGTCTGTGCTGATTTAT 769
QY	852 CGTGTCTGAGACTCCATTCATCATATTCATCTGTGATGAGGCTGTGGGAGACCTTCCA 911
DB	770 TGTCTGCTGAGACCCCATTCACATCTATATGTCATCATTAAGACATGATACAGATTCAGA 829
QY	912 CAGCAGACTGCTCTCTCCAGCTATTAATTTCTGATCGCTTAAAGCTATTAACCAAGTAG 971
DB	830 AACCACTTTCAGACTGTTCTGTGGCACTTCTGATTTGCTTGGGTTACAAACACACTG 889
QY	972 CTGGAATCCATTCCTACAGCCCTTTCTTATAGAAAATTTCAAGCGGTGTTCCGGAGCT 1031
DB	890 CTGGAACCCAGTCTTATATGCTTCGATATGAATACTTCAACAGATGTTTAAAGAGTT 949

CC inflammation, learning and memory disorders, drug dependence, stress-
 CC related neuronal dysfunctions, etc. The polypeptide or nucleic acid is
 CC also useful for generating animal models of orphanin FR receptor-mediated
 CC disease state. This is the cDNA sequence of rat orphanin FQ receptor
 CC (OFQR) splice variant OFQR-c
 XX
 XX

Sequence 1387 BP; 252 A; 403 C; 356 G; 376 T; 0 U; 0 Other;

Query Match 32.7%; Score 377.6; DB 7; Length 1387;
 Best Local Similarity 63.9%; Pred. No. 1.4e-82;
 Matches 607; Conservative 0; Mismatches 334; Indels 9; Gaps 2;

```

QY 153 CGCGACATCTCCCGGCCATCCCGGTCAATCAAGGGGCTACTCCGTAGTTCGT 212
DB 403 CCGCTTCTGCCCCCTTGGACTCAAGGTCAACATCGTGGGCTCTACTTGGCTGTGCAT 462
QY 213 CGTGGGCTTGTGGGCACTCGCTGTGCTATGTTCTGTATCTCCATACCAAGATGAA 272
DB 463 CGGGGGGCTCTGGGGAACTGCCTCGTCAATGATGATCTCTCAGGACACCAAGATGAA 522
QY 273 GACAGCAACCAATTATATATTTAACTGGCTTTGGCAGATGCTTTAGTTACTACAC 332
DB 523 GACAGTACCAATTATATATTTAACTGGCAGCTGTGATACCTGTGCTTGTCTAAC 582
QY 333 CATGCCCTTTCAGAGTACGCTCTACTGTGATGAATTCCTGAGCTTTGGGAGTGTCTGTG 392
DB 583 ACTGCCCTTTCAGGGGACAGACATCTCTACTGGGCTTCTGAGCAATTTGGAAATGCACTCTG 642
QY 393 CAAGATAGTAAATTTCCATGATTTACTACAAATGTTCAACAGATCTTCACTTACAT 452
DB 643 CAAGACTGTCAATTGCTATGACTACTACAAATGTTTACAGACATTTTACTCTGACCGC 702
QY 453 GATGAGCGTGAACCGCTACATTGCGCTGTGCCACCCCGTGAAGGCTTTGACTCCGAC 512
DB 703 CATGAGCGTGAACCGCTATGTGGCTATCTGCCACCTATCCGCTTGAATGTTGCGAC 762
QY 513 ACCCTTGAAGGCAAGATCATCAATATCGCATCTGGCTGTGCTGTGATCTGTGGCAT 572
DB 763 ATCCAGCAAAAGCCCAAGGCTGTATATGTGCGCATATGAGCCCTTGCTTCACTGTGTGTG 822
QY 573 CTCTGCATATGCTCTTGAAGGACCAAAAGTCAAGGAAAGACGTGATGATTTGAGTCTC 632
DB 823 TCCTGTGGCATCATCGGTTCAGACAAAGT-----GGAAGATGAAGATGAGTGCCT 876
QY 633 CTTCGACTTCCAGATGATGACTACTCTCTGTGGGACCTCTTCATGAAATCTGCGCTTT 692
DB 877 GGTGGAGATCCCTGCCCTCAGGACTATTTGGGG---CCCTGTAATCGCCATCTGCATCTT 933
QY 693 CATCTTGTGCTGTGATCCCTGTGCTCATCATGCTGTGCTACACCTGATATGATCTCT 752
DB 934 CTTTCTTCTTCATCATCTCTGTGTGATCATCTGTGTGTACAGCCTTCATGATGTG 993
QY 753 GCGTCTCAAGAGCGTCCGCTCTCTTCTGTGCTCCAGAGAAAGATCGAACCCTGTGATG 812
DB 994 AGGACTCTGTGTGTCTGTCTGTCTTCAAGCTCCCGGAAAGAGACCAAACTGTGGGG 1053
QY 813 GATCAACAGACTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 872
DB 1054 TATCTACTGACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 1113
QY 873 CATATTCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 932
DB 1114 GGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1173
QY 933 CTATTAATCTGTGATGCTTGAAGCTATACCAACAGTACCTGAATCCCATCTCTACAC 992
DB 1174 CCGGAGCTTCTGACAGCCCTGTGGGCTATGTCAACATTTGCTCAATCCATCTCTATAC 1233
QY 993 CTTTCTTGAATAAATTCAAGCGTGTTCGGGACCTTGTCTTGTCTTCACTGAAGATGAG 1052
DB 1234 TTTCTCGATGAGAACTTCAAGGCTGTGTGAAAGTCTGTGTGTGTGTGTGTGTGTGTG 1293
QY 1053 GATGAGCGGACAGACATGAGAGTCCGAAATATAGTTTCAAGGATCTCTG 1102

```

DB 1294 CGGGAGATGACAGGTTTCTGATCGTGTGCGGAGCATTTGCCAAGATGTTG 1343

RESULT 90

AA089233
 ID AA089233 standard; cDNA; 1567 BP.

AC AA089233;
 XX
 XX 25-MAR-2003 (revised)
 DT 20-OCT-1995 (first entry)
 XX
 DE Rat oploid receptor cDNA.
 XX
 KW Opioid receptor; MOR-1; gene therapy; diagnostic; ss.
 XX
 OS Rattus sp.
 XX
 FH Key location/Qualifiers
 FT CDS 173..1276
 FT /*tag= a

W09507983-A1.

23-MAR-1995.

13-SEP-1994; 94WO-US010358.

13-SEP-1993; 93US-00120601.

(INDV) UNIV INDIANA FOUND.

XX
 XX Yu L;

DR MPI; 1995-131351/17.

P-PSDB; AAR71968.

PT New nucleic acid encoding new human mu opioid receptor - and related
 PT vectors, transformed cells, antibodies etc., useful in diagnosis,
 PT treatment and drug screening.

PS Example 9; Page 218-222; 266pp; English.

XX The cDNA given in AA089233 was isolated from a rat brain library by low
 CC stringency hybridization with rat mu opioid receptor cDNA (AA089222). The
 CC clone encoded a 367-amino acid protein (AAR71968) that showed high
 CC homology with mu, kappa and delta opioid receptors but lacked affinity
 CC for their ligands, suggesting it to be a novel member of the opioid
 CC receptor family. (Updated on 25-MAR-2003 to correct PN field.)
 XX

Sequence 1567 BP; 313 A; 440 C; 402 G; 412 T; 0 U; 0 Other;

Query Match 32.7%; Score 377.6; DB 2; Length 1567;
 Best Local Similarity 63.9%; Pred. No. 1.4e-82;
 Matches 607; Conservative 0; Mismatches 334; Indels 9; Gaps 2;

```

QY 153 CGCGACATCTCCCGGCCATCCCGGTCAATCAAGGGGCTACTCCGTAGTTCGT 212
DB 222 CGCTTCTGCCCCCTTGGACTCAAGGTCAACATCGTGGGCTCTACTTGGCTGTGCAT 351
QY 213 CGTGGGCTTGTGGGCACTCGCTGTGCTATGTTCTGTATCTCCATACCAAGATGAA 272
DB 352 CGGGGGGCTCTGGGGAACTGCCTCGTCAATGATGATCTCTCAGGACACCAAGATGAA 411
QY 273 GACAGCAACCAATTATATATTTAACTGGCTTTGGCAGATGCTTTAGTTACTACAC 332
DB 412 GACAGTACCAATTATATATTTAACTGGCAGCTGTGATACCTGTGCTTGTCTAAC 471
QY 333 CATGCCCTTTCAGAGTACGCTCTACTGTGATGAATTCCTGAGCTTTGGGAGTGTCTGTG 392
DB 472 ACTGCCCTTTCAGGGGACAGACATCTCTACTGGGCTTCTGAGCAATTTGGAAATGCACTCTG 531

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QY 393 CAAGATAGTAAATTCATGATTACTACAAAGTTCACACAGATCTTCACCTTGACAT 452
DB 532 CAAGACTGTCTTCTGATCTGATCTACACATGTTTACACAGACTTTTACTCTGACCC 591
QY 453 GATGACCGTGACCCGCTACATTCGCGTGTGCCACCCCGTGAAGGCTTTGGACTCCGAC 512
DB 592 CATGAGCGTAGACCGCTATGTGGCTATCTGCCACCTTACCGGCTTGATGATTTGGAC 651
QY 513 ACCCTTGAAGCAAGATCATATATCTGCATCTGGCTGTCTGTCTATCTGTTGGCAT 572
DB 652 ATCCAGCAAGGCCAGCGCTTAAATGTGGCATATGGGCCCTTGCGCTTCAGTGGTGTCT 711
QY 573 CTCTGCAATAGTCTCTTGAGAGCACCAAGTCAAGGAGAGCGTGCATGTGATGAGTGTCT 632
DB 712 TCTGTGTGCATCATAGGCTTTCAGACACAGT-----GGAAGATGAAGATGAGTGTCT 765
QY 633 CTTGAGTTCCAGATGATGACTACTCTGTGTGGGACCTTTCAATGAAGTCTGCGTCTT 692
DB 766 GGTGAGATCCCTGCCCCCTCAGGACTATTTGGGG---CCCTGATTTGCCATCTGCATCTT 822
QY 693 CATCTTTGGCTTCGTGATCCCTGTCTCTCATCATCATCTGTCTGTACACCTTGATGATCT 752
DB 823 CTTTTTTTCTTCATCATCTCTGTGTGTATCATCTCTGTCTGTACAGCTCATATGATTCG 882
QY 753 GCGCTCAAGAGACGTCGGGCTCCTTTCTGTGCTCCGAGAGAAAGATGCAACCTGGGTAG 812
DB 883 AGGACTCTGTGTGTCTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 942
QY 813 GATCAACGAGCTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 872
DB 943 TATCACTGACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1002
QY 873 CATATTCATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 932
DB 1003 GGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1062
QY 933 CTATATCTTCTGATCTGCTTGTAGGCTATACCAAGTGTAGCTGAATCCATCTCTACGC 992
DB 1063 CCGGCGCTTCTGCAACGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1122
QY 993 CTTTCTTGTATGAAAATTTCAGCGGCTTTCCGGAATTCTGTCTTTTCACTGAAGATGAG 1052
DB 1123 TTTCTGTGATGAACTTTCAGGCGCTTGTGAAGATTTCTGTGTGTGTGTGTGTGTGT 1182
QY 1053 GATGAGCGGCGAGACACTAGACAGTCCGAATATCAGTTCAAGATCTCG 1102
DB 1183 CCGGAGATGACGTTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1232
```

RESULT 91
AAA59510
ID AAA59510 standard; cDNA; 1567 BP.

XX AAA59510;
XX 14-NOV-2000 (first entry)
XX cDNA encoding a rat mu opioid receptor polypeptide.
XX
XX mu opioid receptor; transcription regulatory polypeptide;
XX opiod receptor-like polypeptide; ss.
OS Rattus sp.
XX
XX
XX Key Location/Qualifiers
XX CDS 173..1276
XX FT /*tag= a
XX FT /product= "mu opioid receptor"
XX
XX US6103492-A.
XX 15-AUG-2000.

```
PF 07-JUL-1997; 97US-00889108.  
XX 08-MAR-1993; 93US-00056886.  
PR 13-SEP-1993; 93US-00120601.  
PR 13-SEP-1994; 94US-00305518.  
XX  
XX (INDV ) UNIV INDIANA.  
XX  
XX Yu L;  
DR WPI; 2000-542550/49.  
DR P-PSDB; AAB07868.  
XX  
XX Novel nucleic acids encoding mu opioid receptor for expressing large  
PT quantities opiod receptors which are useful for screening and evaluating  
PT subtype-selective drugs and as probes or primers.  
XX  
XX Example 9; Col 105-110; 86pp; English.
```

The present sequence encodes a mu opioid receptor protein. The specification also describes a transcription regulatory polypeptide and an opiod receptor-like polypeptide. Human mu opiod receptor CC polynucleotides are useful as a source of probes and primers, which may be used as diagnostic tools to detect normal and abnormal DNA sequences in DNA derived from patients cells. They are also used as a means for detecting and isolating other members of the polypeptide family and related polypeptides from a DNA library potentially containing such sequences. The polynucleotide is used for preparing large quantities of CC opiod receptor which on expression in microorganism can be useful for evaluating subtype-selective drugs

Sequence 1567 BP; 313 A; 440 C; 402 G; 412 T; 0 U; 0 Other;

Query Match 32.7%; Score 377.6; DB 3; Length 1567;
Best Local Similarity 63.9%; Pred. No. 1.4e-82;
Matches 607; Conservative 0; Mismatches 334; Indels 9; Gaps 2;

```
QY 153 CGCGGACATCTCCCGGCGCATCCCGTGCATATCAGCGGCTTACTCCGATGTTTGT 212
DB 292 GCGCTTCTGCCCCCTTGACTCAAGTACCATGTGGGGCTCTACTCTTGGCTGTGTGAT 351
QY 213 CGTGGGCTTGTGGGCACTCGCTGTGCATGTTGTGTATCATCCGATACACAAAGATGAA 272
DB 352 CGGGGGGCTCCTGGGGAACCTCGTGTATGTATGTATCTTCAGGACACACAAAGATGAA 411
QY 273 GACAGCAACCAATTTATATTTTAACTTGTGCAATGCTTTAGTTACTACAC 332
DB 412 GACAGCTACCAAACTTATATTTTAACTTGTGCACTGCTGTATCCCTGTGCTTGTAC 471
QY 333 CATGCCCTTCAAGTACGCTCTGATGATGATTTCCGCGCTTTGGGAGTGTGTG 392
DB 472 ACTGCCCTTCAAGGCGACAGACATCTTACTGTGGCTTCTGCGCATTTTGGAAATGAC 531
QY 393 CAAGATAGTAAATTCATGATTACTACAAAGTTCACACAGTTCCTTCACTTGACCAT 452
DB 532 CAAGACTGTCTTCTGATCTGATCTACACATGTTTACACAGACTTTTACTCTGACCC 591
QY 453 GATGACCGTGACCCGCTACATTCGCGTGTGCCACCCCGTGAAGGCTTTGGACTCCGAC 512
DB 592 CATGAGCGTAGACCGCTATGTGGCTATCTGCCACCTTACCGGCTTGATGATTTGGAC 651
QY 513 ACCCTTGAAGCAAGATCATATATCTGCATCTGGCTGTCTGTCTATCTGTTGGCAT 572
DB 652 ATCCAGCAAGGCCAGCGCTTAAATGTGGCATATGGGCCCTTGCGCTTCAGTGGTGTCT 711
QY 573 CTCTGCAATAGTCTCTTGAGAGCACCAAGTCAAGGAGAGCGTGCATGTGATGAGTGTCT 632
DB 712 TCTGTGTGCATCATAGGCTTTCAGACACAGT-----GGAAGATGAAGATGAGTGTCT 765
QY 633 CTTGAGTTCCAGATGATGACTACTCTGTGTGGGACCTTTCAATGAAGTCTGCGTCTT 692
DB 766 GGTGAGATCCCTGCCCCCTCAGGACTATTTGGGG---CCCTGATTTGCCATCTGCATCTT 822
```



```
XX 11-DEC-2002 (first entry)
DT CDNA encoding human mu1 opioid receptor fragment.
XX
XX
XX
XX Human; mu1 opioid receptor; gene; ss; morphine; receptor;
XX intracellular calcium.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
XX CDS 1..945
XX FT /product= "Mu1 opioid receptor fragment"
XX FT /transl_except= (pos:885..887,aa:Leu)
XX
XX WO200268594-A2.
XX
XX 06-SEP-2002.
XX
XX 22-FEB-2002; 2002WO-US005452.
XX
XX 22-FEB-2001; 2001US-0270479P.
XX PR
XX 05-DEC-2001; 2001US-0336677P.
XX PR
XX
XX (RESU-) RES FOUND SUNY.
XX
XX Cadet P, Stefano GB;
XX
XX WPI; 2002-706977/76.
XX DR
XX P-PSDB; ABG32258.
XX
XX New isolated nucleic acid molecule encoding a polypeptide having mu3
XX opiate receptor activity, useful as research tools for exploring the
XX interactions, molecular mechanisms and relationship of morphine with the
XX mu3 opiate receptor.
XX
XX Claim 5; Page 32; 52pp; English.
XX
XX This invention relates to a novel nucleic acid molecule encoding a
XX polypeptide having mu3 opiate receptor activity. Mu opioid receptors
XX exhibit a high binding specificity for morphine. The invention also
XX comprises a method for identifying a mu3 opiate receptor agonist or
XX antagonist. The nucleic acids and polypeptides of the invention are
XX useful as research tools for exploring the interactions of morphine with
XX the mu3 opiate receptor, the molecular mechanisms by which morphine
XX induces intracellular calcium concentration changes and the relationship
XX of mu3 opiate receptors with other mu opioid receptors. They are also
XX useful for identifying a mu3 opiate receptor agonist or antagonist. The
XX present sequence represents a CDNA sequence encoding a fragment of the
XX human mu1 opioid receptor of the invention
XX
XX Sequence 945 BP; 250 A; 252 C; 171 G; 272 T; 0 U; 0 Other;
XX
XX Query Match 32.5%; Score 375.6; DB 6; Length 945;
XX Best Local Similarity 67.9%; Pred. No. 3.7e-82;
XX Matches 557; Conservative 0; Mismatches 254; Indels 9; Gaps 2;
XX
XX 268 ATGAAGACGACGAACCAATTACATATTAACTGGCTTTGGCAGATCCTTAGTTACT 327
XX 1 ATGAAGACGACGAACCAATTACATATTAACTGGCTTTGGCAGATCCTTAGTTACT 327
XX
XX 328 ACAACCATGCCCTTTAGAGTACGGTCTTCTGATGAATTCCTGGCCTTTGGGGATGTG 387
XX 61 AGTACCCCTGCCCTTCAGAGTGAATTTCTAATGGAACATGGCCATTTGGAAACATC 120
XX
XX 388 CAGTGAAGATGATTAATTTCCATTTCTCAACATGTTACCGACGATCTTCACTTG 447
XX 121 CTTTGCAAGATGATGATCTCCATAGTTACTATTAAGATGTTACCGACGATCTTCACTTG 180
XX
XX 448 ACCATGATGAGCGGTGAGCGCTACATGTCGCTGTGACCCCGGTGAAGCTTGAAGCTTC 507
XX 181 TGCACCATGAGTGTGATGATGATATTTGAGAGTGTGCACCCGTGTCAAGGCTTAAGTTTC 240
```

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QY 508 CGCAGACCGCTGAAGGGCAAGATCATCAATATTCGATCTGGCTGTCGTCATCTGTT 567
DB 241 GGTACTCCCGAAGAAAGCCAAATATTAATGATGTCGCACTGATCTCTTTACGCCATT 300
QY 568 GGCATCTCTGCAATATGATCTTTGAGGCAACAAAGTCAGAGGAAGAGTGTATTTAG 627
DB 301 GGTCTCTGTAATGTTATGATGGCTACCAAAATACAGGCAA-----GGTTCAATGAT 354
QY 628 TGCTCTTGCAGTTCCCGAATGATGATCACTCTGCTGTGGACCTTTGATGAAGATCTGC 687
DB 355 TGTACACTCAATATTC--TCAATCAACCTGTGATCTGGAAACCTGTAAGATCTGT 411
QY 688 GTTTCATCTTTCCTTGGCTGATGATCCCTGTCATCATCATGTCGTGTACACCTGTATG 747
DB 412 GTTTTCATCTTTCCTTTCATTAATGCAATGCTCATCATTAACGCTGTCTATGATGATG 471
QY 748 ATCTCGCTCTCAAGAGCGTCCGCTCTTTCTGGCTCCGAGAGAAAGATCGCAACTG 807
DB 472 ATCTGGCGCTCAAGAGTGTCCGATGCTCTCTGGCTCCAAAGAAAGAGCAAGATCTT 531
QY 808 CGTAGATCAACCAAGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 867
DB 532 CGAAGATCACCAAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 591
QY 868 ATTCAATATTCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 927
DB 592 ATTCAATATTCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 651
QY 928 TTCACATTTATCTTGTGATGCTTGTAGCTATACCAACAGTAGCTGAATCCATTCTC 987
DB 652 GTTCTGTGCACTTCTGTGATGCTTGTAGCTATACCAACAGTAGCTGAATCCATTCTC 711
QY 988 TACGCTTTTCTGATGAAATCTTCAAGGGGCTTTCCGGGACTTGTGCTTTCATCTGAAG 1047
DB 712 TATGATTTCTGATGAAATCTTCAAGGGGCTTTCCGGGACTTGTGCTTTCATCTGAAG 771
QY 1048 ATGAGATGAGCGGCGAGACGACGTAGCAGAGTCCGAATA 1087
DB 772 TCCACATTTGAGCAACAAATCTCCATCGAATTCGTCA 811
RESULT 94
AAT90381
ID AAT90381 standard; cDNA; 1452 BP.
XX
XX AAT90381;
XX
XX 23-JAN-1998 (first entry)
XX
XX Rat methadone-specific opioid receptor MSOR cDNA.
XX
XX Methadone-specific opioid receptor; MSOR; rat; psychoactive drug; ss.
XX
XX Ratcus sp.
XX
XX US5658783-A.
XX
XX 19-AUG-1997.
XX
XX 08-NOV-1993; 93US-00149093.
XX
XX 08-NOV-1993; 93US-00149093.
XX
XX (UYOR-) UNIV OREGON HEALTH SCI.
XX
XX Civeilli O, Grandy DK, Bunzow JR;
XX
XX WPI; 1997-424240/39.
```


DR P-PSDB; AAM26582.

XX New isolated mammalian methadone-specific opioid receptor gene - used to
PT develop products for screening for compounds which can be used as
PT psychoactive drugs.

XX Claim 1; Col 17-20; 26pp; English.

XX This nucleotide sequence encodes a novel, claimed rat methadone-specific
CC opioid receptor (MSOR) (see AAM26582). It was isolated from a rat brain
CC library using degenerate primers (see AAT90382-83) based on the putative
CC 3rd and 7th transmembrane regions of a mouse delta-opioid receptor. Also
CC claimed are: (1) a hybridisation probe; (2) a recombinant expression
CC construct that is capable of expressing the MSOR in eukaryotic or
CC prokaryotic cell transformants; and (3) a transformed cell culture that
CC expresses the MSOR. The probes can be used to determine the pattern,
CC amount and extent of expression of the MSOR gene in various tissues of
CC mammals, including humans, as well as in the detection and diagnosis of
CC genetic disease, or the detection of novel related receptor genes

XX Sequence 1452 BP; 276 A; 414 C; 377 G; 385 T; 0 U; 0 Other;

Query Match 31.9%; Score 368; DB 2; Length 1452;

Best Local Similarity 63.3%; Pred. No. 3.2e-80;

Matches 601; Conservative 0; Mismatches 340; Indels 9; Gaps 2;

```

QY 153 GCGGCATCTCCCGCCATCCCGTCAATCAGCGGGCTTACTCCGTAGTTCGT 212
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 301 CCGCTTCCCGCCCTTGAGCTCAAGGTCACATCGGGGCTCATCTTGCTGTGCAT 360
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 213 CGTGGGCTTGAGGACATCGGTGTCATGTTGATCATCCGATACACAAGATGA 272
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 361 CCGGGGGCTCTGGGGAAGTCTGCTCATGATGATCTCTAGGACACCCAGATGA 420
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 273 GACAGCAACCAATTATTAATTAACCTGCTTGGAGATGCTTATTAATTAACA 332
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 421 GACAGTACCAATTATTAATTAATGAGACAGTGGATGATCCCTGTCTGTAC 480
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 333 CATGCCCTTTCAGATGAGTCTGATGAAATCTGCGCTTTGGGAGTGTCTG 392
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 481 ACTGCCCTTTCAGGAGCAGACATCTACTGGGCTTCTGCGCATTTGGGAAAG 540
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 393 CAAGATAGTAATTTCCATGATTAATTAACAAGATGTTACAGAGATCTTAC 452
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 541 CAAGATGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 600
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 453 GATGAGCGTGAACCGCTACATGCTGTCGCAACCCCGTGAAGGCTTTGAGCT 512
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 601 CATGAGCGTGAACCGCTATGTCGTCATGTCGCAACCCCGTGAAGGCTTTG 660
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 513 ACCCTTGAAGCAAGATCATCAATATCTGATCTGCTGCTGCTCATCTGTTG 572
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 661 ATTCAGCAAGGCCAGGCTTATGTCGCAATATGAGGCTTGGCTTCAAGTGT 720
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 573 CTCTGCAATAGCTCTTGGAGGACCAAGATGAGGAAAGCTGATGATGAGGTC 632
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 721 TCTGTGTCATATGAGTTCAGACAGT-----GAAATGAAGATGAGTGGCT 774
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 633 CTTCAGTTCAGATGATGATCTCTGTCGAGGAGCTTTCATGATGATGCTT 692
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 775 GGTGAGATTCCTGCGCCCTCAGAGCTATTGGGG---CCTGTATTTGGCAT 831
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 693 CATCTTGGCTTGTGATCTCTGCTCATCATCATCATGCTGTGTCACACCTG 752
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 832 CCTTTTTCCTTCATCATCTCTGTCGATCATCTCTGCTGCTTACAGCTCAT 891
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 753 GGTTCAGAGAGTGGCTCTCTTCTGCTCCGAGGAAAGATCGCAACCTGTG 812
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 892 AGCACTTGTGTGTGCTGTCTTTCAGGCTCCCGAGAGAGACCGAAACCTGT 951
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 813 GATCAGCAGATGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 872
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 952 TATCATCTGATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1011

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QY 873 CATATTCATCTGTGTGAGAGCTGTGGGAGACCTCCACAGACAGTCTCTCCAG 932
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1012 GGTGTGTGTCTGTGTTCAGAGAGCTGGGTTCAGCCAGGTATGAGACTGTCCAT 1071
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 933 CTATTACTTTCATCGCTTATGAGCTATPACCAAGATGACCTGAATCCATTC 992
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1072 CCGGAGCTTCTCAGACAGCCCTGGGCTATGTCAAGTGTCTCAATCCATTC 1131
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QY 993 CTTCCTTGTATGAAACTTCAACCGGTGTTTCCGGGACTTCTGCTTCACTGA 1052
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QY 1053 GATGAGCGGAGACAGACATGACAGAGTCCGAATACGTTCAAGATCTTG 1102
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DB 1192 CCGGAGATGACAGTTCATGATGATGTCGAGCATGTCACCAAGATTTTG 1241
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RESULT 95

AAT89585

ID AAT89585 standard; cDNA; 1452 BP.

AC AAT89585;

DT 12-JAN-1998 (first entry)

DE Rat orphanin FQ receptor cDNA clone LC132.

KW Orphanin FQ receptor; binding; locomotor disease; diagnosis; treatment;

KW opiate inhibitor; opiate induced hypothermia; drug design;

KW morphine induced analgesia; methadone specific opioid receptor; ss.

OS Rattus sp.

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Claim 5; Page 42-43; 68pp; English.

AAT89585 is rat orphanin FQ (OFQ) receptor cDNA clone LC132. Highly specific peptides that bind the OFQ receptor were identified as OFQ receptor inhibitors. The peptides can be used to antagonise a physiological effect of an opiate in an animal. The peptides antagonise opiate induced hypothermia and morphine induced analgesia in animals. They may also be used in the diagnosis and treatment of locomotor disease. The peptides may also be used in the design of a methadone specific opioid receptor (MSOR), in drug design and for the isolation of endogenous receptors for anti-opioid agonists and antagonists found in

CC plasma, serum, lymph, cerebrospinal fluid etc
XX Sequence 1452 BP; 276 A; 414 C; 377 G; 385 T; 0 U; 0 Other;

Query Match 31.9%; Score 368; DB 2; Length 1452;
Best Local Similarity 63.3%; Pred. No. 3.2e-80;
Matches 601; Conservative 0; Mismatches 340; Indels 9; Gaps 2;

QY 153 CGCGCAATCTCCCGGCATCCCGTCACTCAACGGGGGTCTACTCCGTAGTGTCT 212
DB 301 CGCCTTCTCGCCCTTGAAGGTACCACTCGGGGCTCATCTTGGCTGTGTCAT 360
QY 213 CGTGGGCTTGGGCACTCGCTGTGTCATGTTTGGTATCCGATACACAAAGATGA 272
DB 361 CGGGGGCTTCCGGGAATGCTGCTGATGTATGTGATCTCAGACACCAAGATGA 420
QY 273 GACAGCAACCAATTATTAATTTAACTGCTTTGGGAGATGCTTAACTACAAAC 332
DB 421 GACAGCTACCAATTATTAATTTAACTGACATGCTGATACCTGTCTTGTCTAAC 480
QY 333 CATGCCCTTTAGAGACGTCTACTGTATGTAATTCCTGGCCCTTTGGGGATGTCTGT 392
DB 481 ACTGCCCTTCCAGGGGACAGACATCTACTGGGCTTGGCCATTTGGGAAAGCACTTG 540
QY 393 CAAGATAGTAATTTCCATGATTACTACAACATGTTCAACAGCATCTTACCTTGACAT 452
DB 541 CAAGACTGTCAATGCTATGACTACTACAACATGTTTACAGACATTTACTCTGACCC 600
QY 453 GATGACGTGACCCGCTACATTCGCTGTGCCACCCCGTGAAGGCTTTGGACTTCGCAC 512
DB 601 CATGACCGTAGACCCCTATGTGGCTATCGCACCCCTATCCGTCCTTGAATGTTCCGAC 660
QY 513 ACCCTTGAAGGAAGATCATATATCTGCATCTGGCTGTGTGTCTATCTGTGGCAT 572
DB 661 ATCCAGCAAGCCCAAGCTGTTAATGTGGCCATATGGCCCTTCACTGTGGTGT 720
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QY 753 GGTCTCAAGAGCGTCCGGCTCTCTTCTGTGCTCCGAGAAAGATCGCAACTGCGTAG 812
DB 892 AGGACTGTGTGTCTCTCTCTTCAAGGCTCCGGGGAAGAACCGAAACTGTGGGG 951
QY 813 GATCAACGACTGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 872
DB 952 TATCACTGCACTGT 1011
QY 873 CATATTCATCTCTGT 932
DB 1012 GGT 1071
QY 933 CTATATCTTCTGATCGCTTAGGCTATATCAACAGTATGCTGAATCCCATCTCTACGC 992
DB 1072 CCGTGGCTTCTGCAAGCCCTGGGCTATGTCAACAGTTGTCTCATCTCTCTATGC 1131
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QY 1053 GATGAGCGGCGAGAGACTATGAGAGTCCGAATATACGTTCAAGATCTCG 1102
DB 1192 CCGGAGATGACGGTTTCTGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1241

RESULT 96
AAV56017
ID AAV56017 standard; cDNA; 1452 BP.

XX AC AAV56017;
XX AC AAV56017;
XX DT 08-DEC-1998 (first entry)
XX XX

DE Rat methadone-specific opioid receptor (MSOR) protein encoding cDNA.

KW MSOR; methadone-specific opioid receptor; screening assay; inhibition;
KW psychotropic agent; therapeutic drug; ss.

OS Rattus sp.

PH Key Location/Qualifiers
FT 5'UTR 1..181
FT CDS /tag= a
FT 182..1285
FT /tag= b
FT /product= "Rat MSOR"
FT 1283..1452
FT 3'UTR /tag= c

PN US5821067-A.
PN 13-OCT-1998.

PF 15-AUG-1997; 97US-00911245.

PR 08-NOV-1993; 93US-00149093.

PA (OREG-) STATE OF OREGON.

PI Civeili O, Bunzow JR, Grandy DK;

DR WPI, 1998-567655/48.

DR P-PSDB; AAM80549.

PT Screening assays for opioid receptor ligands - using cells expressing

PT recombinant methadone-specific opioid receptor.

PS Example 1; Fig 1A-C; 26pp; English.

XX CC This cDNA encodes a rat methadone-specific opioid receptor (MSOR)
XX CC protein. A recombinant expression construct containing the MSOR encoding
XX CC nucleic acid can be used to transform a host cell for the recombinant
XX CC production of the protein. This can be used in the screening assays of
XX CC the invention for screening for a compound that binds to a mammalian
XX CC MSOR. The method is for quantitatively measuring inhibition of the
XX CC methadone-specific opioid receptor, which is useful for screening
XX CC psychotropic agents for use as therapeutic drugs which do not have
XX CC deleterious side effects

SQ Sequence 1452 BP; 276 A; 414 C; 377 G; 385 T; 0 U; 0 Other;

Query Match 31.9%; Score 368; DB 2; Length 1452;
Best Local Similarity 63.3%; Pred. No. 3.2e-80;
Matches 601; Conservative 0; Mismatches 340; Indels 9; Gaps 2;

QY 153 CGCGCAATCTCCCGGCATCCCGTCACTCAACGGGGGTCTACTCCGTAGTGTCT 212
DB 301 CGCCTTCTCGCCCTTGAAGGTACCACTCGGGGCTCATCTTGGCTGTGTCAT 360
QY 213 CGTGGGCTTGGGCACTCGCTGTGTCATGTTTGGTATCCGATACACAAAGATGA 272
DB 361 CGGGGGCTTCCGGGAATGCTGCTGATGTATGTGATCTCAGACACCAAGATGA 420
QY 273 GACAGCAACCAATTATTAATTTAACTGCTTTGGGAGATGCTTAACTACTACAAAC 332
DB 421 GACAGCTACCAATTATTAATTTAACTGACATGCTGATACCTGTCTTGTCTAAC 480
QY 333 CATGCCCTTTAGAGACGTCTACTGTATGTAATTCCTGGCCCTTTGGGGATGTCTGTG 392

Search completed: August 31, 2004, 03:56:22
Job time : 554 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 31, 2004, 02:26:37 ; Search time 602 Seconds
(without alignments)
9434.096 Million cell updates/sec

Title: US-09-904-584-1

Perfect score: 1154
Sequence: 1 atgagatccccgacccagat.....ccagatgactagctgtgga 1154

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3237270 seqs, 2460713050 residues

Total number of hits satisfying chosen parameters: 6474540

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database :

Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	1152.4	99.9	1154	12	US-09-904-584-4
5	1152.4	99.9	1154	12	US-09-904-584-5
6	1152.4	99.9	1154	12	US-09-904-584-6
7	1152.4	99.9	1154	12	US-09-904-584-7
8	1146	99.3	1182	15	US-10-225-567A-147
9	1146	99.3	1182	15	US-10-345-680-19
10	1146	99.3	1182	16	US-10-305-720-117
11	1143	99.3	1182	17	US-10-283-975A-80
12	1143	99.0	1143	15	US-10-318-661-1
13	1137.8	98.6	1284	15	US-10-318-661-3
14	1135	98.4	1143	15	US-10-345-680-21

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17	996.2	86.3	1275	15	US-10-318-661-7	Sequence 7, Appli
18	981	85.0	1875	15	US-10-318-661-13	Sequence 13, Appli
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27	446.4	38.7	1618	10	US-09-841-720-1	Sequence 3, Appli
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31	434.8	37.7	1245	15	US-10-080-917-8	Sequence 8, Appli
32	434.8	37.7	1388	15	US-10-185-083-26	Sequence 26, Appli
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34	434.8	37.7	1431	15	US-10-080-917-6	Sequence 6, Appli
35	434.8	37.7	2149	15	US-10-080-917-12	Sequence 12, Appli
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41	432.6	37.5	2851	15	US-10-185-083-21	Sequence 21, Appli
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47	432.4	37.5	1365	9	US-09-761-962-11	Sequence 11, Appli
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49	432.4	37.5	1373	15	US-10-185-083-51	Sequence 51, Appli
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Db 421 AACATGTTACCAACGATCTTCACTTGACATGATGAGGTGACCGCTACCTTCCGTG 480
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RESULT 3
US-09-904-584-3
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; Publication No. US2004009704A1
; GENERAL INFORMATION:
; APPLICANT: Kreek, Mary Jeanne
; APPLICANT: Yulev, Vadim
; APPLICANT: Laforge, Karl Steven
; TITLE OF INVENTION: Alleles of the Human Kappa Opioid
; TITLE OF INVENTION: Receptor Gene, Diagnostic Methods Using Said Alleles, and
; TITLE OF INVENTION: Methods of Treatment Based Thereon
; FILE REFERENCE: 600-1-285X
; CURRENT APPLICATION NUMBER: US/09/904,584
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 60/218,300
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1154
; TYPE: DNA
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 1153; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 661 TGGTGGGAACTCTTCATGAAAGATGCGCTTCCTTCATCTTTGCTGCTGCTGCTGCTG 720
Db 661 TGGTGGGAACTCTTCATGAAAGATGCGCTTCCTTCATCTTTGCTGCTGCTGCTGCTG 720
Qy 721 ATCATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
Db 721 ATCATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
Qy 781 GGCTCCCGAAGAAAGATGCAACCTGCGTAGATCACAAGACTGCTGCTGCTGCTGCTG 840
Db 781 GGCTCCCGAAGAAAGATGCAACCTGCGTAGATCACAAGACTGCTGCTGCTGCTGCTG 840
Qy 841 GCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
Db 841 GCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
Qy 901 AGCACTCCCGACAGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
Db 901 AGCACTCCCGACAGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
Qy 961 ACCAAGCTAGGCTGATCCCATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
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Db      961  ACCAAGTAGAGCTGATCCATCTCTAGACCTTTCTTGATGAAACCTCAAGCGGTG 1020
Qy      1021  TTCGGGAGATTCTGCTTTTCCACTGAAGATGAGATGAGCGGAGAGCACTAGCAGATC 1080
Db      1021  TTCGGGAGATTCTGCTTTTCCACTGAAGATGAGATGAGCGGAGAGCACTAGCAGATC 1080
Qy      1081  CGAAATPACAGTTGAGGATCTGCTTACCTGAGGAGCATGAGATGAGATTAACACAGTA 1140
Db      1081  CGAAATPACAGTTGAGGATCTGCTTACCTGAGGAGCATGAGATGAGATTAACACAGTA 1140
Qy      1141  TGACTAGTGTGGA 1154
Db      1141  TGACTAGTGTGGA 1154

RESULT 4
US-09-904-584-4
; Sequence 4, Application US/0904584
; Publication No. US20040097704A1
; GENERAL INFORMATION:
; APPLICANT: Kreek, Mary Jeanne
; APPLICANT: Yuforov, Vadim
; APPLICANT: LaForge, Karl Steven
; TITLE OF INVENTION: Alleles of the Human Kappa Opioid
; TITLE OF INVENTION: Receptor Gene, Diagnostic Methods Using Said Alleles, and
; TITLE OF INVENTION: Methods of Treatment Based Thereon
; FILE REFERENCE: 600-1-285N
; CURRENT APPLICATION NUMBER: US/09/904,584
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 60/218,300
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FaSTSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1154
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-904-584-4

Query Match      99.9%; Score 1152.4; DB 12; Length 1154;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1153; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1  ATGGAATCTCCCGATCCAGATCTTTCCGCGGAGAGCCGCGCTTACCTGCGCCCGGAGCGCC 60
Db      1  ATGGAATCTCCCGATCCAGATCTTTCCGCGGAGAGCCGCGCTTACCTGCGCCCGGAGCGCC 60
Qy      61  TGCCTGCCCCCAACAGACGAGCGCTGTGTTCCCGGCTGGGCGGAGCCGAGCCGAGCAACGAGC 120
Db      61  TGCCTGCCCCCAACAGACGAGCGCTGTGTTCCCGGCTGGGCGGAGCCGAGCCGAGCAACGAGC 120
Qy      121  AGCGCGCGGCTGGAAGAGCGCGAGCTGAGAGCCCGCGCACATCTCCCGGCAATCCCGATC 180
Db      121  AGCGCGCGGCTGGAAGAGCGCGAGCTGAGAGCCCGCGCACATCTCCCGGCAATCCCGATC 180
Qy      181  ATCATCAAGCGCGCTCTACTCCGATGTTGCTGCTGCGGCTTGGTGGGCAACTGCGTGTGTC 240
Db      181  ATCATCAAGCGCGCTCTACTCCGATGTTGCTGCTGCGGCTTGGTGGGCAACTGCGTGTGTC 240
Qy      241  ATGTCATCAAGCGCGCTCTACTCCGATGTTGCTGCTGCGGCTTGGTGGGCAACTGCGTGTGTC 240
Db      241  ATGTCATCAAGCGCGCTCTACTCCGATGTTGCTGCTGCGGCTTGGTGGGCAACTGCGTGTGTC 240
Qy      301  CTGGCTTTGGAGATGCTTTAGTTACTACTAACCATGCGCTTTCAAGATGCGTCTACTTGG 360
Db      301  CTGGCTTTGGAGATGCTTTAGTTACTACTAACCATGCGCTTTCAAGATGCGTCTACTTGG 360
Qy      361  ATGAATTTCTGGCTTTTGGGATGCTGCTGCAAGATAGTAATTTCCATTGATTAATAC 420
Db      361  ATGAATTTCTGGCTTTTGGGATGCTGCTGCAAGATAGTAATTTCCATTGATTAATAC 420
Qy      421  AACATGTTACACAGATCTTCACTTGAACATGATGAGGTGAGACCGGTACATTCGCCGTG 480
Db      421  AACATGTTACACAGATCTTCACTTGAACATGATGAGGTGAGACCGGTACATTCGCCGTG 480
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Db      421  AACATGTTACACAGATCTTCACTTGAACATGATGAGGTGAGACCGGTACATTCGCCGTG 480
Qy      481  TGCACACCCCGTGAAGGCTTTGAGATTTCCGACACCTTTGAAGGCAAGATCATCAATATC 540
Db      481  TGCACACCCCGTGAAGGCTTTGAGATTTCCGACACCTTTGAAGGCAAGATCATCAATATC 540
Qy      541  TGCATCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
Db      541  TGCATCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
Qy      601  GTCAAGGGAAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
Db      601  GTCAAGGGAAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
Qy      661  TGTGGGAGCTCTTCAATGAAGATGCGCTTCTCATCTTTGCTTGTGCTGCTGCTGCTGCTG 720
Db      661  TGTGGGAGCTCTTCAATGAAGATGCGCTTCTCATCTTTGCTTGTGCTGCTGCTGCTGCTG 720
Qy      721  ATCATCATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Db      721  ATCATCATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Qy      781  GGTCTCCGAGAGAAAGATGCAACCTGCTGATGATGATGATGATGATGATGATGATGATGATG 840
Db      781  GGTCTCCGAGAGAAAGATGCAACCTGCTGATGATGATGATGATGATGATGATGATGATGATG 840
Qy      841  GCAATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
Db      841  GCAATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
Qy      901  AGCACTCCCAAGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
Db      901  AGCACTCCCAAGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
Qy      961  ACCAAGTAGAGCTGATCCATCTCTAGACCTTTCTTGATGAAACCTCAAGCGGTG 1020
Db      961  ACCAAGTAGAGCTGATCCATCTCTAGACCTTTCTTGATGAAACCTCAAGCGGTG 1020
Qy      1021  TTCGGGAGATTCTGCTTTTCCACTGAAGATGAGATGAGCGGAGAGCACTAGCAGATC 1080
Db      1021  TTCGGGAGATTCTGCTTTTCCACTGAAGATGAGATGAGCGGAGAGCACTAGCAGATC 1080
Qy      1081  CGAAATPACAGTTGAGGATCTGCTTACCTGAGGAGCATGAGATGAGATTAACACAGTA 1140
Db      1081  CGAAATPACAGTTGAGGATCTGCTTACCTGAGGAGCATGAGATGAGATTAACACAGTA 1140
Qy      1141  TGACTAGTGTGGA 1154
Db      1141  TGACTAGTGTGGA 1154

RESULT 5
US-09-904-584-5
; Sequence 5, Application US/0904584
; Publication No. US20040097704A1
; GENERAL INFORMATION:
; APPLICANT: Kreek, Mary Jeanne
; APPLICANT: Yuforov, Vadim
; APPLICANT: LaForge, Karl Steven
; TITLE OF INVENTION: Alleles of the Human Kappa Opioid
; TITLE OF INVENTION: Receptor Gene, Diagnostic Methods Using Said Alleles, and
; TITLE OF INVENTION: Methods of Treatment Based Thereon
; FILE REFERENCE: 600-1-285N
; CURRENT APPLICATION NUMBER: US/09/904,584
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 60/218,300
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FaSTSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1154
; TYPE: DNA
; ORGANISM: homo sapiens
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US-09-904-584-5

Query Match 99.9%; Score 1152.4; DB 12; Length 1154;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1153; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY 1 ATGAGCTCCCGCATCAGATCTTCCGCGGGAGCGCGGCGCTTACCGCGGCGCCGAGCGGC 60
DB 1 ATGAGCTCCCGCATCAGATCTTCCGCGGGAGCGCGGCGCTTACCGCGGCGCCGAGCGGC 60
OY 61 TGCCTGCCCCCAACAGACAGCGCCCTGTTCCCGGCTGGGCGAGCCGACAGCAACGCGC 120
DB 61 TGCCTGCCCCCAACAGACAGCGCCCTGTTCCCGGCTGGGCGAGCCGACAGCAACGCGC 120
OY 121 AGCGCGGCTGGAGAGACGCGAGCTGGAGCGCGCGCAATCTCCCGGCGCTCCCGGTC 180
DB 121 AGCGCGGCTGGAGAGACGCGAGCTGGAGCGCGCGCAATCTCCCGGCGCTCCCGGTC 180
OY 181 ATCATCACGCGCGGTCTACTCCGTAAGTGTGTCGTGGGCTTGGTGGGCACTCGCTGGTC 240
DB 181 ATCATCACGCGCGGTCTACTCCGTAAGTGTGTCGTGGGCTTGGTGGGCACTCGCTGGTC 240
OY 241 ATGTCGTGATCATCCGATACCAAGATGAAGAGACAGCAACCAATTTACATATTTAAC 300
DB 241 ATGTCGTGATCATCCGATACCAAGATGAAGAGACAGCAACCAATTTACATATTTAAC 300
OY 301 CTGGCTTTGGGAGATGCTTACTTAATAACCATGSCCTTTAGAGATACGGTCTACTTG 360
DB 301 CTGGCTTTGGGAGATGCTTACTTAATAACCATGSCCTTTAGAGATACGGTCTACTTG 360
OY 361 ATGAATTCCTGGACCTTTTGGGGATGTGTCGCAAGATAGTAATTTCCATGATTAATAC 420
DB 361 ATGAATTCCTGGACCTTTTGGGGATGTGTCGCAAGATAGTAATTTCCATGATTAATAC 420
OY 421 AACATGTTACACAGCATCTTACCTTGACCATGATGAGCGTGACCGCTACATTCGCGTG 480
DB 421 AACATGTTACACAGCATCTTACCTTGACCATGATGAGCGTGACCGCTACATTCGCGTG 480
OY 481 TGGCAACCCCGTGAAGGCTTTGGACCTTCGCAACACCTTGAAGGCAAGATCATCAATATC 540
DB 481 TGGCAACCCCGTGAAGGCTTTGGACCTTCGCAACACCTTGAAGGCAAGATCATCAATATC 540
OY 541 TGCATCTGGCTGTGCTGTGATCTGTGGCATCTGTGGCATCTGTGGCATCTGTGGAGGACCAA 600
DB 541 TGCATCTGGCTGTGCTGTGATCTGTGGCATCTGTGGCATCTGTGGCATCTGTGGAGGACCAA 600
OY 601 GTGAGGGAAGAGCTGATGTCATTAAGTGTCTTTCGACGTTCCGATGATGATCTACTCC 660
DB 601 GTGAGGGAAGAGCTGATGTCATTAAGTGTCTTTCGACGTTCCGATGATGATCTACTCC 660
OY 661 TGGTGGGACCTTTCATGAAGATCTGCGCTTTCATCTTGGCTTGTGATCTCTGTCTTC 720
DB 661 TGGTGGGACCTTTCATGAAGATCTGCGCTTTCATCTTGGCTTGTGATCTCTGTCTTC 720
OY 721 ATCATCATCTGTGTGTACACCTGATGATCTGCGCTCAAGAGGCTCGGCTCTTCT 780
DB 721 ATCATCATCTGTGTGTACACCTGATGATCTGCGCTCAAGAGGCTCGGCTCTTCT 780
OY 781 GGTCTCCGAGAGAAAGATCGCAACTGGGTAGATACACAGATCTGCTGTGTGTGTG 840
DB 781 GGTCTCCGAGAGAAAGATCGCAACTGGGTAGATACACAGATCTGCTGTGTGTGTG 840
OY 841 GCAAGCTTCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
DB 841 GCAAGCTTCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
OY 901 AGCACTTCCCAAGACAGAGCTGCTCTCCAGCTATTAATTTCTGATGCTTGAAGCTAT 960
DB 901 AGCACTTCCCAAGACAGAGCTGCTCTCCAGCTATTAATTTCTGATGCTTGAAGCTAT 960
OY 961 ACCAAGCTAGCTGAATCCCATTTCTTAAGCTTTTGTGATGAATACTTCAAGCGGTGT 1020
DB 961 ACCAAGCTAGCTGAATCCCATTTCTTAAGCTTTTGTGATGAATACTTCAAGCGGTGT 1020
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OY 1021 TTCCGGGACCTTCTGCTTCCACTGAAGTGAAGTGAAGCGGCAAGACATTAAGAGATC 1080
DB 1021 TTCCGGGACCTTCTGCTTCCACTGAAGTGAAGTGAAGCGGCAAGACATTAAGAGATC 1080
OY 1081 CGAAATACAGTTCCAGATCTGCTTACCTGAGGAGCATGATGGAGTAAATTAACAGTA 1140
DB 1081 CGAAATACAGTTCCAGATCTGCTTACCTGAGGAGCATGATGGAGTAAATTAACAGTA 1140
OY 1141 TGACTAGTGTGGA 1154
DB 1141 TGACTAGTGTGGA 1154
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RESULT 6

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US-09-904-584-6
; Sequence 6, Application US/09904584
; Publication No. US20040097704A1
; GENERAL INFORMATION:
; APPLICANT: Kreek, Mary Jeanne
; APPLICANT: Yufeyov, Vadim
; TITLE OF INVENTION: LaForge, Karl Steven
; TITLE OF INVENTION: Receptor Gene, Diagnostic Methods using Said Alleles, and
; TITLE OF INVENTION: Methods of Treatment Based Thereon
; FILE REFERENCE: 600-1-285N
; CURRENT APPLICATION NUMBER: US/09/904,584
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 60/218,300
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1154
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-904-584-6
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Query Match 99.9%; Score 1152.4; DB 12; Length 1154;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1153; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY 1 ATGAGCTCCCGCATCAGATCTTCCGCGGGAGCGCGGCGCTTACCGCGGCGCCGAGCGGC 60
DB 1 ATGAGCTCCCGCATCAGATCTTCCGCGGGAGCGCGGCGCTTACCGCGGCGCCGAGCGGC 60
OY 61 TGCCTGCCCCCAACAGACAGCGCCCTGTTCCCGGCTGGGCGAGCCGACAGCAACGCGC 120
DB 61 TGCCTGCCCCCAACAGACAGCGCCCTGTTCCCGGCTGGGCGAGCCGACAGCAACGCGC 120
OY 121 AGCGCGGCTGGAGAGACGCGAGCTGGAGCGCGCGCAATCTCCCGGCGATCCGCGTC 180
DB 121 AGCGCGGCTGGAGAGACGCGAGCTGGAGCGCGCGCAATCTCCCGGCGATCCGCGTC 180
OY 181 ATCATCACGCGCGGTCTACTCCGTAAGTGTGTCGTGGGCTTGGTGGGCACTCGCTGGTC 240
DB 181 ATCATCACGCGCGGTCTACTCCGTAAGTGTGTCGTGGGCTTGGTGGGCACTCGCTGGTC 240
OY 241 ATGTCGTGATCATCCGATACCAAGATGAAGAGACAGCAACCAATTTACATATTTAAC 300
DB 241 ATGTCGTGATCATCCGATACCAAGATGAAGAGACAGCAACCAATTTACATATTTAAC 300
OY 301 CTGGCTTTGGGAGATGCTTACTTAATAACCATGSCCTTTAGAGATACGGTCTACTTG 360
DB 301 CTGGCTTTGGGAGATGCTTACTTAATAACCATGSCCTTTAGAGATACGGTCTACTTG 360
OY 361 ATGAATTCCTGGACCTTTTGGGGATGTGTCGCAAGATAGTAATTTCCATGATTAATAC 420
DB 361 ATGAATTCCTGGACCTTTTGGGGATGTGTCGCAAGATAGTAATTTCCATGATTAATAC 420
OY 421 AACATGTTACACAGCATCTTACCTTGACCATGATGAGCGTGACCGCTACATTTGCGGTG 480
DB 421 AACATGTTACACAGCATCTTACCTTGACCATGATGAGCGTGACCGCTACATTTGCGGTG 480
```


QY 1021 TTCGGGACCTTCTGCTTCCACTGAGATGAGATGAGCGGACAGACCTAGACAGATC 1080
DB 1021 TTCGGGACCTTCTGCTTCCACTGAGATGAGATGAGCGGACAGACCTAGACAGATC 1080
QY 1081 CGAAATACAGTTGAGGATCTGCTTAACTGAGGAGCATGATGAGATGATTAACCACTA 1140
DB 1081 CGAAATACAGTTGAGGATCTGCTTAACTGAGGAGCATGATGAGATGATTAACCACTA 1140
QY 1141 TGACCTAGCTGTGGA 1154
DB 1141 TGACCTAGCTGTGGA 1154

RESULT 8
US-10-225-567A-147
; Sequence 147, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenn C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 147
; LENGTH: 1182
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-225-567A-147

Query Match 99.3%; Score 1146; DB 15; Length 1182;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1149; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ATGACTCCCGATCCAGATCTTCCGCGGGAGCCGGCCCTACTGCGCCCGAGCGCC 60
DB 14 ATGAAATCCCGATCCAGATCTTCCGCGGGAGCCGGCCCTACTGCGCCCGAGCGCC 73
QY 61 TGCCGCGCCCGCAAGAGAGCGCTGTTCCCGGCTGGGCGAGCCCGCAAGAGAGGCG 120
DB 74 TGCCGCGCCCGCAAGAGAGCGCTGTTCCCGGCTGGGCGAGCCCGCAAGAGAGGCG 133
QY 121 AGCGCGGCTCGAGAGAGCGAGCTGAGCGCCGCGACATCTCCCGGCAATCCCGGTC 180
DB 134 AGCGCGGCTCGAGAGAGCGAGCTGAGCGCCGCGACATCTCCCGGCAATCCCGGTC 193
QY 181 ATCATCAGCGGCTCTACTCCGTAGTGTTCGTGCTGGGCTTGTGGGCACTCGCTGTC 240
DB 194 ATCATCAGCGGCTCTACTCCGTAGTGTTCGTGCTGGGCTTGTGGGCACTCGCTGTC 253
QY 241 ATGTCGATCATCCGATACCAAAAGATGAAGAGAGCAACCAATTTACATATTTTAC 300
DB 254 ATGTCGATCATCCGATACCAAAAGATGAAGAGAGCAACCAATTTACATATTTTAC 313
QY 301 CTGCGTTGGAGATGCTTTAGTTACTTAAACAATGCCCCCTTTCAGAGTACGCTACTTG 360
DB 314 CTGCGTTGGAGATGCTTTAGTTACTTAAACAATGCCCCCTTTCAGAGTACGCTACTTG 373
QY 361 ATGAATCTGGGCTTTTGGGAGTGTCTGTGCAAGATGATTAATTTCCATTGATTACTAC 420
DB 374 ATGAATCTGGGCTTTTGGGAGTGTCTGTGCAAGATGATTAATTTCCATTGATTACTAC 433
QY 421 AACATGTTACAGAGATCTTACCTTGACCAATGATGAGCGGAGCCGCTACATGGCGGTG 480
DB 434 AACATGTTACAGAGATCTTACCTTGACCAATGATGAGCGGAGCCGCTACATGGCGGTG 493
QY 481 TGCCACCCCGTAGAGGCTTTGGAATTCGCGACACCCCTTGAAGGCAAAAGATCATCATATC 540

DB 494 TGCCACCCCGTAGAGGCTTTGGAATTCGCGACACCCCTTGAAGGCAAAAGATCATCATATC 553
QY 541 TGCAATCTGCTGCTGTGTCTATCTGTTGGCATCTCTGCAATATGCTTTGGAGGACCAAA 600
DB 554 TGCAATCTGCTGCTGTGTGTCTATCTGTTGGCATCTCTGCAATATGCTTTGGAGGACCAAA 613
QY 601 GTCAAGGAGAGAGCTGATGTCATTTGAGTGTCTTGGAGTTCCAGATGATGATCTACTCC 660
DB 614 GTCAAGGAGAGAGCTGATGTCATTTGAGTGTCTTGGAGTTCCAGATGATGATCTACTCC 673
QY 661 TGGTGGACCTTTTATGAAGATGCGGTCTTTCATCTTTTGGCTTGTGATCTGTCTC 720
DB 674 TGGTGGACCTTTTATGAAGATGCGGTCTTTCATCTTTTGGCTTGTGATCTGTCTC 733
QY 721 ATCATCATCTGCTCTACACCTTATGATCTGTGCTCAAGACGCTCCGCTCTTCT 780
DB 734 ATCATCATCTGCTCTACACCTTATGATCTGTGCTCAAGACGCTCCGCTCTTCT 793
QY 781 GGCTCCGAGAGAAAGATCGCACTGTGATGATCAACAGACTGTCTGTGTGTG 840
DB 794 GGCTCCGAGAGAAAGATCGCACTGTGATGATCAACAGACTGTCTGTGTGTG 853
QY 841 GCACTCTTCTGCTGTCTGACTCCCATTCATCATATTCATCTGTGTGAGGCTCTG 900
DB 854 GCGGTTTTCGTGCTGTGACTCCCATTCATCATATTCATCTGTGTGAGGCTCTG 913
QY 901 AGCACTTCCACAGACAGCTGCTCTCCAGCTATTAATCTTCCATCTGCTTATG 960
DB 914 AGCACTTCCACAGACAGCTGCTCTCCAGCTATTAATCTTCCATCTGCTTATG 973
QY 961 ACCAAGATAGCTGAATCCCATCTCTACAGCTTCTTGTGTAAGAACTTCAAGCGGTGT 1020
DB 974 ACCAAGATAGCTGAATCCCATCTCTACAGCTTCTTGTGTAAGAACTTCAAGCGGTGT 1033
QY 1021 TTCGGGACCTTCTGCTTCCACTGAGATGAGATGAGCGGACAGACCTAGACAGTCTC 1080
DB 1034 TTCGGGACCTTCTGCTTCCACTGAGATGAGATGAGCGGACAGACCTAGACAGTCTC 1093
QY 1081 CGAAATACAGTTGAGGATCTGCTTAACTGAGGAGCATGAGGATGATTAACCACTA 1140
DB 1094 CGAAATACAGTTGAGGATCTGCTTAACTGAGGAGCATGAGGATGATTAACCACTA 1153
QY 1141 TGACTAGCTGTGGA 1154
DB 1154 TGACTAGCTGTGGA 1167

RESULT 9
US-10-345-680-19
; Sequence 19, Application US/10345680
; Publication No. US20030148394A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Silos-Santiago, Immaculada
; APPLICANT: Venkateswarlu, Karicheti
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,
; TITLE OF INVENTION: 12303, 985, 11237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
; FILE REFERENCE: MP102-012P1NM OMNI
; CURRENT APPLICATION NUMBER: US/10/345,680
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US 60/349,511
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/360,500
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/365,041
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/374,063
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/403,468
; PRIOR FILING DATE: 2002-08-14

PRIOR APPLICATION NUMBER: US 60/414,262
PRIOR FILING DATE: 2002-09-27
PRIOR APPLICATION NUMBER: US 60/419,986
PRIOR FILING DATE: 2002-10-21
PRIOR APPLICATION NUMBER: US 60/423,809
PRIOR FILING DATE: 2002-11-05
PRIOR APPLICATION NUMBER: US 60/429,797
PRIOR FILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 66
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 19
LENGTH: 1182
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (14) ... (1156)
US-10-345-680-19

Query Match 99.3%; Score 1146; DB 15; Length 1182;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1149; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ATGAACTCCCGATCCAGATCTTCGCGGGAGAGCCGCCCTTACCTGCGCCCGAGCGCC 60
DB 14 ATGAATCCCGATTCAGATCTTCGCGGGAGAGCTGGCCCTTACCTGCGCCCGAGCGCC 73
QY 61 TGCCTGCCCCCAACAGAGCGCCCTGCTTCCCGCTGGCGGAGCCCGAGCAAGCGGC 120
DB 74 TGCCTGCCCCCAACAGAGCGCCCTGCTTCCCGCTGGCGGAGCCCGAGCAAGCGGC 133
QY 121 AGCGCGGCTCGAGAGAGCGAGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGG 180
DB 134 AGCGCGGCTCGAGAGAGCGAGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGG 193
QY 181 ATCATCAGGCGGCTTACTCCGTAAGTGTGCTGCGGAGCGCGGAGCGCGGAGCGCGG 240
DB 194 ATCATCAGGCGGCTTACTCCGTAAGTGTGCTGCGGAGCGCGGAGCGCGGAGCGCGG 253
QY 241 ATGTTTCGATCATCCGATACCAAAAGATGAAGAGCAACCAATTTACATATTAAAC 300
DB 254 ATGTTTCGATCATCCGATACCAAAAGATGAAGAGCAACCAATTTACATATTAAAC 313
QY 301 CTGGCTTGGAGAGATGCTTGAATTAACAACCAATGAGCGCTTACGCTACTTG 360
DB 314 CTGGCTTGGAGAGATGCTTGAATTAACAACCAATGAGCGCTTACGCTACTTG 373
QY 361 ATGAATTCCTGAGCTTTTGGGAGATGCTGTCAGAGATGAATTTCCATTGATTAC 420
DB 374 ATGAATTCCTGAGCTTTTGGGAGATGCTGTCAGAGATGAATTTCCATTGATTAC 433
QY 421 AACATGTTCAACAGATCTTCACTTGAACATGATGAGCGTGAGCGCTTACATGCGGTG 480
DB 434 AACATGTTCAACAGATCTTCACTTGAACATGATGAGCGTGAGCGCTTACATGCGGTG 493
QY 481 TGGCAACCCCGGAGAGCTTGGAGATTCGCGACACCCCTTGAAGGCAAAATATCAATATC 540
DB 494 TGGCAACCCCGGAGAGCTTGGAGATTCGCGACACCCCTTGAAGGCAAAATATCAATATC 553
QY 541 TGCATTCGAGCTGCTGCTCATCTGTTGGCATCTTTCGAAATAGTCTTGGAGGCAACAA 600
DB 554 TGCATTCGAGCTGCTGCTCATCTGTTGGCATCTTTCGAAATAGTCTTGGAGGCAACAA 613
QY 601 GTCAGGGAAGAGCTGATGATGAAGTGTCTTGGCATGCTTCCAGATGATGATGATCTCC 660
DB 614 GTCAGGGAAGAGCTGATGATGAAGTGTCTTGGCATGCTTCCAGATGATGATGATCTCC 673
QY 661 TGGTGGAGCTCTTCATGAAGTGTGCTTCACTTTCGCTTGTGATGATGATGATGATGAT 720
DB 674 TGGTGGAGCTCTTCATGAAGTGTGCTTCACTTTCGCTTGTGATGATGATGATGATGAT 733
QY 721 ATCATCATGCTGCTGATACACCTGATGATGATGATGATGATGATGATGATGATGATGAT 780

DB 734 ATCATCATGCTGCTGATACACCTGATGATGATGATGATGATGATGATGATGATGATGAT 793
QY 761 GAGTCCCGAGAGAAAGATGCAACCTGGAGATGATGATGATGATGATGATGATGATGATGAT 840
DB 794 GAGTCCCGAGAGAAAGATGCAACCTGGAGATGATGATGATGATGATGATGATGATGATGAT 853
QY 841 GAGTCTTGTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
DB 854 GAGTCTTGTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 913
QY 901 AGCACTTCCAGAGAGAGCTGCTTTCAGAGATGATGATGATGATGATGATGATGATGATGAT 960
DB 914 AGCACTTCCAGAGAGAGCTGCTTTCAGAGATGATGATGATGATGATGATGATGATGATGAT 973
QY 961 ACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
DB 974 ACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1033
QY 1021 TTCCGGAGCTTCTGCTTCACTGAGAGATGATGATGATGATGATGATGATGATGATGATGAT 1080
DB 1034 TTCCGGAGCTTCTGCTTCACTGAGAGATGATGATGATGATGATGATGATGATGATGATGAT 1093
QY 1081 CGAAATACAGTTCAAGATCTGCTTCACTGAGAGATGATGATGATGATGATGATGATGATGAT 1140
DB 1094 CGAAATACAGTTCAAGATCTGCTTCACTGAGAGATGATGATGATGATGATGATGATGATGAT 1153
QY 1141 TGACTAGTGTGGA 1154
DB 1154 TGACTAGTGTGGA 1167

RESULT 10
US-10-305-720-1417
Sequence 1417, Application US/10305720
Publication No. US20040010136A1
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice K.; Seilheimer, Jeffrey J.
TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression
FILE REFERENCE: PA-0002-1 CON
CURRENT APPLICATION NUMBER: US/10/305,720
PRIOR FILING DATE: 2002-11-26
PRIOR APPLICATION NUMBER: 09/016,434
NUMBER OF SEQ ID NOS: 1490
SOFTWARE: PERL Program
SEQ ID NO 1417
LENGTH: 1182
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc. feature
OTHER INFORMATION: GenBank ID No. US20040010136A1 9532059
US-10-305-720-1417

Query Match 99.3%; Score 1146; DB 16; Length 1182;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1149; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ATGAACTCCCGATCCAGATCTTCGCGGGAGAGCCGCCCTTACCTGCGCCCGAGCGCC 60
DB 14 ATGAATCCCGATTCAGATCTTCGCGGGAGAGCTGGCCCTTACCTGCGCCCGAGCGCC 73
QY 61 TGCCTGCCCCCAACAGAGCGCCCTGCTTCCCGCTGGCGGAGCCCGAGCAAGCGGC 120
DB 74 TGCCTGCCCCCAACAGAGCGCCCTGCTTCCCGCTGGCGGAGCCCGAGCAAGCGGC 133
QY 121 AGCGCGGCTCGAGAGAGCGAGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGG 180
DB 134 AGCGCGGCTCGAGAGAGCGAGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGG 193
QY 181 ATCATCAGGCGGCTTACTCCGTAAGTGTGCTGCGGAGCGCGGAGCGCGGAGCGCGG 240
DB 194 ATCATCAGGCGGCTTACTCCGTAAGTGTGCTGCGGAGCGCGGAGCGCGGAGCGCGG 253

Db 734 ATCATCATGTCGTCTGACACCTGATGATTCCTGCTCTCAAGAGCGCTCGCTCTTCT 793
Qy 781 GGCCTCCGAGAGAAAGATCGCAACCTGGTAGGATCACAGACTGCTCTGCTGGTGGTG 840
Db 794 GGCCTCCGAGAGAAAGATCGCAACCTGGTAGGATCACAGACTGCTCTGCTGGTGGTG 853
Qy 841 GCAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
Db 854 GCGGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 913
Qy 901 AGCACTCTCCACAGACAGCTGCTCTCTCCAGCTATTAATCTTGATGCTGCTTAACTAT 960
Db 914 AGCACTCTCCACAGACAGCTGCTCTCTCCAGCTATTAATCTTGATGCTGCTTAACTAT 973
Qy 961 ACCAAGCTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
Db 974 ACCAAGCTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1033
Qy 1021 TTCCGGGACTTCTGCTTCTCACTGAGATGAGATGAGAGCGGACAGCACTAGCAGATC 1080
Db 1034 TTCCGGGACTTCTGCTTCTCACTGAGATGAGATGAGAGCGGACAGCACTAGCAGATC 1093
Qy 1081 CGAATATACGTTTACAGATCTGCTTACCTGAGGAGCATGATGGATGAATTAACAGTA 1140
Db 1094 CGAATATACGTTTACAGATCTGCTTACCTGAGGAGCATGATGGATGAATTAACAGTA 1153
Qy 1141 TGACTAGTCTGGA 1154
Db 1154 TGACTAGTCTGGA 1167

RESULT 12

US-10-318-661-1
; Sequence 1, Application US/10318661
; Publication No. US20030167476A1
; GENERAL INFORMATION:
; APPLICANT: Conklin, Bruce R.
; TITLE OF INVENTION: Selective Target Cell Activation By
; TITLE OF INVENTION: Expression of A G Protein-coupled Receptor Activated
; FILE REFERENCE: UCAL-049CIP2
; CURRENT FILING DATE: 2003-05-05
; PRIOR FILING DATE: 1997-03-25
; PRIOR APPLICATION NUMBER: US 08/622,348
; PRIOR FILING DATE: 1996-03-26
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1143
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-318-661-1

Query Match 99.0%; Score 1143; DB 15; Length 1143;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGACTCTCCGAGATCGAATCTTTCGGGGGAGCGGCGCTTACTGCGCCCGAGCGCC 60
Db 1 ATGACTCTCCGAGATCGAATCTTTCGGGGGAGCGGCGCTTACTGCGCCCGAGCGCC 60
Qy 61 TGCTGCGCCCGAGAGAGCGGCTGTTTCCGGGCTGGGCGAGCGCCGAGAGAGAGG 120
Db 61 TGCTGCGCCCGAGAGAGCGGCTGTTTCCGGGCTGGGCGAGCGCCGAGAGAGAGG 120
Qy 121 AGCGCGGCTCGAGAGAGCGGAGCTGAGCGCGGAGCATCTCCCGGAGATCCCGGTC 180
Db 121 AGCGCGGCTCGAGAGAGCGGAGCTGAGCGCGGAGCATCTCCCGGAGATCCCGGTC 180

Qy 181 ATCATCAGCGGCTCTACTCCGTAAGTTCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
Db 181 ATCATCAGCGGCTCTACTCCGTAAGTTCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
Qy 241 ATGTTGCTGATCATCGATACCAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
Db 241 ATGTTGCTGATCATCGATACCAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
Qy 301 CTGGTTTGGAGAGATGCTTGTATTAATCAACCAATGCTTGTGAGAGAGAGAGAGAGAG 360
Db 301 CTGGTTTGGAGAGATGCTTGTATTAATCAACCAATGCTTGTGAGAGAGAGAGAGAGAG 360
Qy 361 ATGAATTCCTGAGCTTGTGGGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
Db 361 ATGAATTCCTGAGCTTGTGGGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
Qy 421 AACATGTTACACAGATCTTCACTTGAATGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
Db 421 AACATGTTACACAGATCTTCACTTGAATGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
Qy 481 TGCCACCCCGGAGAGAGCTTGGAGCTTCCGACACCCCTTGAAGAGAGAGAGAGAGAGATC 540
Db 481 TGCCACCCCGGAGAGAGCTTGGAGCTTCCGACACCCCTTGAAGAGAGAGAGAGAGATC 540
Qy 541 TGCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
Db 541 TGCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
Qy 601 GTCAAGGAGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
Db 601 GTCAAGGAGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
Qy 661 TGCTGAGAGAGCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 720
Db 661 TGCTGAGAGAGCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 720
Qy 721 ATCATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Db 721 ATCATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Qy 781 GGCCTCCGAGAGAAAGATCGCAACCTGGTAGGATCACAGACTGCTGCTGCTGCTGCTG 840
Db 781 GGCCTCCGAGAGAAAGATCGCAACCTGGTAGGATCACAGACTGCTGCTGCTGCTGCTG 840
Qy 841 GCAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
Db 841 GCAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
Qy 901 AGCACTCTCCACAGACAGCTGCTCTCCAGCTATTAATCTTGATGCTGCTTAACTAT 960
Db 901 AGCACTCTCCACAGACAGCTGCTCTCCAGCTATTAATCTTGATGCTGCTTAACTAT 960
Qy 961 ACCAAGCTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
Db 961 ACCAAGCTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
Qy 1021 TTCCGGGACTTCTGCTTCTCACTGAGATGAGATGAGAGCGGACAGCACTAGCAGATC 1080
Db 1021 TTCCGGGACTTCTGCTTCTCACTGAGATGAGATGAGAGCGGACAGCACTAGCAGATC 1080
Qy 1081 CGAATATACGTTTACAGATCTGCTTACCTGAGGAGCATGATGGATGAATTAACAGTA 1140
Db 1081 CGAATATACGTTTACAGATCTGCTTACCTGAGGAGCATGATGGATGAATTAACAGTA 1140
Qy 1141 TGA 1143
Db 1141 TGA 1143

RESULT 13

US-10-318-661-3
; Sequence 3, Application US/10318661
; Publication No. US20030167476A1

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; GENERAL INFORMATION:
; APPLICANT: Conklin, Bruce R.
; TITLE OF INVENTION: Selective Target Cell Activation By
; TITLE OF INVENTION: Expression of A G Protein-Coupled Receptor Activated
; TITLE OF INVENTION: Superiorly By Synthetic Ligand
; FILE REFERENCE: UCAL-049CIP2
; CURRENT APPLICATION NUMBER: US/10/318,661
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 09/341,446
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US97/05334
; PRIOR FILING DATE: 1997-03-25
; PRIOR APPLICATION NUMBER: US 08/622,348
; PRIOR FILING DATE: 1996-03-26
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1284
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified KOR
; US-10-318-661-3

Query Match      98.6%  Score 1137.8;  DB 15;  Length 1284;
Best Local Similarity 99.8%;  Pred. No. 0;
Matches 1139;  Conservative 0;  Mismatches 2;  Indels 0;  Gaps 0;

QY  2  TGAAGTCCCGGATCCGATCTTCCGCGGAGAGCCCGGAGCCCTAAGCTGCGCGGAGCGGCT 61
DB  113  TCGACTCCCGGATCCGATCTTCCGCGGAGAGCCCGGAGCCCTAAGCTGCGCGGAGCGGCT 172
QY  62  GCTTGGCCCCCAACGACGCGCGCTGCTTCCGCGGAGAGCCCGGAGCCCTAAGCTGCGCGGAG 121
DB  173  GCTTGGCCCCCAACGACGCGCGCTGCTTCCGCGGAGAGCCCGGAGCCCTAAGCTGCGCGGAG 232
QY  122  GCGCGGAGTCCGAGAGAGCGGAGCTGAGAGCCCGGAGCCCTAAGCTGCGCGGAGCGGCT 181
DB  233  GCGCGGAGTCCGAGAGAGCGGAGCTGAGAGCCCGGAGCCCTAAGCTGCGCGGAGCGGCT 292
QY  182  TCATCAGCGGAGTCTACTCCGATGCTTCCGCGGAGAGCCCGGAGCCCTAAGCTGCGCGGAG 241
DB  293  TCATCAGCGGAGTCTACTCCGATGCTTCCGCGGAGAGCCCGGAGCCCTAAGCTGCGCGGAG 352
QY  242  TGTTCGTATCATCCGATACACAAAGATGAGAGACGACCAACCACTTACATATTAC 301
DB  353  TGTTCGTATCATCCGATACACAAAGATGAGAGACGACCAACCACTTACATATTAC 412
QY  302  TGGCTTGGAGATCTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAA 361
DB  413  TGGCTTGGAGATCTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAA 472
QY  362  TGAATTCCTGGCTTTGGGAGTGTCTGTGCAAGATGTAATTTCAATTGATTA 421
DB  473  TGAATTCCTGGCTTTGGGAGTGTCTGTGCAAGATGTAATTTCAATTGATTA 532
QY  422  ACATTTTACCAAGATCTTCACTTGAACATGATGAGAGTGAACCGGATACATTTGCGGT 481
DB  533  ACATTTTACCAAGATCTTCACTTGAACATGATGAGAGTGAACCGGATACATTTGCGGT 592
QY  482  GCCACCCCGTGAAGCTTTGAGCTTCCGACACACCTTGAAGGCAAAAGATCATATATCT 541
DB  593  GCCACCCCGTGAAGCTTTGAGCTTCCGACACACCTTGAAGGCAAAAGATCATATATCT 652
QY  542  GCATCTGGCTGTCTGTATCTTGTGATCTGTGATCTGTGATCTGTGATCTGTGATCTGTGAT 601
DB  653  GCATCTGGCTGTCTGTATCTTGTGATCTGTGATCTGTGATCTGTGATCTGTGATCTGTGAT 712
QY  602  TCAGGAGAGAGTGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 661
DB  713  TCAGGAGAGAGTGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 772
QY  662  GGTGGAGCTTCTTATGAAGATCTGATCTTATCTTATCTTATCTTATCTTATCTTATCTTAT 721
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DB  773  GGTGGAGCTTCTTATGAAGATCTGATCTTATCTTATCTTATCTTATCTTATCTTATCTTATCT 832
QY  722  TCATCATCTGCTGTATCAACCTGTATGATCTGCTGTATCAAGAGCTGCGGCTCTTCTTCTG 781
DB  833  TCATCATCTGCTGTATCAACCTGTATGATCTGCTGTATCAAGAGCTGCGGCTCTTCTTCTG 892
QY  782  GCTCCGAGAGAGATGCAAGCTGCTGTATGATCAACAGCTGCTGTATGATGATGATGATGAT 841
DB  893  GCTCCGAGAGAGATGCAAGCTGCTGTATGATCAACAGCTGCTGTATGATGATGATGATGAT 952
QY  842  CAGTCTGCTGCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 901
DB  953  CAGTCTGCTGCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1012
QY  902  GCACCTCCACAGACAGCTGCTCTTCCAGCTTATCTTATCTTATCTTATCTTATCTTATCTT 961
DB  1013  GCACCTCCACAGACAGCTGCTCTTCCAGCTTATCTTATCTTATCTTATCTTATCTTATCTT 1072
QY  962  CCAACAGTGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1021
DB  1073  CCAACAGTGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1132
QY  1022  TCCGAGACTTCTGCTTCCACTGAGATGAGATGAGAGCGGAGCACTGAGAGATCC 1081
DB  1133  TCCGAGACTTCTGCTTCCACTGAGATGAGATGAGAGCGGAGCACTGAGAGATCC 1192
QY  1082  GAAATACAGTTCAGATCTGCTTACCTGAGAGGATGATGATGATGATGATGATGATGATGAT 1141
DB  1193  GAAATACAGTTCAGATCTGCTTACCTGAGAGGATGATGATGATGATGATGATGATGATGAT 1252
QY  1142  G 1142
DB  1253  G 1253

RESULT 14
US-10-345-680-21
; Sequence 21, Application US/10345680
; Publication No. US20030148394A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Sinos-Santiago, Immaculada
; APPLICANT: Venkateswarlu, Karibeti
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 143S, 559, 34021, 44099, 25278,
; TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46656, 62553, 302, 323,
; FILE REFERENCE: MP102-012P1RNM OMNI
; CURRENT APPLICATION NUMBER: US/10/345,680
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US 60/349,511
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: US 60/360,500
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/365,041
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/374,063
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/403,468
; PRIOR FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: US 60/414,262
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: US 60/419,986
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/423,809
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 60/429,797
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 1143
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; TYPE: DNA
 ; ORGANISM: Homo Sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)... (1143)
 ; US-10-345-680-21

Query Match 98.4%; Score 1135; DB 15; Length 1143;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 1138; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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QY 1 ATGACATCCCCGATCCAGATCTTCCGCGGGAGCCGCGCCCTACCTGCGCCCGAGCGCC 60
DB 1 ATGGAATCCCGGATTCAGATCTTCCGCGGGAGCTCGGCTTACCTGCGCCCGAGCGCC 60
QY 61 TGCCTGCCCCCAACAGACGCGCTGTTTCCGCGTGGGCGGAGCCCGACAGCAACGCGC 120
DB 61 TGCCTGCCCCCAACAGACGCGCTGTTTCCGCGTGGGCGGAGCCCGACAGCAACGCGC 120
QY 121 AGCGCGGCTGGAGAGACGCGGAGCTGGAGCCCGGCGCATCTCCCGGCGATCCCGGTC 180
DB 121 AGCGCGGCTGGAGAGACGCGGAGCTGGAGCCCGGCGCATCTCCCGGCGATCCCGGTC 180
QY 181 ATCATCAGCGCGGTCTACTCCGTAAGTGTTCGTCGCGCTTGTGGGCAACTCGCTGCTC 240
DB 181 ATCATCAGCGCGGTCTACTCCGTAAGTGTTCGTCGCGCTTGTGGGCAACTCGCTGCTC 240
QY 241 ATGTTCTGATCATCCGATACCAAAAGATGAAGACAGCAACCAATTTACATATTAAAC 300
DB 241 ATGTTCTGATCATCCGATACCAAAAGATGAAGACAGCAACCAATTTACATATTAAAC 300
QY 301 CTGGCTTTGGCAGATGCTTTAGTTACTACACCATGCGCCCTTCAAGATACGGTCTACTTG 360
DB 301 CTGGCTTTGGCAGATGCTTTAGTTACTACACCATGCGCCCTTCAAGATACGGTCTACTTG 360
QY 361 ATGAATTCCTGCGCTTTTGGGGATGTGCTGTGSCAAGATAGTAATTTCCATTGATTACTAC 420
DB 361 ATGAATTCCTGCGCTTTTGGGGATGTGCTGTGSCAAGATAGTAATTTCCATTGATTACTAC 420
QY 421 AACATGTTACACAGATCTTCACTTGAACCATGATGAGCGTGAACCGCTACATTCGGTG 480
DB 421 AACATGTTACACAGATCTTCACTTGAACCATGATGAGCGTGAACCGCTACATTCGGTG 480
QY 481 TGGCAACCCCGTGAAGGCTTTGGAATTTCCGCAACCCCTTGAAGGCAAAATCATCAATATC 540
DB 481 TGGCAACCCCGTGAAGGCTTTGGAATTTCCGCAACCCCTTGAAGGCAAAATCATCAATATC 540
QY 541 TGCATCTGGCTGCTGTGCTCATCTGTGGCATCTCTGCAATATGCTCTTGGAGGACCAAA 600
DB 541 TGCATCTGGCTGCTGTGCTCATCTGTGGCATCTCTGCAATATGCTCTTGGAGGACCAAA 600
QY 601 GTCAAGGAAAGACGTGATGTCAATTGAGTCTCTTGAAGTCCAGATGATGACTACTCC 660
DB 601 GTCAAGGAAAGACGTGATGTCAATTGAGTCTCTTGAAGTCCAGATGATGACTACTCC 660
QY 661 TGGTGGGACCTTCTCATGAAGATCTGCGTCTTCACTTTGCGCTTGTGATCTCTGCTC 720
DB 661 TGGTGGGACCTTCTCATGAAGATCTGCGTCTTCACTTTGCGCTTGTGATCTCTGCTC 720
QY 721 ATCATCATGCTGTGCTACACCTGATGATCTGCGCTCAAGAGGCTCGGCTCTTCTCT 780
DB 721 ATCATCATGCTGTGCTACACCTGATGATCTGCGCTCAAGAGGCTCGGCTCTTCTCT 780
QY 781 GAGTCCGAGAGAAAGATCGCAACCTGCGTAGAGATCACAGACTGCTCTGTGTGTGTG 840
DB 781 GAGTCCGAGAGAAAGATCGCAACCTGCGTAGAGATCACAGACTGCTCTGTGTGTGTG 840
QY 841 GCAAGCTTCTGCTGTGCTGAGCTCCCATTCACATTTCAATCTCTGTGTGTGTGTG 900
DB 841 GCGGTTTCTGCTGTGCTGAGCTCCCATTCACATTTCAATCTCTGTGTGTGTGTG 900
QY 901 AGCACTCCCAAGACAGCTGCTCTCTGAGCTATTAATTGATGAGCTCTAGGCTAT 960
DB 901 AGCACTCCCAAGACAGCTGCTCTCTGAGCTATTAATTGATGAGCTCTAGGCTAT 960
  
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DB 901 AGCACTCCCAAGACAGCTGCTCTCTGAGCTATTAATTGATGAGCTCTAGGCTAT 960
QY 961 ACCAATCAGTACGCTTAATTCCTTCTTACAGGCTTTCTTGAATGAATTTCAAGCGGT 1020
DB 961 ACCAATCAGTACGCTTAATTCCTTCTTACAGGCTTTCTTGAATGAATTTCAAGCGGT 1020
QY 1021 TTCGGGACTTGTGCTTTTCACTGAAGATGAGAGTGAAGCGGACAGCACTAGCAGATC 1080
DB 1021 TTCGGGACTTGTGCTTTTCACTGAAGATGAGAGTGAAGCGGACAGCACTAGCAGATC 1080
QY 1081 CGAAATATACAGTTACAGATCTGCTTACCTGAGGAGCATGATGAGATGAATTAACAGTA 1140
DB 1081 CGAAATATACAGTTACAGATCTGCTTACCTGAGGAGCATGATGAGATGAATTAACAGTA 1140
QY 1141 TGA 1143
DB 1141 TGA 1143
  
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RESULT 15

US-09-826-509-542
 ; Sequence 542, Application US/09826509
 ; Publication No. US20030204073A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lehmann-Bruinsma, Karin
 ; APPLICANT: Liaw, Chen W.
 ; APPLICANT: Lin, I-Lin
 ; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G
 ; FILE REFERENCE: AREN-207
 ; CURRENT APPLICATION NUMBER: US/09/826, 509
 ; PRIOR FILING DATE: 2001-04-05
 ; PRIOR APPLICATION NUMBER: 60/195, 747
 ; PRIOR FILING DATE: 2000-04-07
 ; PRIOR APPLICATION NUMBER: 09/170,496
 ; PRIOR FILING DATE: 1998-10-13
 ; NUMBER OF SEQ ID NOS: 589
 ; SOFTWARE: PatentIn Version 2.1
 ; SEQ ID NO 542
 ; LENGTH: 1143
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-826-509-542

Query Match 98.1%; Score 1131.8; DB 11; Length 1143;
 Best Local Similarity 99.4%; Pred. No. 0;
 Matches 1136; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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QY 1 ATGACATCCCCGATCCAGATCTTCCGCGGGAGCCGCGCCCTACCTGCGCCCGAGCGCC 60
DB 1 ATGGAATCCCGGATTCAGATCTTCCGCGGGAGCTCGGCTTACCTGCGCCCGAGCGCC 60
QY 61 TGCCTGCCCCCAACAGACGCGCTGTTTCCGCGTGGGCGGAGCCCGCAACAGAGCC 120
DB 61 TGCCTGCCCCCAACAGACGCGCTGTTTCCGCGTGGGCGGAGCCCGCAACAGAGCC 120
QY 121 AGCGCGGCTGGAGAGACGCGAGCTGAGGCGCGGCAATCTCCCGGCAATCCCGGTC 180
DB 121 AGCGCGGCTGGAGAGACGCGAGCTGAGGCGCGGCAATCTCCCGGCAATCCCGGTC 180
QY 181 ATCATCAGGGGCTGTACTCCGTAGTGTTCGTCGTGGGCTTGTGGGCAACTCGCTGCTC 240
DB 181 ATCATCAGGGGCTGTACTCCGTAGTGTTCGTCGTGGGCTTGTGGGCAACTCGCTGCTC 240
QY 241 ATGTTCTGATCATCCGATACCAAAAGATGAAGACAGCAACCAATTTACATATTAAAC 300
DB 241 ATGTTCTGATCATCCGATACCAAAAGATGAAGACAGCAACCAATTTACATATTAAAC 300
QY 301 CTGGCTTTGGCAGATGCTTTAGTTACTACAAACATGCGCTTTCAAGATACGGTCTACTTG 360
DB 301 CTGGCTTTGGCAGATGCTTTAGTTACTACAAACATGCGCTTTCAAGATACGGTCTACTTG 360
QY 361 ATGAATTCCTGCGCTTTTGGGGATGTGCTGTGSCAAGATAGTAATTTCCATTGATTACTAC 420
  
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Db 361 ATGAAATCTGCGCTTTGGGGATGCTGTGCAAGATGATTAATTTCCATGATTACTAC 420
Qy 421 AACATGTTACACAGATCTTCACTTGAACATGATGAGCGTGAGCCGTTACATGGCGTG 480
Db 421 AACATGTTACACAGATCTTCACTTGAACATGATGAGCGTGAGCCGTTACATGGCGTG 480
Qy 481 TGCAACCCCGTGAAGGCTTTGGAATCTTGGCAACACCCCTTGAAGGCAAAATATCAATATC 540
Db 481 TGCAACCCCGTGAAGGCTTTGGAATCTTGGCAACACCCCTTGAAGGCAAAATATCAATATC 540
Qy 541 TGCACTGTGCTGTCTGTCACTGTGTGCACTTCTGCAATAGTCTTGAAGGCAACAA 600
Db 541 TGCACTGTGCTGTCTGTCACTGTGTGCACTTCTGCAATAGTCTTGAAGGCAACAA 600
Qy 601 GTCAAGGAAAGCTGTGATGTCAATGATGCTTGTGCACTTCCAGATGATGACTACTCC 660
Db 601 GTCAAGGAAAGCTGTGATGTCAATGATGCTTGTGCACTTCCAGATGATGACTACTCC 660
Qy 661 TGGTGGGACCTCTTCATGAAGATCGGTCTTCATCTTGCCTTGATGCTGCTGCTC 720
Db 661 TGGTGGGACCTCTTCATGAAGATCGGTCTTCATCTTGCCTTGATGCTGCTGCTC 720
Qy 721 ATCATCATCTGTCTGTACACCTGTATGATCTGTGCTCAAGAGCGTCCGCTCTTCT 780
Db 721 ATCATCATCTGTCTGTACACCTGTATGATCTGTGCTCAAGAGCGTCCGCTCTTCT 780
Qy 781 GCGTCCGAGAAAGATCGCACTGCTGATGATCAACAGATCTGTCTGCTGCTGCTG 840
Db 781 GCGTCCGAGAAAGATCGCACTGCTGATGATCAACAGATCTGTCTGCTGCTGCTG 840
Qy 841 GCACTCTGTCTGTCTGTGAGCTCCATTCATCTCTGCTGCTGCTGCTGCTGCTG 900
Db 841 GCGGTTTCTGTCTGTCTGTGAGCTCCATTCATCTCTGCTGCTGCTGCTGCTGCTG 900
Qy 901 AGCACTTCCACAGACAGCTGTCTCTCAAGCTATTAATCTGTGATGCTTGAAGCTAT 960
Db 901 AGCACTTCCACAGACAGCTGTCTCTCAAGCTATTAATCTGTGATGCTTGAAGCTAT 960
Qy 961 ACCAAGATGCTGATCTTCACTTCTGAGCTTCTTGAATGAAATCTTCAAGGCTGT 1020
Db 961 ACCAAGATGCTGATCTTCACTTCTGAGCTTCTTGAATGAAATCTTCAAGGCTGT 1020
Qy 1021 TTCGGGACCTCTGTCTTCACTGAAGATGAGATGAGCGGACAGACTAGAGAGTCTC 1080
Db 1021 TTCGGGACCTCTGTCTTCACTGAAGATGAGATGAGCGGACAGACTAGAGAGTCTC 1080
Qy 1081 CGAAATACAGTTCAGATCTGCTTACCTGAGGAGCATGATGGATGAATTAACAGTA 1140
Db 1081 CGAAATACAGTTCAGATCTGCTTACCTGAGGAGCATGATGGATGAATTAACAGTA 1140
Qy 1141 TGA 1143
Db 1141 TGA 1143

RESULT 16
US-10-318-661-5

; Sequence 5, Application US/10318661
; Publication No. US20030167476A1
; GENERAL INFORMATION:
; APPLICANT: Conklin, Bruce R.
; TITLE OF INVENTION: Selective Target Cell Activation By
; TITLE OF INVENTION: Expression of A G Protein-Coupled Receptor Activated
; FILE REFERENCE: UCAL-049CIP2
; CURRENT APPLICATION NUMBER: US/10/318,661
; PRIOR FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 09/341,446
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US97/05334
; PRIOR FILING DATE: 1997-03-25
; PRIOR APPLICATION NUMBER: US 08/622,348

; PRIOR FILING DATE: 1996-03-26
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1275
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: RASL OR1
US-10-318-661-5

Query Match 86.7%; Score 1001; DB 15; Length 1275;
Best Local Similarity 93.1%; Pred. No. 1.2e-279;
Matches 1062; Conservative 0; Mismatches 70; Indels 9; Gaps 1;

Qy 2 TGAATCCCGATTCAGATCTTCCGCGGAGCCGCGCTTACTGCGGCCCGGAGCCCT 61
Db 113 TCGACTCCCGATTCAGATCTTCCGCGGAGCCGCGCTTACTGCGGCCCGGAGCCCT 172
Qy 62 GCGTCCCGGAG 121
Db 173 GCGTCCCGGAG 232
Qy 122 GCGCGGCTGAG 181
Db 233 GCGCGGCTGAG 292
Qy 182 TCATCAAGGCGGTACTTCCGTAGTGTCTGTGCGGCTGTGTGGGAACTCGCTGTGCA 241
Db 293 TCATCAAGGCGGTACTTCCGTAGTGTCTGTGCGGCTGTGTGGGAACTCGCTGTGCA 352
Qy 242 TGTTCGTGATCATCCGATPACAAAGATGAAGACAGAACCAATTTAATTAAC 301
Db 353 TGTTCGTGATCATCCGATPACAAAGATGAAGACAGAACCAATTTAATTAAC 412
Qy 302 TGGCTTTGGAGATGCTTATGATTAATCAACATGCTTTCAGAGTACGCTTACTTGA 361
Db 413 TGGCTTTGGAGATGCTTATGATTAATCAACATGCTTTCAGAGTACGCTTACTTGA 472
Qy 362 TGAATTCCTGCGCTTTGGGAGATGCTGTGCAAGATGATTAATTTCAATGATTAACA 421
Db 473 TGAATTCCTGCGCTTTGGGAGATGCTGTGCAAGATGATTAATTTCAATGATTAACA 532
Qy 422 ACATGTTACACAGATCTTCACTTGAACATGATGAGCGGCTACATTCCTGCTGT 481
Db 533 ACATGTTACACAGATCTTCACTTGAACATGATGAGCGGCTACATTCCTGCTGT 592
Qy 482 GCCACCCGAGAGAGCTTTGACTTCGCAACACCTTGAAGGCAAAATCATTAATCT 541
Db 593 GCCACCCGAGAGAGCTTTGACTTCGCAACACCTTGAAGGCAAAATCATTAATCT 652
Qy 542 GCATCTGCTGTCTGTCTGTCTGTGTGCACTTCTGCAATAGTCTTGGAGGACCAAG 601
Db 653 GCATCTGCTGTCTGTCTGTGTGCACTTCTGCAATAGTCTTGGAGGACCAAG 712
Qy 602 TCAGGAAAGAGTCAATGATGATGAGTCTTGCAGTTCAGATGATGATGATGATGAT 661
Db 713 CCGGAGATGAGAGAGTATGACAGCTTCCAGTTCAGAGCTTCCAGAGCTTCCAGAGCTT 763
Qy 662 GGTGGACCTTTCATGAAGATCTGCTTTCATCTTGTGCTTGTGATCTTGTCTCTCA 721
Db 764 ACTGGACACTGATCAAGATCTGCTTTCATCTTGTGCTTGTGATCTTGTCTCTCA 823
Qy 722 TCATCATCTGTCTGTACACCTGTATGATCTGTGCTTCAAGAGGCTCCGCTCTTCTG 781
Db 824 TCATCATCTGTCTGTACACCTGTATGATCTGTGCTTCAAGAGGCTCCGCTCTTCTG 883
Qy 782 GCTCCGAGAAAGATCGCAACCTGCTGATGATCAACAGCTGCTGCTGCTGCTGCTG 841
Db 884 GCTCCGAGAAAGATCGCAACCTGCTGATGATCAACAGCTGCTGCTGCTGCTGCTG 943
Qy 842 CAGTCTTCTGTCTGTGATCTTCCATTCATTCATTCATTCATTCATTCATTCATTCAT 901


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; CURRENT APPLICATION NUMBER: US/10/318,661
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 09/341,446
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US97/05334
; PRIOR FILING DATE: 1997-03-25
; PRIOR APPLICATION NUMBER: US 08/622,348
; PRIOR FILING DATE: 1996-03-26
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 1875
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Ro3 (Rig)
US-10-318-661-13
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Query Match      85.0%; Score 981; DB 15; Length 1875;
Best Local Similarity 92.6%; Pred. No. 9e-274;
Matches 1045; Conservative 0; Mismatches 75; Indels 9; Gaps 1;
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QY 15 CCAAGATCTTCGCGGGAGCCGCGCTTAACTGCGCCCGGAGCGCTTGCTGCCCCCAA 74
DB 756 CGAGCTGTACCGCGGGAGCCGCGCTTAACTGCGCCCGGAGCGCTTGCTGCCCCCAA 815
QY 75 CAGCAGCGCCGCTGTTCCCGGCTGGGCGAGCCGAGCAAGCAAGCGAGCGCGCGCTCGGA 134
DB 816 CAGCAGCGCCGCTGTTCCCGGCTGGGCGAGCCCGCAAGCAAGCGAGCGCGCGCTCGGA 875
QY 135 GAGCGCGAGCTGAGCGCCGCGCAATCTCCCGGCAATCCCGGCTCATCATCAGCGCGGT 194
DB 876 GAGCGCGAGCTGAGCGCCGCGCAATCTCCCGGCAATCCCGGCTCATCATCAGCGCGGT 935
QY 195 CTACTCCGTAGTGTTCGTGCTGGGCTTGGTGGGCAATCTGCTGTGATGTTCTGTATCAT 254
DB 936 CTACTCCGTAGTGTTCGTGCTGGGCTTGGTGGGCAATCTGCTGTGATGTTCTGTATCAT 995
QY 255 CCGATACCAAGATGAGAGCAAGCAACCAATTAACTTAATTAATTAATTAATTAATTAATTA 314
DB 996 CCGATACCAAGATGAGAGCAAGCAACCAATTAACTTAATTAATTAATTAATTAATTAATTA 1055
QY 315 TGCCTTAAGTAACTAACAACATCCCTTTAGAGTACGCTTCACTGATGATTAATTCCTGGCC 374
DB 1056 TGCCTTAAGTAACTAACAACATCCCTTTAGAGTACGCTTCACTGATGATTAATTCCTGGCC 1115
QY 375 TTTTGGGAGTGTCTGTGCAAGATGATTAATTCATTAATTAATTAATTAATTAATTAATTA 434
DB 1116 TTTTGGGAGTGTCTGTGCAAGATGATTAATTCATTAATTAATTAATTAATTAATTAATTA 1175
QY 435 CATCTCACTTGAACATGATGAGGTGAGCGGCTAACATTCGCGGTGCAACCGCGTAA 494
DB 1176 CATCTCACTTGAACATGATGAGGTGAGCGGCTAACATTCGCGGTGCAACCGCGTAA 1235
QY 495 GGCCTTTGAGCTTCCGCAACCCCTTTGAAGCAAGATCATCATATCTGATCTGCTGCT 554
DB 1236 GGCCTTTGAGCTTCCGCAACCCCTTTGAAGCAAGATCATCATATCTGATCTGCTGCTGCT 1295
QY 555 GTCTGATCTGTGGCAATCTTCAATATGCTCTTGAAGCAACCAAGTCAAGGAAGAGCT 614
DB 1296 GGCATCATCTGTGGTATATAGCGATAGTCTTGGGGTGAACCAACCCCGGAGTGAAGC 1355
QY 615 CGATGTCAATGAGTCTCTTGAAGTATCCCAATGATGATGATGATGATGATGATGATGATGAT 674
DB 1356 AGTGTATGACAGCTTCAGTTCCCAAGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1406
QY 675 CATGAAGATCTGCTCTTCAATCTTGTGCTTGTGATTCCTGCTCATCATCATCATCATCATCAT 734
DB 1407 GACCAAGATCTGCTCTTCAATCTTGTGCTTGTGATTCCTGCTCATCATCATCATCATCATCAT 1466
QY 735 CTACACCTGATGATCTGCTGCTCAAGAGCTCGGCTCTCTTCTGCTCCGAGAGAA 794
DB 1467 CTACACCTGATGATCTGCTGCTCAAGAGCTCGGCTCTCTTCTGCTCCGAGAGAA 1526
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QY 795 AGATCGCAACTGGTAGATCACCAAGCTGGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 854
DB 1527 AGATCGCAACTGGTAGATCACCAAGCTGGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1586
QY 855 CTGCTGAGCTCCCAATTCATATTTATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 914
DB 1587 CTGCTGAGCTCCCAATTCATATTTATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1646
QY 915 CACAGCTGCTCTTCACAGCTTATTTATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 974
DB 1647 CACAGCTGCTCTTCACAGCTTATTTATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1706
QY 975 GAATCCCATCTCTACAGCTTCTTTGATGAAATCTTCAAGCGGTGTGTGTGTGTGTGTGTGTGT 1034
DB 1707 GAATCCCATCTCTACAGCTTCTTTGATGAAATCTTCAAGCGGTGTGTGTGTGTGTGTGTGTGT 1766
QY 1035 CTTTCCACTGAAAGATGAGATGAGCGGCAAGCACTAGCAGAGTCCGAATTAACATTTCA 1094
DB 1767 CTTTCCACTGAAAGATGAGATGAGCGGCAAGCACTAGCAGAGTCCGAATTAACATTTCA 1826
QY 1095 GGATCTGCTTACCTGAGGAGCATCATGATGGATGAATTAACAGATATGA 1143
DB 1827 GGATCTGCTTACCTGAGGAGCATCATGATGGATGAATTAACAGATATGA 1875
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RESULT 19

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US-10-318-661-15
; Sequence 15, Application US/10318661
; Publication No. US20030167476A1
; GENERAL INFORMATION:
; APPLICANT: Konklin, Bruce R.
; TITLE OF INVENTION: Selection Target Cell Activation By
; TITLE OF INVENTION: Expression of A G Protein-Coupled Receptor Activated
; FILE REFERENCE: UCAL-049CIP2
; CURRENT APPLICATION NUMBER: US/10/318,661
; PRIOR APPLICATION NUMBER: US 09/341,446
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US97/05334
; PRIOR FILING DATE: 1997-03-25
; PRIOR APPLICATION NUMBER: US 08/622,348
; PRIOR FILING DATE: 1996-03-26
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 1875
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Ro3A (Rig A)
US-10-318-661-15
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Query Match      83.6%; Score 965; DB 15; Length 1875;
Best Local Similarity 91.7%; Pred. No. 4e-269;
Matches 1035; Conservative 0; Mismatches 85; Indels 9; Gaps 1;
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QY 15 CCAAGATCTTCGCGGGAGCCGCGCTTAACTGCGCCCGGAGCGCTTGCTGCCCCCAA 74
DB 756 CGAGCTGTACCGCGGGAGCCGCGCTTAACTGCGCCCGGAGCGCTTGCTGCCCCCAA 815
QY 75 CAGCAGCGCCGCTGTTCCCGGCTGGGCGAGCCGAGCAAGCAAGCGAGCGCGCTCGGA 134
DB 816 CAGCAGCGCCGCTGTTCCCGGCTGGGCGAGCCCGCAAGCAAGCGAGCGCGCTCGGA 875
QY 135 GAGCGCGAGCTGAGCGCCGCGCAATCTCCCGGCAATCCCGGCTCATCATCAGCGCGGT 194
DB 876 GAGCGCGAGCTGAGCGCCGCGCAATCTCCCGGCAATCCCGGCTCATCATCAGCGCGGT 935
QY 195 CTACTCCGTAGTGTTCGTGCTGGGCTTGGTGGGCAATCTGCTGTGATGTTCTGTATCAT 254
DB 936 CTACTCCGTAGTGTTCGTGCTGGGCTTGGTGGGCAATCTGCTGTGATGTTCTGTATCAT 995
```

OY	255	CCGATATACCAAGAGTGAAGACGACGACCAACATTTACATATTTAACTCGGCTTTGGACGA	314
Db	996	CCGATATACCAAGAGTGAAGACGACGACCAACATTTACATATTTAACTCGGCTTTGGACGA	1055
OY	315	TGCTTTAGTTACTACAAACATGCGCTTTACAGATACGGTCTACTGATGTAATTTCCGTGCC	374
Db	1056	TGCTTTAGTTACTACAAACATGCGCTTTACAGATACGGTCTACTGATGTAATTTCTTGGCC	1115
OY	375	TTTTGGGAGTGTGCTGTGCAGATATGTAAATTTCCATTGATTACTACAAATGTTCAACAG	434
Db	1116	TTTTGGAGATGTGCTGTGCAGATATGTCAATTTCCATTGACTACTCAACATGTTTACAG	1175
OY	435	CATCTTCACTTGACCACTGATGATGAGGGTGGACCGCTACATATGCGGTGTCACCCCGTAA	494
Db	1176	CATATTTCACTTGACCACTGATGATGAGTGGACCGCTTACATGCGGTGTCACCCGTGTA	1233
OY	495	GCGCTTTGAGACTTCCGACACACCTTGTAAGGCAAAAGATCATCATATCTGATCTGGCTGT	554
Db	1236	AGCTTTGGATTTTCGAAACACTTTTBAAGCAAAAGATCATCATCTGATTTGGTCTACT	1295
OY	555	GTCGTTCATCTGTGGCATCTCTGCATATGTCTTTGAGGACCAAAAGTCAGGAAAGAGCT	614
Db	1296	GGCATCATCTGTGGTATATACGCATATGTCTTTGGGGTGACCCAAACCCCGGAGTGGAGC	1355
OY	615	CGATGTCAATGAGTGTGCTCGTCCAGATGCCAGATATGATACATCTCTGGTGGAGACTCTG	674
Db	1356	AGTGTATATGACAGCTTCCAGTTTCCACAGCCC-----CAGCTGTACTGGAGACATGT	1405
OY	675	CATGAAAGATCTGCGTCTTCATCTTTGCTTCGTGATGCCGTGCTCATCATCATCATGTCTG	734
Db	1407	GACCAAGATCTGCGTCTTCATCTTTGCTTCGTGATGCCGTGCTCATCATCATCATGTCTG	1466
OY	735	CTACACCTCGATGATCTTGCCTCTCAAGAGCGTCCGGCTCCTTTCTGGCTCCGAGAGAA	794
Db	1467	CTACACCTCGATGATCTTGCCTCTCAAGAGCGTCCGGCTCCTTTCTGGCTCCGAGAGAA	1526
OY	795	AGATGCAACCGCGCTAGAGATCACAGACTGGTCCGTGGGAGTGGAGGAGCTTCTGCTGT	854
Db	1527	AGATGCAACCGCGCTAGAGATCACAGACTGGTCCGTGGGAGTGGAGGAGCTTCTGCTGT	1586
OY	855	CTGCTGAGCTCCGATTCATATATTCATCTCTGGTGGAGGCTCTGGGAGACCTCCACAG	914
Db	1587	CTGCTGAGCTCCGATTCATATATTCATCTAGTTCAGGCTCTGGGAGAGCACTCCACAG	1646
OY	915	CACAGCTGCTCTCTCCAGCTATTACTTCTGCATGCGCTTAAGCTATACCAACAGTAGCT	974
Db	1647	CACAGCTGCTCTCTCCAGCTATTACTTCTGCATGCGCTTAAGCTATACCAACAGTAGCT	1706
OY	975	GAATGCCATTCCTACAGCGCTTTCTTGATGAAAACTTCAAGCGGATTTTCCGGGACTTCTG	1034
Db	1707	GAATGCCATTCCTACAGCGCTTTCTTGATGAAAACTTCAAGCGGATTTTCCGGGACTTCTG	1766
OY	1035	CTTTCCTACTGAAGATGAGATGAGACGGCGACAGCACTAGCAGAGTCCGAAATACAGTTCA	1094
Db	1767	CTTTCCTACTGAAGATGAGATGAGACGGCGACAGCTAGCTAGAGTCCGAAATAGCTTCA	1826
OY	1095	GGATCTCTCTTACCTGAGAGACATGGAATGGGATGGAATTAACAGATATGA 1143	
Db	1827	GGATCTCTCTTACCTGAGAGACATGGAATGGGATGGAATTAACAGATATGA 1875	
RESULT 20			
US-09-214-904-5			
; Sequence 5, Application US/09214904			
; Patent No. US20010047519A1			
; GENERAL INFORMATION:			
; APPLICANT:			
; TITLE OF INVENTION: TRANSGENIC ANIMAL IN WHICH THE EXPRESSION			
; NUMBER OF SEQUENCES: 6			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			

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: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/214,904
: FILING DATE:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/FR97/01262
: FILING DATE:
: APPLICATION NUMBER: FR 96.08810
: FILING DATE: 15-JUL-1996
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1408 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 184..1323
: US-09-214-904-5

Query Match      78.9% Score 910.8: DB 9: Length 1408:
Best Local Similarity 86.8% Pred. NO.1,9e-253;
Matches 1002; Conservative 0; Mismatches 152; Indels 0; Gaps 0

OY      1  ATGGACTCCCGATCCAGATCTTCGCGGGAGCCGGGCTTACTGCGCCCCGAGCGCC 60
Db      184  ATGAGTGTCCCATTCATCATCTTCGAGAGATTCAGGCGCTTACTGCTCTCCAGTGT 243

OY      61  TGCCTGCCCCCAACAGCAGCGCTGTGTTCCGGCTG3GCGGAGCCGACAGCAAGCGC 120
Db      244  TGCCTTCTCCCAACAGCAGCGCTGTGTTCCCAACTGGGCGAATCCACAGTAATGCG 303

OY      121  AGCGCCGGCTGGAGAGACGCGCAGCTGGAGCCCGCGCATCTCCCGGCGCATCCCGGTC 180
Db      304  AGTGGGGCTCAGAGATCAGACGCTGGAGTCCGCGCATCTTCGCGCATCTCCGTT 363

OY      181  ATCATCAAGCGGCTCTACTCCGTAAGTTCGTCGTGGGCTTGGTGGGCAACTCGCTGTC 240
Db      364  ATCATCAAGCGGCTCTACTCTGTGTATTGTGTGGGCTTGGTGGGCAACTCTGTGTC 423

OY      241  ATGTTGCGATCATCCGATACCAAAAGATGAAGACAGCAACCAACATTTACATATTAAAC 300
Db      424  ATGTTGCGATCATCCGATACCAAGATGAAGACCGCAACCAACATTTACATATTAAAC 483

OY      301  CTGGCTTTGGAGATGCTTTAGTTACTACAAACATGCCCCCTTCAAGATACGGTCTTACTTG 360
Db      484  CTGGCTTTGGAGATGCTTTGGTTACTACAACTAAGCCCCCTTCAAGATGCTGTCTTACTTG 543

OY      361  ATGAATTCCTGGCCCTTTGGGGAGATGTGCTGTGCAAGATAGTAATTTCATTTACTAC 420
Db      544  ATGAATTCCTGGCCCTTTGGGGAGATGTGCTGTGCAAGATAGTTGTATTTCCATTGACTAC 603

OY      421  AACATGTTTACACAGCATCTTCACTTGAACCATGATGAGCGTGACCGCTCAATTCGCGTG 480
Db      604  AACATGTTTACAGCATATTTCACCTTGAACCATGATGAGTGGACCGCTCAATTCGCGTG 663

OY      481  TGCACACCCCGTGAAGGCTTTGACCTTCCGACACCCCTTGAAGGCAAAATCATCAATATC 540
Db      664  TGCACACCCCGTGAAGGCTTTGACCTTCCGACACCTTGAAGGCAAAAGATCATCAATATC 723

OY      541  TGCATCTGGCGCTGTGCTGATCTGTTGGACATCTGTGAATATGTCCTTGAAGGCAACAA 600
Db      724  TGCATCTGGCGCTGTGCTGATCTGTTGGATATATGAGGATATGTCCTTGAAGGCAACAA 783

OY      601  GTCAAGGAAGAAGTCGATGATCTATTGAGTGTCTCTTGCATTTCCAGATGATGACTACTCC 660
Db      784  GTCAAGGAAGAAGTGTGATGATGATGATGCTCTCTTGCATTTCCAGATGATGATATTTCC 843

OY      661  TGTGTGGAGCTCTTCAATGAAGATCTGCGCTTTCACTTTTGGCTTGTGATCCCTGTCTTC 720

```

Db 844 TGGTGGGATCTCTTATGAAGAATCTGTGTCTTGTCTTTCCTTTGTATGCCAGTCTTC 903
Qy 721 ATCATCATGTCTGTCTACACCTGATGATCTGCGTCTCAAGAGCGCTCCGCTCTTCT 780
Db 904 ATCATCATGTCTGTCTACACCTGATGATCTGCGCTCAAGAGTGTCCGCTCTTCT 963
Qy 781 GGCCTCCGAGAGAAAGATGCAACCTGCGTAGATCAGCAGACTGGTCTGCTGGTGGTG 840
Db 964 GGCCTCCGAGAGAAAGATGCAACCTGCGCTCAAGAGTGTGTGCTGGTGGTGGT 1023
Qy 841 GCAATCTTGTGTCTGTCTGATGATCTCCATTCACATATTCATCTGTGTGAGGCTCTG 900
Db 1024 GCAGTCTTCATCATCTGTGTGACCCCATTCACATCTTATCTCTGTGTGAGGCTCTG 1083
Qy 901 ACCACTTCCAGAGACAGAGCTGTCTCTGACATATTAATCTGTGATGAGGCTTACGCT 960
Db 1084 ACCACTTCCAGAGACAGAGCTGTCTCTGACATATTAATCTGTGATGAGGCTTACG 1143
Qy 961 ACCAAGAGAGCTGTGATCTCCATTCCTGAGGCTTGTGATGAGGCTTGTGAGGCTGT 1020
Db 1144 ACCAAGAGAGCTGTGATCTCCATTCCTGAGGCTTGTGATGAGGCTTGTGAGGCTGT 1203
Qy 1021 TTCCGGAGCTTCTGTCTTCTCACTGAAAGATGAGATGAGAGCGGACAGCACTAGAGCT 1080
Db 1204 TTAGGGAGCTTCTGTCTTCTCACTGAAAGATGAGATGAGAGCGGACAGCACTAGAG 1263
Qy 1081 GCAATATCAGATCTGAGATCTGCTTACCTGAGGAGCATCGATGGATGAATTAACAGTA 1140
Db 1264 ACAAACAGATCTGAGATCTGCTTACCTGAGGAGCATCGATGGATGAATTAACAGTA 1323
Qy 1141 TGACTAGTCTGGA 1154
Db 1324 TGACTAGTCTGGA 1337

RESULT 21

US-10-318-661-17
; Sequence 17, Application US/10318661
; Publication No. US20030167476A1
; GENERAL INFORMATION:
; APPLICANT: Conklin, Bruce R.
; TITLE OF INVENTION: Selective Target Cell Activation By
; TITLE OF INVENTION: Expression of A G Protein-Coupled Receptor Activated
; FILE REFERENCE: UCAL-049CIP2
; CURRENT APPLICATION NUMBER: US/10/318,661
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 09/341,446
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US97/05334
; PRIOR FILING DATE: 1997-03-25
; PRIOR APPLICATION NUMBER: US 08/622,348
; PRIOR FILING DATE: 1996-03-26
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 1911
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: R1g-mua
US-10-318-661-17

Query Match 76.2% Score 879.4; DB 15; Length 1911;
Best Local Similarity 88.6%; Pred. No. 2,8e-244;
Matches 968; Conservative 0; Mismatches 116; Indels 9; Gaps 1;

Qy 15 CCAATCTTCCGCGGAGAGCGGCGCTTACCTGCGCCCGAGCGCTGCTGCCCCCAA 74
Db 756 CGAGCTGTACCGCGGAGAGCGGCGCTTACCTGCGCCCGAGCGCTGCTGCCCCCAA 815
Qy 75 CAGACGCGCTGCTTCCCGGCTGGGCGGAGCCGAGCAGCAAGCGGCGGCTGGGA 134
Db 134 CAGACGCGCTGCTTCCCGGCTGGGCGGAGCCGAGCAGCAAGCGGCGGCTGGGA 134

Db 816 CAGACGCGCTGCTTCCCGGCTGGGCGGAGCCGAGCAGCAAGCGGCGGCTGGGA 875
Qy 135 GAGCGCGAGCTGAGAGCCCGGAGCATCTCCCGGCAATCCCGGTATCATCACGCGGT 194
Db 876 GAGCGCGAGCTGAGAGCCCGGAGCATCTCCCGGCAATCCCGGTATCATCACGCGGT 935
Qy 195 CTACTCCGTATGTTCCGCGGCGCTGCGGAGCACTCGGTGATGATGATGATGAT 254
Db 936 CTACTCCGTATGTTCCGCGGCGCTGCGGAGCACTCGGTGATGATGATGATGAT 995
Qy 255 CCGATACCAAAAGATGAGAGCAGCAACCAATTTAATTTAATTTAATTTAATTTAATTTA 314
Db 996 CCGATACCAAAAGATGAGAGCAGCAACCAATTTAATTTAATTTAATTTAATTTAATTTA 1055
Qy 315 TGCTTTAGTTACTAACCAATGCGCTTTCAAGATGAGGCTTACTTGAATTTCTGCGC 374
Db 1056 TGCTTTAGTTACTAACCAATGCGCTTTCAAGATGAGGCTTACTTGAATTTCTGCGC 1115
Qy 375 TTTTGGGAGATGCGTGAAGATGATGATTTTCAATTTACTTACTTACTTACTTACTTACT 434
Db 1116 TTTTGGGAGATGCGTGAAGATGATGATTTTCAATTTACTTACTTACTTACTTACTTACT 1175
Qy 435 CATCTTCACTTGAACATGATGAGCGTGAACCGCTACATTTGCGGTGCGACCCGTGA 494
Db 1176 CATATTCACCTTGAACATGATGATGATGAGCGGTATCATTTGCGGTGCGACCCGTGA 1235
Qy 495 GGCCTTGAATCTTCCGAGACCCCTTGAAGCAAAATATCATATTTCTGATCTGGCTGCT 554
Db 1236 AGCTTTGATTTTCCGAACACCTTGAAGCAAAATATCATCATCTGCAATTTGGCTACT 1295
Qy 555 GTGCTCATCTGTGGCATCTCTGCAATGATCTTGAAGCAACCAATGCGGAGGAGAGCT 614
Db 1296 GGCATCATCTGTGTGATATCAGGATGATCTTTGGGTGACCAACCCCGGATGAGAGC 1355
Qy 615 CGATGCAATGAGTGTCTTCTGCACTTCCAGATGATGATGATGATGATGATGATGATGAT 674
Db 1356 AGTGTATGACGCTCCAGATTTCCCAAGCC-----CAGCTGATGAGGAGCACTGT 1406
Qy 675 CATGAATCTGCGCTTCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 734
Db 1407 GACCAAGATCTGCTTCTCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1466
Qy 735 CTACACCTGATGATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 794
Db 1467 CTACACCTGATGATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1526
Qy 795 AGATCGCACTGCTGATGATCAACAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 854
Db 1527 AGATCGCACTGCTGATGATCAACAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1586
Qy 855 CTGCTGACCTCCCATTTCAATTTCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 914
Db 1587 CTGCTGACCTCCCATTTCAATTTCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1646
Qy 915 CACAGCTGCTCTCTCAGCTATTACTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 974
Db 1647 CACAGCTGCTCTCTCAGCTATTACTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1706
Qy 975 GAATCCATTTCTTACGCTCTTCTTGTGATAAACTTCAAGCGGTGTTCCGGAGCTTCTG 1034
Db 1707 GAATCCATTTCTTACGCTCTTCTTGTGATAAACTTCAAGCGGTGTTCCGGAGCTTCTG 1766
Qy 1035 CTTTCCAGTAAGATGAGTGAAGAGGCGGAGAGCACTAGAGAGTCCGAATACAGTTCA 1094
Db 1767 CATCCCAACTCTGTCCAGATGAGAGCAAACTCACTGAGATCTGCTGAGAACACTAG 1826
Qy 1095 GATCTCTGTAC 1107
Db 1827 GAAACATCTCTCC 1839

RESULT 22
US-10-027-632-188121/c

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/ Sequence 188121, Application US/10027632
/ Publication No. US20020198371A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
/ FILE REFERENCE: 108827.129
/ CURRENT APPLICATION NUMBER: US/10/027,632
/ PRIOR FILING DATE: 2002-04-30
/ PRIOR APPLICATION NUMBER: US 60/218,006
/ PRIOR FILING DATE: 2000-07-12
/ PRIOR APPLICATION NUMBER: US 60/198,676
/ PRIOR FILING DATE: 2000-04-20
/ PRIOR APPLICATION NUMBER: US 60/193,483
/ PRIOR FILING DATE: 2000-03-29
/ PRIOR APPLICATION NUMBER: US 60/185,218
/ PRIOR FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: US 60/167,363
/ PRIOR FILING DATE: 1999-11-23
/ PRIOR APPLICATION NUMBER: US 60/156,358
/ PRIOR FILING DATE: 1999-09-28
/ PRIOR APPLICATION NUMBER: US 60/146,002
/ PRIOR FILING DATE: 1999-08-09
/ NUMBER OF SEQ ID NOS: 325720
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 188121
/ LENGTH: 585
/ TYPE: DNA
/ ORGANISM: Human
US-10-027-632-188121
```

Query Match 40.8%; Score 470.6; DB 13; Length 585;

Best Local Similarity 99.8%; Pred. No. 6.9e-126; Matches 470; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
QY 684 CTGCGTCTTCATCTTGGCTTCGTGATCCCTGTCCTCATCATCATGTCGTACACCT 743
DB 585 CTGCGTCTTCATCTTGGCTTCGTGATCCCTGTCCTCATCATCATGTCGTACACCT 526
QY 744 GATGATCCTGCGTCTCAAGAGCGTCCGCTCTTTCTGCTCCCGAGAGAAAGATCGCA 803
DB 525 GATGATCCTGCGTCTCAAGAGCGTCCGCTCTTTCTGCTCCCGAGAGAAAGATCGCA 466
QY 804 CTTGGTGAAGATCACAGACTGCTCTGATGCTGAGTGGAGCTTCGTGCTGAGAC 863
DB 465 CTTGGTGAAGATCACAGACTGCTCTGATGCTGAGTGGAGCTTCGTGCTGAGAC 406
QY 864 TCCCATTCACATATTTCATCTGCTGAGAGCTCTGGGAGACCTCCACAGACAGCTGC 923
DB 405 TCCCATTCACATATTTCATCTGCTGAGAGCTCTGGGAGACCTCCACAGACAGCTGC 346
QY 924 TCTCTCCAGCTATTACTTCTGATGCGCTTGAAGCTATACCAACAGTAGCTGAATCCCAT 983
DB 345 TCTCTCCAGCTATTACTTCTGATGCGCTTGAAGCTATACCAACAGTAGCTGAATCCCAT 286
QY 984 TCTCTACGCTTTCTTGATGAAAACCTTCAAGGGGTGTTCCGGGACTTCTGCTTCCACT 1043
DB 285 TCTCTACGCTTTCTTGATGAAAACCTTCAAGGGGTGTTCCGGGACTTCTGCTTCCACT 226
QY 1044 GAAAGATGAGATGAGAGCGGACAGACACTAGAGAGTCCGAATATACAGTTCAAGATCTGC 1103
DB 225 GAAAGATGAGATGAGAGCGGACAGACACTAGAGAGTCCGAATATACAGTTCAAGATCTGC 166
QY 1104 TTACTGAGGAGCATCGATGGAGTGAATTAACCAAGTAGACTAGTCGTGGA 1154
DB 165 TTACTGAGGAGCATCGATGGAGTGAATTAACCAAGTAGACTAGTCGTGGA 115
```

```
RESULT 23
US-10-027-632-188122/c
/ Sequence 188122, Application US/10027632
/ Publication No. US20020198371A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
/ FILE REFERENCE: 108827.129
/ CURRENT APPLICATION NUMBER: US/10/027,632
/ PRIOR FILING DATE: 2002-04-30
/ PRIOR APPLICATION NUMBER: US 60/218,006
/ PRIOR FILING DATE: 2000-07-12
/ PRIOR APPLICATION NUMBER: US 60/198,676
/ PRIOR FILING DATE: 2000-04-20
/ PRIOR APPLICATION NUMBER: US 60/193,483
/ PRIOR FILING DATE: 2000-03-29
/ PRIOR APPLICATION NUMBER: US 60/185,218
/ PRIOR FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: US 60/167,363
/ PRIOR FILING DATE: 1999-11-23
/ PRIOR APPLICATION NUMBER: US 60/156,358
/ PRIOR FILING DATE: 1999-09-28
/ PRIOR APPLICATION NUMBER: US 60/146,002
/ PRIOR FILING DATE: 1999-08-09
/ NUMBER OF SEQ ID NOS: 325720
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 188122
/ LENGTH: 585
/ TYPE: DNA
/ ORGANISM: Human
US-10-027-632-188122
```

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/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
/ FILE REFERENCE: 108827.129
/ CURRENT APPLICATION NUMBER: US/10/027,632
/ PRIOR FILING DATE: 2002-04-30
/ PRIOR APPLICATION NUMBER: US 60/218,006
/ PRIOR FILING DATE: 2000-07-12
/ PRIOR APPLICATION NUMBER: US 60/198,676
/ PRIOR FILING DATE: 2000-04-20
/ PRIOR APPLICATION NUMBER: US 60/193,483
/ PRIOR FILING DATE: 2000-03-29
/ PRIOR APPLICATION NUMBER: US 60/185,218
/ PRIOR FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: US 60/167,363
/ PRIOR FILING DATE: 1999-11-23
/ PRIOR APPLICATION NUMBER: US 60/156,358
/ PRIOR FILING DATE: 1999-09-28
/ PRIOR APPLICATION NUMBER: US 60/146,002
/ PRIOR FILING DATE: 1999-08-09
/ NUMBER OF SEQ ID NOS: 325720
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 188122
/ LENGTH: 585
/ TYPE: DNA
/ ORGANISM: Human
US-10-027-632-188122
```

Query Match 40.8%; Score 470.6; DB 13; Length 585;

Best Local Similarity 99.8%; Pred. No. 6.9e-126; Matches 470; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 684 CTGCGTCTTCATCTTGGCTTCGTGATCCCTGTCCTCATCATCATGTCGTACACCT 743
DB 585 CTGCGTCTTCATCTTGGCTTCGTGATCCCTGTCCTCATCATCATGTCGTACACCT 526
QY 744 GATGATCCTGCGTCTCAAGAGCGTCCGCTCTTTCTGCTCCCGAGAGAAAGATCGCA 803
DB 525 GATGATCCTGCGTCTCAAGAGCGTCCGCTCTTTCTGCTCCCGAGAGAAAGATCGCA 466
QY 804 CTTGGTGAAGATCACAGACTGCTCTGATGCTGAGTGGAGCTTCGTGCTGAGAC 863
DB 465 CTTGGTGAAGATCACAGACTGCTCTGATGCTGAGTGGAGCTTCGTGCTGAGAC 406
QY 864 TCCCATTCACATATTTCATCTGCTGAGAGCTCTGGGAGACCTCCACAGACAGCTGC 923
DB 405 TCCCATTCACATATTTCATCTGCTGAGAGCTCTGGGAGACCTCCACAGACAGCTGC 346
QY 924 TCTCTCCAGCTATTACTTCTGATGCGCTTGAAGCTATACCAACAGTAGCTGAATCCCAT 983
DB 345 TCTCTCCAGCTATTACTTCTGATGCGCTTGAAGCTATACCAACAGTAGCTGAATCCCAT 286
QY 984 TCTCTACGCTTTCTTGATGAAAACCTTCAAGGGGTGTTCCGGGACTTCTGCTTCCACT 1043
DB 285 TCTCTACGCTTTCTTGATGAAAACCTTCAAGGGGTGTTCCGGGACTTCTGCTTCCACT 226
QY 1044 GAAAGATGAGATGAGAGCGGACAGACACTAGAGAGTCCGAATATACAGTTCAAGATCTGC 1103
DB 225 GAAAGATGAGATGAGAGCGGACAGACACTAGAGAGTCCGAATATACAGTTCAAGATCTGC 166
QY 1104 TTACTGAGGAGCATCGATGGAGTGAATTAACCAAGTAGACTAGTCGTGGA 1154
DB 165 TTACTGAGGAGCATCGATGGAGTGAATTAACCAAGTAGACTAGTCGTGGA 115
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```
RESULT 24
US-10-027-632-188121/c
/ Sequence 188121, Application US/10027632
/ Publication No. US20030204075A9
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
/ FILE REFERENCE: 108827.129
/ CURRENT APPLICATION NUMBER: US/10/027,632
/ PRIOR FILING DATE: 2002-04-30
/ PRIOR APPLICATION NUMBER: US 60/218,006
/ PRIOR FILING DATE: 2000-07-12
/ PRIOR APPLICATION NUMBER: US 60/198,676
/ PRIOR FILING DATE: 2000-04-20
/ PRIOR APPLICATION NUMBER: US 60/193,483
/ PRIOR FILING DATE: 2000-03-29
/ PRIOR APPLICATION NUMBER: US 60/185,218
/ PRIOR FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: US 60/167,363
/ PRIOR FILING DATE: 1999-11-23
/ PRIOR APPLICATION NUMBER: US 60/156,358
/ PRIOR FILING DATE: 1999-09-28
/ PRIOR APPLICATION NUMBER: US 60/146,002
/ PRIOR FILING DATE: 1999-08-09
/ NUMBER OF SEQ ID NOS: 325720
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 188121
/ LENGTH: 585
/ TYPE: DNA
/ ORGANISM: Human
US-10-027-632-188121/c
```

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; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 188121
; LENGTH: 585
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-188121
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Query Match      40.8%; Score 470.6; DB 16; Length 585;
Best Local Similarity 99.8%; Pred. No. 6.9e-126;
Matches 470; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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OY 684 CTGGCTCTTCATCTTTGGCTTCGTCGATCCCTGCTCATCATCATCTGCTGACACCT 743
DB 585 CTGGCTCTTCATCTTTGGCTTCGTCGATCCCTGCTCATCATCATCTGCTGACACCT 526
OY 744 GATGATCTCGGCTCAAGAGCGCTCCGCTCTTTCTGCTCCGAGAGAAAGATCGCAA 803
DB 525 GATGATCTCGGCTCAAGAGCGCTCCGCTCTTTCTGCTCCGAGAGAAAGATCGCAA 466
OY 804 CCTGCGTAGAGATCAACAGACTGCTGTCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 863
DB 465 CTTGCGTAGAGATCAACAGACTGCTGTCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 406
OY 864 TCCCATTCACATATTCATCTCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 923
DB 405 TCCCATTCACATATTCATCTCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 346
OY 924 TCTCTCAGCTATTACTTCTGTCATGCTTGAAGCTTATACCAAGATGCTGAATCCCAT 983
DB 345 TCTCTCAGCTATTACTTCTGTCATGCTTGAAGCTTATACCAAGATGCTGAATCCCAT 286
OY 984 TCTCTACGCTTTCTTGATGAAAACCTTGAAGCGGTGTTCCGGGACTTCTGCTTCCACT 1043
DB 285 TCTCTACGCTTTCTTGATGAAAACCTTGAAGCGGTGTTCCGGGACTTCTGCTTCCACT 226
OY 1044 GAAAGTAGAGATGAGCGGAGAGACCTAGACAGATCCGAAATACAGTTCAAGATCTGTC 1103
DB 225 GAAAGTAGAGATGAGCGGAGAGACCTAGACAGATCCGAAATACAGTTCAAGATCTGTC 166
OY 1104 TTACCTGAGGACATCGATGGAGTGAATTAACCAAGTATGACTAGTCTGTGGA 1154
DB 165 TTACCTGAGGACATCGATGGAGTGAATTAACCAAGTATGACTAGTCTGTGGA 115
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RESULT 25
US-10-027-632-188122/c
; Sequence 188122, Application US/10027632
; Publication No. US20030204075a9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
```

```
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 188122
; LENGTH: 585
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-188122
```

```
Query Match      40.8%; Score 470.6; DB 16; Length 585;
Best Local Similarity 99.8%; Pred. No. 6.9e-126;
Matches 470; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 684 CTGGCTCTTCATCTTTGGCTTCGTCGATCCCTGCTCATCATCATCTGCTGACACCT 743
DB 585 CTGGCTCTTCATCTTTGGCTTCGTCGATCCCTGCTCATCATCATCTGCTGACACCT 526
OY 744 GATGATCTCGGCTCAAGAGCGCTCCGCTCTTTCTGCTCCGAGAGAAAGATCGCAA 803
DB 525 GATGATCTCGGCTCAAGAGCGCTCCGCTCTTTCTGCTCCGAGAGAAAGATCGCAA 466
OY 804 CCTGCGTAGAGATCAACAGACTGCTGTCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 863
DB 465 CTTGCGTAGAGATCAACAGACTGCTGTCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 406
OY 864 TCCCATTCACATATTCATCTCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 923
DB 405 TCCCATTCACATATTCATCTCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 346
OY 924 TCTCTCAGCTATTACTTCTGTCATGCTTGAAGCTTATACCAAGATGCTGAATCCCAT 983
DB 345 TCTCTCAGCTATTACTTCTGTCATGCTTGAAGCTTATACCAAGATGCTGAATCCCAT 286
OY 984 TCTCTACGCTTTCTTGATGAAAACCTTGAAGCGGTGTTCCGGGACTTCTGCTTCCACT 1043
DB 285 TCTCTACGCTTTCTTGATGAAAACCTTGAAGCGGTGTTCCGGGACTTCTGCTTCCACT 226
OY 1044 GAAAGTAGAGATGAGCGGAGAGACCTAGACAGATCCGAAATACAGTTCAAGATCTGTC 1103
DB 225 GAAAGTAGAGATGAGCGGAGAGACCTAGACAGATCCGAAATACAGTTCAAGATCTGTC 166
OY 1104 TTACCTGAGGACATCGATGGAGTGAATTAACCAAGTATGACTAGTCTGTGGA 1154
DB 165 TTACCTGAGGACATCGATGGAGTGAATTAACCAAGTATGACTAGTCTGTGGA 115
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RESULT 26
US-09-841-720-1
; Sequence 1, Application US/09841720
; Publication No. US20030068672A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Lei
; TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND
; METHODS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
```

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/ COUNTRY: USA
/ ZIP: 77210
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent in Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/841,720
/ FILING DATE: 24-Apr-2001
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/120,601
/ FILING DATE: 13-SEP-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Wilson, Mark B.
/ REGISTRATION NUMBER: 37,259
/ REFERENCE/DOCKET NUMBER: INDA:002
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 512/418-3000
/ TELEFAX: 512/474-7577
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1618 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 214..1407
/ SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-841-720-1

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Query Match 38.7%; Score 446.4; DB 10; Length 1618;
 Best Local Similarity 66.9%; Pred. No. 1.2e-118;
 Matches 668; Conservative 0; Mismatches 321; Indels 9; Gaps 2;

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QY 110 ACAGCAGCGGACGCGGCTGCGAGAGACGCGAGCTGGAGCCCGGACATCTCCCGG 169
DB 350 ACCGACCGGCGTTGGCGGAGACGACGCTTGCCTTGACCGGACCCCTTCATGG 409
QY 170 CCATCCCGGTCAATCAACGCGGCTCTACTCCGTAGTTCGTGCGCTTGATGGGCA 229
DB 410 TCACAGCCATTACATCATGCGCCCTCTATCTATGCTGTGTAAGTGGGCTCTTCGGA 469
QY 230 ACTCGCTGTCATGTTCTGATCATCCGATACAAAGATGAAGACGACCAACATTT 289
DB 470 ACTTCCTGTCATGTATGTGATTTGAATACACAAATGAAGACTGCCACCAACATCT 529
QY 290 ACATATTTAACTGGCTTTGGAGAGATGCTTAGTTACTACACATGCCCTTTCAGAGTA 349
DB 530 ACATTTTCAACTCTGCTCTGCGAGACGCTTACGACGACGACGACCTCTTTCAGAGTG 589
QY 350 CGGTCTACTGATGATTCCTGCGCTTTTGGGATGTGCTGCAAGATAGTAATTTCCA 409
DB 590 TCAACTACTGATGGGAACATGCGCTTCGGAACATCTCTGCAAGATGATGATCTCAA 649
QY 410 TTGATTTACTACAAATGTTACACAGCATCTTACCTTGACATGATGACGTCGCT 469
DB 650 TAGATTTACTACAAATGTTACACAGCATCTTACCTTGACATGATGACGTCGCT 709
QY 470 ACATGCGCTGTCGACCCCGGAGAGCTTTGGAATTCGCGACACCTTGAAGGCAAGA 529
DB 710 ACATGCTGCTGTCGACCCGACGACGCTTGAATTTCCGTAACCCCGCAAAATGCAAAA 769
QY 530 TCATCAATATCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 589
DB 770 TCGTCAAGCTGTCGACACTGATCTCTCTCTCTGCAATGCTGCTGCTGCTGCTGCTGCT 829
QY 590 GAGGACCAAAAGTCAAGGAAAGAGCTGATGATGATGATGATGATGATGATGATGATG 649
DB 830 CAACCACAAAATACAGGCGAGGCTC-----CATAGATGACACCTCAGCTTCTCCACC 883

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QY 650 ATGACTACTCTGTGTGAGACCTCTTCATGAAAGATGCGCTTCATCTTGGCTTCGTGA 709
DB 884 CAACCTGTGACTGGAGAACCTGCTC---AAATCTGTCTTTATCTTCGCTTCATCA 940
QY 710 TCCCTGCTCTCATCATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 769
DB 941 TGCCGATCTCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1000
QY 770 GCGCTCTTCTGCGCTCCGAGAGAAAGATGCAACCTGCTGATGATGATGATGATGATGAT 829
DB 1001 GCATCTATCTGCGCTCCAAAGAAAGACAGAAATCTGCGAGATCACCCGAAATGCTC 1060
QY 830 TGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 889
DB 1061 TGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1120
QY 890 AGGCTCTGCGGAGACCTCCACAGACAGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCT 949
DB 1121 AAGCGCTGATACGATTCAGAAACACATTTACAGACGCTTCTGCGACCTTCTGATG 1180
QY 950 CCTTAGGCTATACCAACAGTACCTGATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1009
DB 1181 CTGGGGTTTACACGAAACAGCTGCTGATTCAGATTCAGATTCAGATTCAGATTCAGAT 1240
QY 1010 TCAAGCGGATGTTCCGAGACTTCTGCTTCCACTGAAAGATGAGATGAGAGCGAGAGA 1069
DB 1241 TCAGCGATGCTTTCAGAGATGCTTCTGATTCAGATTCAGATTCAGATTCAGATTCAG 1300
QY 1070 CTAGCAGATCGGAATACAGTTCAAGATCTGCTTAC 1107
DB 1301 CCATCGAGTCCGTCAGAAACACTAGGAAACATCCCTCC 1338

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RESULT 27
 US-09-841-720-3
 ; Sequence 3, Application US/09841720
 ; Publication No. US20030068672A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Yu, Lei
 ; TITLE OF INVENTION: MU OPTOID RECEPTORS: COMPOSITIONS AND METHODS
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: Arnold, White & Durkee
 ; STREET: P.O. Box 4433
 ; CITY: Houston
 ; STATE: Texas
 ; COUNTRY: USA
 ; ZIP: 77210
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/841,720
 ; FILING DATE: 24-Apr-2001
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/120,601
 ; FILING DATE: 13-SEP-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Wilson, Mark B.
 ; REGISTRATION NUMBER: 37,259
 ; REFERENCE/DOCKET NUMBER: INDA:002
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 512/418-3000
 ; TELEFAX: 512/474-7577
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1618 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single

TOPOLOGY: linear
FEATURE: cds
NAME/KEY: CDS
LOCATION: 339..1232
SEQUENCE DESCRIPTION: SEQ ID NO: 3
US-09-841-720-3

Query Match 38.7%; Score 446.4; DB 10; Length 1618;
Best Local Similarity 66.9%; Pred. No. 1.2e-118;
Matches 668; Conservative 0; Mismatches 321; Indels 9; Gaps 2;

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OY 110 ACAGACGCGACGCGCGCTCGAGAGACGCGAGCTGAGCCCGGACATCTCCCGG 169
DB 350 ACCGACCGCGGCTTGGCGGGAACGACAGCTGTGCCCTAGACCGGACCGCTTCATG 409
OY 170 CCATCCCGGTCAATCAACGCGGTCTACTCCGTAGTGTTCGTGCGGCTTGTGGGCA 229
DB 410 TCACAGCCATACCATCATGCGCCCTACTCTATCGTGTGTAGTGGGCTTCCGGA 469
OY 230 ACTCGGTGTCAATGTTCTGTGATCCGATACCAAAAGTGAAGACAGCAACCAATTT 289
DB 470 ACTTCGTGTCAATGATGATGATGATGAACCAAAATGAAGACTGCGACCAACATCT 529
OY 290 ACATATTTACCTGGCTTTGGCAGATGCTTAGTTACTACCAACAGCCCTTTCAGAGTA 349
DB 530 ACATTTTCACTTGTCTGTGCGAGAGCGCTTAGCGACAGTACACTGCGCTTTCAGAGTG 589
OY 350 CGGTCTACTGATGATTAATCTCGGCTTTGGGAGATGCTGTGCAAGATAGTAATTTCA 409
DB 590 TCACATCTACTGATGAGGAACATGCGCCCTTCGAAACCATCTCTGCAAGATCTGATCTCA 649
OY 410 TTGATTTACTACAAACATGTTACACAGATCTTCACTTACCAATGATGAGCGGTGAC 469
DB 650 TAGATTTACTACAAACATGTTACACAGATTAATCACTCTGCAACATGAGCGGTGAC 709
OY 470 ACATTCGCGTGTGCGACCGCGCTTGAAGGCTTGGACCTTCGCAACCTTGAAGGAAAGA 529
DB 710 ACATTCGCGTGTGCGACCGCGCTTGAAGGCTTGGACCTTTCGCAACCTTGAAGGAAAGA 769
OY 530 TCATCAATATCTGCAATCTGTGCTGTGTGTCATCTGTTGGCATCTCTGCAATAGTCTTG 589
DB 770 TCGTCAAGCTGTGCAACCTGATCTCTCTTCTGCAATGCTGTGCTGATGATGTTCAATG 829
OY 590 GAGGACCAAAAGTGAAGGGAAGACGTCATGATGATGATGATGATGATGATGATGATG 649
DB 830 CAACCAAAATATACAGGAGGAGGCTC-----CATGATTTGACCTTCAAGTTCTCCACC 883
OY 650 ATGACTACTCTGTGAGGACCTCTTCAAGATGATGATGATGATGATGATGATGATGATG 709
DB 884 CAACCTGTGATCGGAGAACTGCTC---AAATCTGTGTCTTTATCTTCCGCTTTCATCA 940
OY 710 TCCCTGTCTCTATCATCATCTGTCTGTACCTGTATGATCTGTGCTTCAAGAGCTTC 769
DB 941 TCCCATCTCTATCATCATCTGTGTGTACGCGCTGTATGATCTTATGACTCAAGAGCTTC 1000
OY 770 GGCCTCTTTCGCGCTCCCGAGAGAAAGATTCGCACTGCGTGAATGATGATGATGATG 829
DB 1001 GCATCTTATCGGCTTCCAAAGAAAGACAGAAATCTGCGAGATCAACCGGATGTGTC 1060
OY 830 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 889
DB 1061 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1120
OY 890 AGGCTCTGGGAGACCTTCCACAGACAGAGCTGCTCTCCAGCTATTAATTTGTGATCG 949
DB 1121 AAGGCTCTATCAAGATTCAGAAACCAATTCAGACCGTTCCTGGGACATTCGCAATG 1180
OY 950 CCTTAGGCTATACCAAGATGAGCTGAATCCCATTTCTTACGCGCTTGTGATGAAACT 1009
DB 1181 CTTTGGGTTTACAGAAAGCTGCTGAATCCAGTTCTTTACGCTTCTTGTGATGAAACT 1240
OY 1010 TCAAGCGGTGTTTCCGGGACTTCTGCTTTCATGAAAGATGAGATGAGAGCGGAGCA 1069
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DB 1241 TCAAGCGATGCTTACAGAGATTTCTGCATCCCACTGCTCCAGCATGGAAGAAACT 1300
OY 1070 CTAGCAGATCCGAAATACATTCAGATTCCTGCTTAC 1107
DB 1301 CCATCGAGTCCGTTCAGAACTAGGGAACATCCCTCC 1338
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RESULT 28

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US-10-185-083-25
; Sequence 25, Application US/10185083
; Publication No. US20030050467A1
; GENERAL INFORMATION:
; APPLICANT: Memorial Sloan Kettering Cancer Center
; APPLICANT: Pasteur, Gavril
; APPLICANT: Pan, Ying-Xian
; TITLE OF INVENTION: Multiple Splice Variants of the Mu-Opioid Receptor Gene
; FILE REFERENCE: 83002-2007.1
; CURRENT APPLICATION NUMBER: US/10/185,083
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 60/302,072
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 1464
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-185-083-25
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Query Match 37.8%; Score 436.2; DB 15; Length 1464;
Best Local Similarity 64.7%; Pred. No. 1e-115;
Matches 683; Conservative 0; Mismatches 363; Indels 9; Gaps 2;

```
OY 92 CCGGCTGGGCGGACCGGACGACAAAGCGCGGCTCGAGAGACCGCACTGAGC 151
DB 174 CCGACCATGGGGGTCGGAACCGCACGACCTGGGCGGAGAGACAGCTGCGCTCGA 233
OY 152 CCGGACATCTCCCGGCGCATCCCGGTCAATCAAGGGGCTTACTCGGTAGTGTTC 211
DB 234 CCGGACATCTCCATATATACCGGCATCAAGATCAAGATGAGGCTTCTTCAATCGTGGC 293
OY 212 TCGGCGCTTGTGGGCACTCGCTGTGATGTTGATCATTCGATCATTCGATCAACAAAGTGA 271
DB 294 TGTGTGGGCTCTTCGAAATCTCTGTGATGATGATGATGATGATGATGATGATGATG 353
OY 272 AGACAGCAACCAATTTAATATTAACTGCTTTGGAGATGTTAGTAACTAACAA 331
DB 354 AGACTGCACCAACATCATTAATTTCAACCTTGTGCGAGATGCTTAGCCACAGTA 413
OY 332 CCAATGCCCTTTCAGAGTACGCTCACTTGAATGAAATTCCTGGCTTTGGGAGTGTCT 391
DB 414 CCGGCGCTTTCAGAGTGAATTTAATTTAATGGAATGGAATGGAATGGAATGGAATG 473
OY 392 GCAAGATGATTAATTTCAATGATTTACTACAAATGTTCAACAGATCTTCACTTGACCA 451
DB 474 GCAAGATGATGATTCATGATGATTTACTATAAATGTTCAACAGATTTACCTCTGCA 533
OY 534 CCAATGATGTTGATTCATATCATTCATTCAGTTCGACACCTGTCAAGGCTTATGATTCG 593
DB 512 CACCTTGAAGGCAAAAGATATGATATTCAGATTCAGATTCAGATTCAGATTCAGATTC 571
OY 594 CTCCCGCAAAATGCAAAATTAATTAATGTGCAACTGATGATCTCTTTCAGCAATGTGTC 653
DB 572 TCTCTGCAATAGTCTTGTGAGGCAACAAAGTCAAGGGAAGAGCTGATGATGATGATG 631
OY 654 TTCTGTGAATGTTTATAGGCTACAAACAAATATAGGGA-----GTTTCATGATGAT 707
OY 632 CTTTGAATTCAGATGATGATCTCTGTGTGGACCTTTCATGAAAGATCTGCGCT 691
DB 708 CACTTAACATCTC---TCATCAACCTGTGATGAGAAACCTGTGAAAGATCTGTGTT 764
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;; PRIOR FILING DATE: 2001-02-22
;; PRIOR APPLICATION NUMBER: US 60/336,677
;; PRIOR FILING DATE: 2001-12-05
;; NUMBER OF SEQ ID NOS: 28
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 10
;; LENGTH: 1239
;; TYPE: DNA
;; ORGANISM: Rattus norvegicus
US-10-080-917-10

Query Match 37.7%; Score 434.8; DB 15; Length 1239;
Best Local Similarity 66.3%; Pred. No. 2.5e-115;
Matches 660; Conservative 0; Mismatches 327; Indels 9; Gaps 2;

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QY 92 CCGGCTGGGCGGAGCCCGACAGCAAGGAGCGCGGCTCGAGAGACGGCAGCTGGAGC 151
DB 119 CCGAGCCCATCGGCTCGAAGCCGACCGACCTGGGCGGAGAGACGCCCTGCTCCGCA 178
QY 152 CCGGCGACATCTCCCGGCGCATCCGGTCATCATCGCGGGCTTACTCCGTAAGTTGCG 211
DB 179 CCGGCGAGTCCCTCCATGATCAGCGGCATCAGCATGAGCCCTTACTTCCATGCTGCG 238
QY 212 TCGTGGGCTTGGTGGGCACTGCGTGTGATGTCGATTCGATACCAAGATGA 271
DB 239 TGGTGGGCTCTTGGAACTTCTGTGATGATGATGTCAGATACCAAGATGA 298
QY 272 AGACGACCAACCAATTATCATATTAACTGGCTTGGCAGATGCTTATGATTACAA 331
DB 299 AAGCTGCGCAACCAATCATATTTCACCTTGTCTGTGCAATGCTTAAAGCAGCAAGTA 358
QY 332 CCATGCCCCCTTTCAGAGTACGCTCTGATGATGAATTCCTGGGCTTGGGAGTGTGT 391
DB 359 CCTGCCCCCTTCAGAGTGTGATTAACCTAATGGAACATGGCATTGGAAACATCTTT 418
QY 392 GCAAGATGTAATTTTCATTGATTACTACACATGTTACCGACATCTTACCTTGACCA 451
DB 419 GCAAGATGTAATTTTCATTGATTACTAATCATGTTACCGACATCTTACCTTGCA 478
QY 492 TGATGAGGTGAGCGGCTCATTTGCGGTGCGACCCCGTGAAGGCTTGGACTTCCGCA 511
DB 479 CCAATAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 538
QY 512 CACCTTGAAGGCAAGATCATCAATATCTGATGCTGCTGTGCTCATCTGTTGCA 571
DB 539 CTCCCGAAGTCCAAATATATCATGCTGCACTGATCTCTTCAAGCATGTGTC 598
QY 572 TCTGTGCAATGCTCTTGGAGGCAACAAAGTCAGGAAGAGTGTGATGATGCT 631
DB 599 TTCTGTATGTTCTATGCTACACAAATACAGGCAAGG-----TTCCATGATGTA 652
QY 632 CTTGCAATGCTCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 691
DB 653 CACTAATGCTCTCTATCCAACTGATGATGATGATGATGATGATGATGATGATGATG 709
QY 692 TCAATCTTGGCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 751
DB 710 TCAATCTTGGCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 769
QY 752 TGGCTTGAAGAGCTCCGGCTCTTCTTGGCTCCCGAGAGAAAGATGCAACTGGCTA 811
DB 770 TGGCTTGAAGAGCTCCGGCTCTTCTTGGCTCCCGAGAGAAAGATGCAACTGGCTA 829
QY 812 GGATTCACAGAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 871
DB 830 GGATTCACAGAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 889
QY 872 ACATATTCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 931
DB 890 ACATATTCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 949
QY 932 GCTATTAATCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 991
```

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DB 950 CTGGCACTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1009
QY 992 CTTTCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1051
DB 1010 CATTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1069
QY 1052 GGATGAGCGGCGAGCAGCTAGCAGAGTCGGAATA 1087
DB 1070 ACATTTGAGCAACAAATCTCAGTCTGAAATTCGTGCA 1105
```

RESULT 31
US-10-080-917-8

;; Sequence 8, Application US/10080917
;; Publication No. US20030054451A1
;; GENERAL INFORMATION:
;; APPLICANT: Cadet, Patrick
;; APPLICANT: Stefano, George B.
;; TITLE OF INVENTION: Opiate Receptors
;; FILE REFERENCE: 09598-006001
;; CURRENT APPLICATION NUMBER: US/10/080,917
;; CURRENT FILING DATE: 2002-02-22
;; PRIOR APPLICATION NUMBER: US 60/270,479
;; PRIOR FILING DATE: 2001-02-22
;; PRIOR APPLICATION NUMBER: US 60/336,677
;; PRIOR FILING DATE: 2001-12-05
;; NUMBER OF SEQ ID NOS: 28
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 8
;; LENGTH: 1245
;; TYPE: DNA
;; ORGANISM: Homo Sapiens
US-10-080-917-8

Query Match 37.7%; Score 434.8; DB 15; Length 1245;
Best Local Similarity 66.3%; Pred. No. 2.5e-115;
Matches 660; Conservative 0; Mismatches 327; Indels 9; Gaps 2;

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QY 92 CCGGCTGGGCGGAGCCCGACAGCAAGGAGCGCGGCTCGAGAGACGGCAGCTGGAGC 151
DB 125 CCGAGCCCATCGGCTCGAAGCCGACCGACCTGGGCGGAGAGACGCCCTGCTCCGCA 184
QY 152 CCGGCGACATCTCCCGGCGCATCCGGTCATCATCGCGGGCTTACTCCGTAAGTTGCG 211
DB 185 CCGGCGAGTCCCTCCATGATGATGATGATGATGATGATGATGATGATGATGATG 244
QY 212 TCGTGGGCTTGGTGGGCACTGCGTGTGATGTCGATTCGATACCAAGATGA 271
DB 245 TGGTGGGCTCTTGGAACTTCTGTGATGATGATGATGATGATGATGATGATGATG 304
QY 272 AGACGACCAACCAATTATCATATTAACTGGCTTGGCAGATGCTTATGATTACAA 331
DB 305 AAGCTGCGCAACCAATCATATTTCACCTTGTCTGTGCAATGCTTAAAGCAGCAAGTA 364
QY 332 CCAATGCCCCCTTTCAGAGTACGCTCTGATGATGAATTCCTGGGCTTGGGAGTGTGT 391
DB 365 CCGTGGCTTCCAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 424
QY 392 GCAAGATGTAATTTTCATTGATTACTACAAATGTTACCGACATCTTACCTTGACCA 451
DB 425 GCAAGATGTAATTTTCATTGATTACTAATCATGTTACCGACATATTCACCTTGCA 484
QY 492 TGATGAGGTGAGCGGCTCATTTGCGGTGCGACCCCGTGAAGGCTTGGACTTCCGCA 511
DB 485 CCAATAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 544
QY 512 CACCTTGAAGGCAAGATCATCAATATCTGATGCTGCTGTGCTCATCTTGGGCA 571
DB 545 CTCCCGAAGTCCAAATATATCATGCTGCAACTGATGATGATGATGATGATGATG 604
QY 572 TCTGTGCAATGCTCTTGGAGGCAACAAAGTCAGGAAGAGTGTGATGATGATGCT 631
DB 605 TTCTGTATGTTCTATGCTACCAAAATACAGGCAAGG-----TTCCATGATGTA 658
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Qy	632	CTTGCAGTTCCCAAGATGATGACTCTCTGGTGGGACCTCTTATGAAAGATTGGCTCT	691
Db	659	CACTAACTTCTCTCATCCAACTGGTACTGGGAAACCTGCG--TGAAGATCTGTGTTT	715
Qy	692	TCATCTTTCCTTCGTGATGCCGTGCTCATATCATGCTGCTGCATCAACCCGATGATCC	751
Db	716	TCATCTTGGCCTTATTATGCAAGTGCATCATATTAACGTGTGCTATGGACTGAGATCT	775
Qy	752	TGCGTCTCAAGAGCGTCCGGCTCCTTTCTGGCTCCGAGAGAGAGATGGCACTGGCTA	811
Db	776	TGCGGCTCAAGAGTGTCCGATGCTCTCTGGCTCCAAAGAAAGACAGATCTTCCAA	835
Qy	812	GGATCACCAGACTGGTCCCTGGGAGTGTGGGACGCTTGTGGTCTGCTGGACTCCCATTC	871
Db	836	GGATCACCAAGATGTGTGCTGGTGTGTGGCTGTCTGTTATGCTCTGTCTGGACTCCCATTC	895
Qy	872	ACATATTTCATCTGTGTGAGAGGCTCTGGGAGACCTCCACAGCAGACTGCTCTTCCA	931
Db	896	ACATTATGTCATCTATTAAAGCCTGGTTACAATCCCAAGAACTACGTTCCAGACTGTTT	955
Qy	932	GCTATTACTTCGTCGATCGCGCTTAAGGCTATACCAAGATGAGCTGAAATCCATTCCTTAG	991
Db	956	CTTGGACCTTCTGCATGTGCTCTAGATTACACAAAGACTGCTCAACCAAGTCTTTATG	1015
Qy	992	CCTTTCTTGATGAAAACTTCAAGCCGATGTTCCGGGACTTCTGCTTCCACTGAGAAATGA	1051
Db	1016	CATTTCGTGATGAAAACTTTCAAGATGCTTCAGAGAGTTGTGATTCCAACCTTCTCA	1075
Qy	1052	GGATGAGCGGCGACAGCACTAGACAGATGCCAATA	1087
Db	1076	ACATTGACCAACAAACTCCACTCGAATTTGTCAGA	1111

```

RESULT 32
US-10-185-083-26
? Sequence 26, Application US/10185083
? Publication No. US20030050467A1
? GENERAL INFORMATION:
? APPLICANT: Memorial Sloan Kettering Cancer Center
? APPLICANT: Pasternak, Gavril
? APPLICANT: Pan, Ying-Xian
? TITLE OF INVENTION: Multiple Splice Variants of the Mu-Opioid Receptor Gene
? FILE REFERENCE: 830002-2007.1
? CURRENT APPLICATION NUMBER: US/10/185, 083
? CURRENT FILING DATE: 2002-06-28
? PRIOR APPLICATION NUMBER: 60/302,072
? PRIOR FILING DATE: 2001-06-29
? NUMBER OF SEQ ID NOS: 53
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 26
? LENGTH: 1388
? TYPE: DNA
? ORGANISM: Homo Sapiens
US-10-185-083-26

```

	Query Match	Similarity	Score	DB	Length
Best Local	66.3%	Pred. No. 2.6e-115			
Matches	660	Conservative	0	Mismatches 327	Indels 9; Gaps 2
QY	92	CCGGCTGTGGGCGAGCCCGCAGCAACGCGCAGCGCCGCTCGGAGGACCGCAGCTGAGGC	151		
Db	174	CCGACCCATGGGGGTCCGAACCGCAACGACCTGGGGGAGAGACGCTGGCCCTCCGA	233		
QY	152	CCGCGCAATCTCCCCGCGCATCCCGGTATCATACGCGCGGTCTAATCCGTAAGTTCG	211		
Db	234	CCGCGAGTCCCTCCATGTATCAACGCGCATCACGATCATGCCCCCTTAATCCATCGGTGCG	293		
QY	212	TCGTGGGCTGGTGGGCAACTGCGTGCATCTTGTGTAATCATCCGATACCAAGATGA	271		
Db	294	TGGTGGGCTCTTCGAAACCTTCCGATCATGTATGTATGTCTCAGATPACCAAGATGA	353		
QY	272	AGACGCAACCAACATTATTAATATTTAACCTGGCTTGTGGAGANTCTTTAGTTACTACAA	331		

Db	354	AGACTGCCACCAACATCTTACATTTTCAACCTTGCTCTGGAGATGCTTACCCACCACTA	413
Qy	332	CCATGACCCTTTCAGAGTACGGTCTACTGTGATGAATTCCTGGCCCTTTGGGATGTGCTG	391
Db	414	CCCTGACCTTCCAGAGTGTGAATTACCTAATGGGAACATGGCCATTTGGAAACATCTTT	473
Qy	392	GCAGAGTATGTAATTTCCATTGATTACTACAAACATGTTTCCACGACATCTTCACTTGACA	451
Db	474	GCAAGATATGATCTCCATAGATTACTATAACATGTTTACCAGACATATTTCAACCTCTGCA	533
Qy	452	TGAAGAGCTGGAACCGCTACATTCGCCGTGGCCACCCCGTGAAGGCTTTGGACCTTCGCA	511
Db	534	CCATGAGTGTGATCGATACATTCGACGTGCGCACCTGTGCMAAGCCTTTGATATTTCCGTA	593
Qy	512	CACCCCTTGAAGGCAAAAGATCATCAATATCTGCACTGGCTGCTCGTCACTCTTGCGCA	571
Db	594	CTCCCCGAAATGCCAAATTTATCAATGTCTGCAACTGATCTCTCTTCAGCCATTGGTC	653
Qy	572	TCTCTGCAATATGTCCTTGGAGGCAACAAAGTCAGGGAAAGTCATGTCATTGATGTCT	631
Db	654	TTCTGTATATGTTATGATGGCTACACAAATATCAGGGCAAG-----TTCCATATATTGTA	707
Qy	632	CCTTGCACTTCCCAAGATGATCATCTCTGTGTGGAGCTCTTATATGAATCTTGGCTCT	691
Db	708	CACATCAATTTCTTCATCTCAACACCTGGATCTGGGAAACCTGCG---TGAAGATCTGTGTTT	764
Qy	692	TCATCTTTGACCTTGATGCCCTGCTCCATCATCATCTGCTGCTGCTACACCTGATGATGCC	751
Db	765	TCATCTTGCCCTTATTAATATGCAAGTGTCTCATCATTAACCGTGTGCTATATGAGATGATATCT	824
Qy	752	TGCGTCTCAAGAGCGTCGGCTCTCTTTCTTGCGCTCCGAGAGAAAGATCGAACCTGCGTA	811
Db	825	TGGCGCTCAAGAGTGCAGATGCTCTGTGGCTCTCAAGAAAGAACAGACGGAATCTTGAA	884
Qy	812	GGATGCACCAACTGCTCTGTGTGTGTGGCAGTCTTCTGTCTGTCTGCACTTCCATTC	871
Db	885	GGATCACCAGAGATGT	944
Qy	872	ACATATTTCATCTGTGTGGAGGCTCTGTGGAGGACCTCCACAGACAGCTGCTCTGCCA	931
Db	945	ACATTTACGTATCATTAAGACCTTGTGTATCAATCCAGAAACTAGTCTCCAGACTGTTT	1004
Qy	932	GCTATTACTTGTGCATGCGCTTATAGCTATAACCAAGTAGCTGATATCCATTTCTACAG	991
Db	1005	CTTGGCACTTGTGATGTGCTCTAGTTATACAAACAGCTGCTCAACCCAGTCTTTATG	1064
Qy	992	CCTTTCTTGATGAACCTTCAAGCGGTGTTCCGGGACTTCTGCTTTCACCTGAAGATGA	1051
Db	1065	CATTTCTGAGTGAACACTTCAACGATGCTTCAAGAGATTTCTGATCCAACTCTTCCA	1124
Qy	1052	GGATGAGCGGCAAGACCTTAGCAGAGTCCGAATA	1087
Db	1125	ACATTTGAGCAACAAATCTCCACTGTGAATTCGTCTGA	1160

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? RESULT 33
? US-10-194-595-26
? Sequence 26, Application US/10194595
? Publication No. US20030068805A1
? GENERAL INFORMATION:
? APPLICANT: Memorial Sloan Kettering Cancer Center
? APPLICANT: Pasternak, Gavril
? APPLICANT: Pan, Ying-Xian
? TITLE OF INVENTION: Multiple Splice Variants of the Mu-Opioid Receptor Gene
? FILE REFERENCE: 830002-2007.1
? CURRENT APPLICATION NUMBER: US/10/194,595
? CURRENT FILING DATE: 2002-07-11
? PRIOR APPLICATION NUMBER: US/09/561,523
? PRIOR FILING DATE: 2002-07-03
? PRIOR APPLICATION NUMBER: 60/302,072
? PRIOR FILING DATE: 2001-06-29
? NUMBER OF SEQ ID NOS: 53

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Qy	692	CCATCTTTGCGCTGGATATCCCTGTCATCATATCATGCTGTGTAACAACCTGATGATCC	751
Dp	902	TCATCTTGCCCTCAATTATATGACAGATGCTCATATTACCGCTGGCTATATGAGATGAATGATT	961
Qy	752	TGCGCTCAAGAGACGTCCGGCTCCTTTCTGAGCTCCGAGAGAAATCGCAACTGCGTA	811
Dp	962	TGCGGCTCAAGATGTCCGCAATGCTCTCTGGCTCCAAAGAAAGACAGAAATCTTCCAA	1022
Qy	812	GGATCACCAAGACTGGTCTGTGGTGGTGGACGTCTTGTGCTGTGCTGAGACTCCATTG	871
Dp	1022	GGATCACCAAGATGGTGGTGGTGGTGGTGGCTGTGTTACCTGTGCTGAGATCCCAATTC	1083
Qy	872	ACATTTGATCCTGGTGGAGAGGCTCTGGGGAGACCTCCACAGCAAGCTGCTCTGTCCA	931
Dp	1082	ACATTTAGCTATCAATTAAAGCTTGGTTTACATCCCAAGAACTACGTTCAGACTGTTT	1144
Qy	932	GCTATTACTTCTGCATCTGCCCTTAGGCTATACACACAGTACGCTGATCCATTCTCTAGC	991
Dp	1142	CTTGGCACTTCTGCATTTGCTCTAGATTACACAAACAGCTGCTCAACCAAGTCTTTATG	1203
Qy	992	CCTTTCTTGATGAAAACTTCAAGCGGTGTTTCCGGAACCTTGTGCTTTCATGAAAGATGA	1051
Dp	1202	CATTTCTGGATGAAAACTTCAACGATGCTCAGAGAGTTCTGTATCCCAACTCTTCCA	1263
Qy	1052	GGATGAGACGGCAGAGCACTAGCAAGTCCGAAATA	1087
Dp	1262	ACATTGAGCAACAAACCTCCATCGAATTGTGTACA	1297

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RESULT 35
US-10-080-917-12
; Sequence 12, Application US/10080917
; Publication No. US20030054451A1
; GENERAL INFORMATION:
; APPLICANT: Cadet, Patrick
; APPLICANT: Stefano, George B.
; TITLE OF INVENTION: Opiate Receptors
; FILE REFERENCE: 09598-006001
; CURRENT APPLICATION NUMBER: US/10/080,917
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: US 60/270,479
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: US 60/336,677
; PRIOR FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 2149
; TYPE: DNA
; ORGANISM: Homo Sapiens
; US-10-080-917-12

```

Query Match	37.7%	Score 434.8;	DB 15;	Length 2149;
Best Local Similarity	66.3%	Pred. No. 3.2e-115;		
Matches 660;	Conservative 0;	Mismatches 327;	Indels 9;	Gaps 2

Qy	92	CCGAGTGGGCGAGGCGGACAGCAACGGGAGGCGCGGCTCGGAGGAGACGGGACGCTGGAGG	151
Db	334	CCGACCCATGGGGTCCGAACGGCACCGACTTGGGGGGGAGAGAACAGCTGTGGCTCCGCA	393
Qy	152	CCGGCGACATCTCCCGGCGCATCCCGGCATCATCAGCGCGGTTACTTCGGTAGTTTCG	211
Db	394	CCGGAGTCCCTCCATGATCAAGCGGCATCAGATATGGCCCTCTACTTCATCGTGTGG	453
Qy	212	TCTGTGGGCTTGGTGGCAACTCGCTGTGCATGTTCTGATCATCCGATACCAAAAGATGA	271
Db	454	TGTGTGGGCTCTTCGGAACCTTCGTGCATGTATGTGTTGTGAGATACCAACAGATGA	513
Qy	272	AGACAGCAACCAACTTACATATTAACTGTGGCTTTGGCGAGTCCGTTTAGTTACTACA	331
Db	514	AGACTGCCACCAACATCTACATTTTCAACTTGTCTGTGGCAGATCCCTTAGGCAACAGTA	573

OY	332	CAATGACCCCTTCAAGATACGGTCTACTTGATGAAATTCCTGAGCCCTTTGGGGAGATGTGCTG	391
Db	574	CCCTGCCCCCTTCAAGAGTGTGAATTAACCTAATGGGACATGGCCATTGGAACCATCTCTT	633
OY	392	GCAAGATAGTAATTTCCATTGATTACTACAAACATGTTACACAGCATCTTGCACCTTGACCA	451
Db	634	GCAAGATAGTATCTCCATAGATTACTATAACATGTTACACAGCATATTACCCCTCTGCA	693
OY	452	TGATAGCGTGGAGCCGCTACATTGCGGTGGCCACCCCGTGAAAGGCTTTGACTTCGGCA	511
Db	694	CCATGAGTGTGATCGATTGACATTGCACTGCGCACCCCTGTCAAGGCGCTTGATTTCCGTA	753
OY	512	CACCCCTTGAAGGGCAAAATGATCAATATCTGCAATCTGGCTGCTGTGTCATCTGTGGCA	571
Db	754	CTCCCCGAATATGCCAAATATTATCAATCTGTGCAACTGGATCTCTCTTCAAGCCATGGTC	813
OY	572	TCTCTGCATATAGTCTCTTGAGAGGCACCAAAAGTCAAGGGAGAAGTCGATGATTAAGTCT	631
Db	814	TTCTCTGTAATGTTATATGGCTACAAACAAATATACAGGCAAG-----TTCCATAGATTGTA	867
OY	632	CTTTGCAGTTCCAGATGATGACTACTCTGCTGGGGAGCTCTTTCATGAAAGATCTGCGTCT	691
Db	868	CACATAATTTCTCATCCAAACCTGATCGGGAAAACTGCG--TGAAATCTGTGTTT	924
OY	692	TGATCTTTGGCTTGGTATCCCTGTCTCTATCATCATGCTCTGTACACCTGATATGATCC	751
Db	925	TGATCTTTCGCTTCATTATGCGCAAGTGCATCATATTACCGTGTGTATGAGCTAGATGATCT	984
OY	752	TGCGTCTCAAGAGCGTCCGGCTCCTTTCTGAGCTCCGAGAAAAAGATCGAACCTGGGTA	811
Db	985	TGCGCTCTCAAGAGTCTCCGATGCTCTGTGGCTTCCAAAGAAAAAGACAGAAATCTTGAA	1044
OY	812	GGATCACACAGCTGGTCTGTGTGTGTGGCAAGTCTTGTGCTGTGTGTGACATCTCCATTC	871
Db	1045	GGATCACACAGATGTGCTGTGTGTGTGTGGCTGTGTTTCACTGCTGTGTGACATCTCCATTC	1104
OY	872	ACATATTATCTGTGTGTGAGGCTCTGTGGAGAGCACTTCCACAGACACAGCTGCTCTGCCA	931
Db	1105	ACATTTAAGTATCATTTAAAGCCTTGTGTACAATCCCAAGAACTGATTCACAAGCTGTTT	1164
OY	932	GCTATTACTCTGCACTGCGCTTAGAGCTATACCAACAGTAGACCTGAATCCCATCTCTACG	991
Db	1165	CTTGGCACTTCTGATTTGCTCTAGGTTACCAAAACAGCTGCTCCAAACCAAGTCTTTATG	1224
OY	992	CTTTTCTTGATGAAAATTCAAGCGGTGTTCCGGGACTTTCTGCTTTCCATGAAAGTGA	1051
Db	1225	CATTTCTGATGAAAACTTCAAAAGATGCTTCAGAGAGTTCTGTATCCCAACCTCTTCCA	1284
OY	1052	GGATGAGCGGCGACAGCACTACAGAGATCCGMAATA	1087
Db	1285	ACATTGAGCAACAACCTCACTGAAATTTGTGAGA	1320

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RESULT 36
US-10-225-567A-195
; Sequence 185, Application US/10225567A
; Publication No. US20030113796A1
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; PRIORITY FILING DATE: 2001-12-19
; PRIORITY FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 185
; LENGTH: 2162
; TYPE: DNA

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? ORGANISM: Homo sapiens
?
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (2061)..(2063)
?
? OTHER INFORMATION: unknown nucleotide
?
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (2091)..(2091)
?
? OTHER INFORMATION: unknown nucleotide
US-10-225-5674-185

```

Query Match	37.7%;	Score 434.8;	DB 15;	length 2162;
Best Local Similarity	66.3%;	Pred. No. 3.2e-115;		
Matches 660;	Conservative	0;	Mismatches 327;	Indels 9; Gaps 2

OY		92	CCGGCTGGAGCGGACGCCCAACAGCAA	CGGCAGCGCCGGCTTCGGAGAACCGCAGCTGAAGC	151
Dp		337	CCGACCATTGTGGGTCCGAACCGCACAA	CTTGGGGGGAGAGACAGCCTGTGCCTCCGA	396
OY		152	CCGGSCAATCTCCCCGGGSCAATCCGGG	CATCATCAAGCGGCTTAACTCCGTAAGTTCCG	211
Dp		397	CCGGCAGTCCCTCAATGATCAAGGCATCA	GCATATGAGCCCTTAATCTCAATCGTGTGG	456
OY		212	TCTGTGGCTTGGATGGCAACTCGCTGTG	CATGTTGTGATCATCCGATAACAAGAATGA	271
Dp		457	TGTGTGGGCTCTTCGGAACCTTCGTGT	CACTGATGTAATGTGAGATACCAAGATGA	516
OY		272	AGACAGCAACCAACATTTACATATTTAA	CTGGCTTTGGCAGATGCTTTAGTTACTAA	331
Dp		517	AGACTGCACCAACATCTACATTTTTCAA	CTTGCTCTGGCAGATCCCTTAGGCACACAGTA	576
OY		332	CCATGACCTTTCAGAGTACGGGTCTACT	GATGAATTCGAGCCTTTTGGGGATGTGCGT	391
Dp		577	CCCTGCCCCTTTCAGAGTGTGAATTTAC	TAAATGGAAACATGGCCATTTTGGAACATCCTTT	636
OY		392	GCAAGATAGTAATTTCCATTTGATTA	CTAACAAATGTTCAACGACATCTTCAACCTTGACCA	451
Dp		637	GCAAGATGTATCTTCATATGATTA	CTATTAACATGTTTACCGACATATTTACACCCGTCTMGCA	696
OY		452	TGATGAGCGGTGACCGCTCAACTATGG	CCGTGTGCACACCCGTGAAGGCTTTGACCTTCGCA	511
Dp		697	CCAATGAGTGTGATCGATACATGGA	ATGGAAGTGCACCCCTGTCAAGGCCCTTAATATTTCCGTA	756
OY		512	CACCCCTTGAAGGCAAAAGATCATCAAT	AATCTGCATCTGCTGTGCTCATCTGTGTGSCA	571
Dp		757	CTCCCCGAAAAGCCAAATTTTCAATG	CTGTGCAACTGSAATCTCTCTTCAAGCATTTGTC	816
OY		572	TCTCTGCAATATGCTCTTGGAGSAC	CAAAAGTCAAGGAAGACGTGCATGTCAATTGATGCT	631
Dp		817	TTCTCTGTAATGTTATGTGCTCAAA	CAAAATTCAGGCAAGG-----TTCCATAGATTGTA	870
OY		632	CCTTGAGAGTCCCGAGATGATGATCA	ATCTCTGTGGGACCTCTTATGANAAGTTCGCCGT	691
Dp		871	CACTTAACATTTCTCATCTCCAA	CTGTGATCTGTGGAAAACTCTG--TGAAGATCTGTGTTT	927
OY		692	TCATCTTTGCTTCGTGATCCCTGTCC	TGCTCATCATCATGCTGTGCTAACACCTGTAGATCC	751
Dp		928	TCATCTTCGCTTCAATTATGCAATG	GTCAATTAACGTGTGCTAATGSACTGATGATCT	987
OY		752	TGCGTCTCAAGAGCGTCCGCTCCTTT	TGTGCTCTCCGAGAGAAAAGTGCACACTTGCGTA	811
Dp		988	TGCGCTTCAAGAGGTCCGCAATGCTCT	CTGTGCTCCAAAAGAAAAGACAGGAATCTTGGA	1047
OY		812	GGATCACACAGCTGATCCTGTGGTGG	AGGAGCTTCGTGTGCTGAGCTCCCATTC	871
Dp		1048	GGATCACACAGGATGTGTGTGGTGG	TGGTGGTGTGTTTCATGCTGTGAGCTCCCATTC	1107
OY		872	ACAATATTCATCTGTGTGAGGCTCT	GTGGAGACACCTCCACAGACAGACTCTCTTCCA	931
Dp		1108	ACAATTTACGTATCATTAAGCCTT	TGGTTACATCCAGAAAACTAAGTCCAGACTGTTT	1167
OY		932	GCAATTAATCTTGTGATGCGCTTAG	GCTTAATACCAAGTAGCTTAATCCATTTCTTACG	991

Db 1168 CTTGGCACTTCTGCATTGCTCTAGATTACAAACAGCTGCTCAACCACTCTTTATG 1222

Qy 992 CCTTCTTGATGAAGAAACCTCAAGGGGTTTCCGGGACTTCTGCTTTCACCTGAAGATGA 1051

Db 1228 CATTCTCGAATGAAGAACTTCAACAGATGCTTCAAGAGGTTCTGTATCCACACTCTTCCA 1287

Qy 1052 GGATGAGAGGGCAGACGACTAGCAGAGTCCGAATA 1087

Db 1288 ACATTGAGCAACAACCTCCACTCGAATTCGTCTGA 1323

RESULT 37
US-10-305-720-1379

```

; Sequence 1379, Application US/10305720
; Publication No. US20040010136A1
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression
; FILE REFERENCE: PA-0002-1 CON
; CURRENT APPLICATION NUMBER: US/10/305,720
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 09/016,434
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 1490
; SOFTWARE: PERL Program
; SEQ ID NO 1379
; LENGTH: 2162
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Genbank ID NO. US20040010136A1 g452072
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1) ... (2162)
; OTHER INFORMATION: a, t, c, g, or other
US-10-305-720-1379

```

Query Match	37.7%	Score 434.8;	DB 16;	Length 2162;
Best Local Similarity	66.3%	Pred. No. 3.2e-115;		
Matches 660; Conservative	0;	Mismatches 327;	Indels 9;	Gaps 2;

Qy	92	CCGGCTGGGGCCGAGCCCGGACAGCAACGGCAGCGCGGTCTGGAGAGCGCGCAGCTGGAGC	151
Db	337	CCGACCCATGCGGTCCGAAACCGCACCAACTGGCGGGAGAGAACAGCTGTGGCCCTCCGA	396
Qy	152	CCGGGCAATCTCCCCGGGCATCCCGGTTCATCATCGCGAGTCTACTCCGTAGTGTGG	211
Db	397	CCGGCAATCCCTCATATACCGGCATACAGATCATGGCCCTTACTCTCCATCGTGTGG	456
Qy	212	TCTGGGCTGTGTGGGCACTCGTGTGATGTTCTGTGATCATCCGATACCAAAAGATGA	271
Db	457	TGGTGGGGCTCTTCGGAACCTCTCGTCATGTATGTGATGTGATCAGATACCAAAAGATGA	516
Qy	272	AGACAGCAACCAATTTACATTTATTTAACCGCTTGGCGAGATGTTAGTTACTACAA	331
Db	517	AGACTGCAACCAATTTACATTTTCAACCTTGTCTGGCGAGATGCTTACGCAACAGTA	576
Qy	332	CCATGCCCTTTCAGAGTACGGTCTACTGTGAATTCCTTGGCCCTTTGGGAGTGTGCTGT	391
Db	577	CCCTGCCCTTTCAGAGTGTGAATTACTTAATGGAAATATGGCCATTTGGAAACCATTCCTTT	636
Qy	392	GCAAGATAGTAAATTTCCATTTGATTTACATCAACATGTTTACACAGATCTTCACTTGACCA	451
Db	637	GCAAGATAGTATCTCATAGATTATCATTAACAATTTTACACAGATATTCACCCCTTGCA	696
Qy	452	TGATGAGCGTGGACCGCTACATTGCCGTGGCCACCCCGTGAAAGCTTTGGACTTTCGCA	511
Db	697	CCATGAGTGTGTGATTCGATTCATTTGCAATCTGCGCACCTGTCTAABGCGCTAGATTTCCGTA	756
Qy	512	CACCTTTGAAGGCAAGATCATCAATATCTGCATCTGGCTGTGCTCATCTGTGGCA	571
Db	757	CTCCCCGAAATGCAAAATATCATATCTGCGCACTGGATCTCTCTTTCAGCCATTTGGTC	816


```

: Publication NO. US20030068805A1
: GENERAL INFORMATION:
: APPLICANT: Memorial Sloan Kettering Cancer Center
: APPLICANT: Pasternak, Gavril
: APPLICANT: Pan, Ying-Xian
: TITLE OF INVENTION: Multiple Splice Variants of the Mu-Opioid Receptor Gene
: FILE REFERENCE: 830002-2007.1
: CURRENT APPLICATION NUMBER: US/10/194,595
: PRIORITY FILING DATE: 2002-07-11
: PRIOR APPLICATION NUMBER: US/09/561,523
: PRIOR FILING DATE: 2002-07-03
: PRIOR APPLICATION NUMBER: 60/3302,072
: PRIOR FILING DATE: 2001-06-29
: NUMBER OF SEQ ID NOS: 53
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 21
: LENGTH: 2951
: TYPE: DNA
: ORGANISM: Mus Sp.
: US-10-194-595-21

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Query Match	37.5%	Score 432.6;	DB 15;	Length 2951;
Best Local Similarity	64.4%;	Pred. No. 1.6e-114;		
Matches 683;	Conservative 0;	Mismatches 369;	Indels 9;	Gaps 2

QY	92	CCGGCTGGGGCCGAGCCGACACAGCAACGGCAGCGCGCTCGAGAGACGCGCAGCTGAGAC	151
Db	185	CCGACCCATGGGGTCTTAACCGCAAGGGGCTTGGCGAGACCAACGCTGTGCCCTCAGA	244
QY	152	CCGGCAATCTCCCCGCCATCCGGGTATATCAAGGGGTTCTACTCCGAGTGTTC	211
Db	245	CCGGAGGCCCTTCATGGTTCAGAGCATCACCATCATGGCCCTCTATTCTATCGTGTGG	304
QY	212	TCTGGGCTTGGTGGGCAACTGCTGTCATCTGTGTATCTATCCGATCAACAAGATGA	271
Db	305	TAGTGGGCTCTTTGGAACTTCCGTGTCATATATGATTTGTAAGATATACCAAAATGA	364
QY	272	AGACAGCAACCAACATTTACATATTTAACTTGGCTTTGGCAGATCCTTTAGTTACTACA	331
Db	365	AGACTGCCACAAACATCTACATTTTCAACTTGTCTGTGGCAGATGCTTACGCCACTAGA	424
QY	332	CCATGCCCCCTTCAAGTACGGTCTATCTATGATGAATTTCCGGGCTTTTGGGATGTGCTGT	391
Db	425	CGTGGCTTTTCAAGGTGTAACTACCTGATGGAAAGTGGCCCTTTGGAAACATCTCT	484
QY	392	GCAAGATAGTATTTCCATGTATTACTACAACATGTTGACACGATCTTCACTTGACCA	451
Db	485	GCAAGATGTAATCTCAATAGCTACTACAAATGTTTACACAGTATCTTCAACCTCTGGA	544
QY	452	TGATGAGGTGGAACGGTACATTTGCCGTGTGCCACCCCGTGAAGCTTTGACCTTCCGA	511
Db	545	CCATGAGGTGAGACCGCTACATTTGCCGTGTGCCACCCGGTCAAGGCCCTGTGATTTCCGA	604
QY	512	CACCCCTGAAGGCAAAAGATCAATCAATATCTGTGATCTGGCTGTGTCATGTGTTGGCA	571
Db	605	CCCCCGGAAATGCCAAATTTGTCAATGTCTGCACATGTGATCTCTCTTCTGCCATTGGTC	664
QY	572	TCTTGTCAATATGTCCTTGGAGGACCAAAAGTCAAGGGAAGAAGTGAATCATTGAAGTCT	631
Db	665	TGCCCGTATGTTATGTGGCAACCAACAAATACAGGCA-----GGGGTCCATAGATTGCA	718
QY	632	CCTTGGAGTTCCAGATGATGATCTACTCTGTGGGACCTCTTCAATGAAGATCTTGGCT	691
Db	719	CCCTCAGTTTCTCATCTCCACATGTGTAAGTGGGAACCTGTCT--AAAATCTGTGTCT	775
QY	692	TCAATCTTTGACCTTGTGATCTCCTGTCCATCATCATGCTGTGTCACCCGTGATATCC	751
Db	776	TCAATCTTGGCTTATCATATGCGGGTCTCATCATCATCACTGTGTGTTATGGAATGAATGATCT	835
QY	752	TGCGTCTCAAGAGGCTCGGCTCTTTTGTGGCTCCGAGAGAAAGATGCACCTTGGTA	811
Db	836	TACACATCAAGAGTGTGCGATGTCTGTGGGCTCCAAAGAAAGACAGGAACCTGGCCA	895

[illegible]

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RESULT 43
US-10-185-083-22
; Sequence 22, Application US/10185083
; Publication NO.: US20030050467A1
; GENERAL INFORMATION:
; APPLICANT: Memorial Sloan Kettering Cancer Center
; APPLICANT: Pasternak, Gavril
; APPLICANT: Pan, Ying-Xian
; TITLE OF INVENTION: Multiple Splice Variants of the Mu-Opioid Receptor Gene
; FILE REFERENCE: 830002-2007.1
; CURRENT APPLICATION NUMBER: US/10/185,083
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 60/302,072
; PRIOR FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 1332
; TYPE: DNA
; ORGANISM: Mus Sp.
US-10-185-083-22

```

Query Match	Similarity	37.5%	Score	432.4	DB	15	Length	1332
Best Local	Similarity	65.8%	Pred.	No.	1.3e-114			
Matches	663	Conservative	0	Mismatches	336	Indels	9	Gaps
QY	92	CCGGCTGGGCCGAGCCCGACAGCAACGGCAGCCGGCTCGAGAGACGCGCAGCTGAGNC	151					
DY	185	CCGACCCATCGGGCTTAACCGACAGGGGGCTGGCGGGAGCCACAGCCTGGCCCTGAGA	244					
QY	152	CCGGGCAATCTCCCGGGCATCCCGGTACTATCAAGGGGCTACTCCGTAGTGTTCG	211					
DB	245	CCGGCAGCCCTTCCATGATGACAGCCATCAACATCAGGCGCTTATTTCTATCGTGTGTG	304					
QY	212	TCGTGGCTTGTGTGGCACTCGTGTGTCATGTTCTGATCATCCGATCAACAAGATGA	271					
DB	305	TAGTGGGCTCTTTTGGAAACTTCTGTGTCATGATGATGATTAAGATATATCCAAATATGA	364					
QY	272	AGACAGCAACCAATTTACATATTTAACTGGCTTTGGCAGATGCTTTAGTTACTACAA	331					
DB	365	AGACTGCCAACCAATCTACATTTTCAACCTTGTCTGGCAGATGCCCTTGGCCACTAGCA	424					
QY	332	CCATGCCCTTTGAGAGTAGCGTCTACTATGATGAATTCGTGGCTTTTGGGGATGTGCTGT	391					
DB	425	CGCTGCCCTTTGAGAGTGTTAATCTACTATGGGAACGTGGCCCTTTGGAAACATCTCTCT	484					
QY	392	GCAAGATAGTAATTTTCATTGATTACTCAACAATGTTTCACAGCATCTTCACTTGACAA	451					

485 GCAGAGTGTGATCTCAATAGACTACTACAAACATGTTCCAGATCTTACCCCTCTGCA 544
QY 452 TGATAGAGTGGACCGCTACATTTGCGTGTGCGACCCCGTGAAGGCTTTGACCTTCCGA 511
Db 545 CCATAGAGTGAACCGCTACATTTGCGTGTGCGACCCCGTGAAGGCTTTGACCTTCCGA 604
QY 512 CACCTTGAAGGCAAGATCATCATATTCGTCATGCTGCTGTGTCATGTGTTGGA 571
Db 605 CCCCCGAAATGCCAAATTTGTCAATGTGTGCACTGATCTCTCTTGTGCAATTTGGTC 664
QY 572 TCTGTCAATAGTCTTGTGAGGCGACCAAGTCAGGAAAGACGTGCATGTGATGAGTGT 631
Db 665 TGCCCGTATGTTCTAGGCAACCAAAATATACAGCAGGAGGTC-----CATAGATTGCA 718
QY 632 CTTTGACATTTCCCAATGATGACTACTCTGCTGTGAGGACCTCTTCATGAAAGATCGCT 691
Db 719 CCTTCACGTTCTCTCATCCCATGATGATGAGGAAACCTGTCTC--AAAATCTGTGTCT 775
QY 692 TCATCTTGGCTTCCGTGATCCCTGTCTCATCATCATGCTGTGCTACACCCGTGATGATCC 751
Db 776 TCATTTTGGCTTTCATCATGCGGCTCTCATCATCATGTGTGTATGAGACTGATGATCT 835
QY 752 TGCGTCTCAAGAGCGTCCGCGCTCTTGTGCTCCGAGAGAAAGATGCAACTGCGTA 811
Db 836 TACGACTCAAGAGTGTCCGCAATGCTGTGCGGCTCCAAAGAAAGACAGAACTGCGCA 895
QY 812 GGATCAACAGACTGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 871
Db 896 GGATCAACCGAGT 955
QY 872 ACATATTCATCTGT 931
Db 956 ACATATGTATGTATCATCAAGACATGATCAAGATTTCCAAACCACTTTCCAGACTGTT 1015
QY 932 GCTATTTACTTGTGATGCTGCTTGTGAGCTATACCAACAGTAGCCTGATCTCTCTACG 991
Db 1016 CTTGACACTTCTGATGCTGCTTGTGAGCTATACCAACAGTAGCCTGATCTCTCTACG 1075
QY 992 CCTTTCTGTGATGAATCTTCAAGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1051
Db 1076 GGTTCCTGTGATGAATCTTCAAGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1135
QY 1052 GGATGACGCGCAGAGCACTAGCAGATCCGAAATATACAGTTCCAGATC 1099
Db 1136 CAATGAAACAGCAAACTCTGCTGAAATCCGTCAAACCACTAGGGAAC 1183

RESULT 44

US-10-194-595-22
; Sequence 22, Application US/10194595
; Publication No. US20030068805A1
; GENERAL INFORMATION:
; APPLICANT: Memorial Sloan Kettering Cancer Center
; APPLICANT: Pasternak, Gavril
; TITLE OR INVENTION: Multiple Splice Variants of the Mu-Opioid Receptor Gene
; FILE REFERENCE: 830002-2007.1
; CURRENT APPLICATION NUMBER: US/10/194,595
; PRIOR FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: US/09/561,523
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 60/302,072
; PRIOR FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 1332
; TYPE: DNA
; ORGANISM: Mus Sp.
US-10-194-595-22

Query Match 37.5%; Score 432.4; DB 15; Length 1332;
Best Local Similarity 65.8%; Pred. No. 1.3e-114;

Matches 663; Conservative 0; Mismatches 336; Indels 9; Gaps 2;

QY 92 CCGGCTGGGCGGAGCGCAGACAGCAAGCGCGGCTCGGAGGAGACGGCGAGCTGGAGC 151
Db 185 CCGAGCCATGCGGCTTAACCGCAGCGAGGCTTTGGGAGGCCACAGCCTGTGCCCTCACA 244
QY 152 CCGGCAACATCTCCCGGCGCATCCCGGTCATCATCAGCGCGGTCTTACTCCGTAGTGTG 211
Db 245 CCGGCAACCGCTTCCATGATGATCAGGCAATCAGCATATGAGCCCTCTATTTCTATGCTGTG 304
QY 212 TCGTGGGCTGTGTGGGCAATCTGCTGTGATGTTGTGTATCATCCGATATCAACAAAGATCA 271
Db 305 TAGTGGGCTCTTTGGAATCTCTGTGATGATGATGATGATGATGATGATGATGATGATGAT 364
QY 272 AGACGCAACCAATTTACATTTAATTTAATCTGCTTTGGCGAGATCTTATGATTACTACAA 331
Db 365 AGACTGCCACCAACATCTACATTTTCAACTTGTCTGTGAGATGCTTGAACACTAGCA 424
QY 332 CCATGCCCTTTCAGAGTACGCTCTACTGATGAAATTTCCGTGCTTTTGGGAGTGTGCTGT 391
Db 425 CGCTGCCCTTTCAGAGTGTAACTATCCTGATGAGAAAGTGTGCTTTGGAACATCTCTCT 484
QY 392 GCAGATGATATTTCCATTTGATTAATTAACAAATGTTCACAGACTTTTACCTTGACCA 451
Db 485 GCAGATGATGATCTCAATAGACTACTCAACATGTTCAACAGTATCTTCACTCTGCA 544
QY 452 TGATAGAGTGGACCGCTACATTTGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 511
Db 545 CCATAGAGTGAACCGCTACATTTGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 604
QY 512 CACCTTGAAGGCAAGATCATCATATTCGTCATGCTGTGCTGTGTCATGTGTTGGA 571
Db 605 CCCCCGAAATGCCAAATTTGTCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 664
QY 572 TCTGTCAATAGTCTTGTGAGGCGACCAAGTCAGGAAAGACGTGCATGTGATGAGTGT 631
Db 665 TGCCCGTATGTTCTAGGCAACCAAAATATACAGCAGGAGGTC-----CATAGATTGCA 718
QY 632 CTTTGCAATTTCCCAATGATGACTACTCTGTGTGAGACTCTTTCATGAAAGATCGCTCT 691
Db 719 CCTTCACGTTCTCTCATCCCATGATGATGAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 775
QY 692 TCATCTTGGCTTCCGTGATGCTGCTCTCATCATCATGCTGTGCTACACCCGTGATGATCC 751
Db 776 TCATTTTGGCTTTCATCATGCGGCTCTCATCATCATGTGTGTATGAGACTGATGATCT 835
QY 752 TGCGTCTCAAGAGCGTCCGCGCTCTTGTGCTCCGAGAGAAAGATGCAACTGCGTA 811
Db 836 TACGACTCAAGAGTGTCCGCAATGCTGTGCGGCTCCAAAGAAAGACAGAACTGCGCA 895
QY 812 GGATCAACAGACTGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 871
Db 896 GGATCAACCGAGT 955
QY 872 ACATATTCATCTGT 931
Db 956 ACATATGTATGTATCATCAAGACATGATCAAGATTTCCAAACCACTTTCCAGACTGTT 1015
QY 932 GCTATTTACTTGTGATGCTGCTTGTGAGCTATACCAACAGTAGCCTGATCTCTCTACG 991
Db 1016 CTTGACACTTCTGATGCTGCTTGTGAGCTATACCAACAGTAGCCTGATCTCTCTACG 1075
QY 992 CCTTTCTGTGATGAATCTTCAAGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1051
Db 1076 GGTTCCTGTGATGAATCTTCAAGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1135
QY 1052 GGATGACGCGCAGAGCACTAGCAGATCCGAAATATACAGTTCCAGATC 1099
Db 1136 CAATGAAACAGCAAACTCTGCTGAAATCCGTCAAACCACTAGGGAAC 1183

RESULT 45
US-09-761-962-3

```

; Sequence 3, Application US/09761962
; Patent No. US20020077285A1
; GENERAL INFORMATION:
; APPLICANT: Memorial Sloan-Kettering Cancer Center
; TITLE OF INVENTION: Identification and Characterization of Multiple Splice
; TITLE OF INVENTION: Variants of Mu-
; TITLE OF INVENTION: Opioid Receptor (MOR-1) Gene
; FILE REFERENCE: 830002-2000.1
; CURRENT APPLICATION NUMBER: US/09/761,962
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/743,872
; PRIOR FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 3
; LENGTH: 1334
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-761-962-3

```

```

Query Match      37.5%; Score 432.4; DB 9; Length 1334;
Best Local Similarity 65.8%; Pred. No. 1.3e-114;
Matches 663; Conservative 0; Mismatches 336; Indels 9; Gaps 2;

```

```

QY 92 CCGGCTGGGCGGAGCCCGACAGCAACGGGCGCGGCTCGAGAGACGGGCGAGCTGGAGC 151
DB 105 CCGACCCATGCGGTCTTAACCGGAGGGGCTTGGGGAGCCAGCCTGTGCTCAGA 244
QY 152 CCGGCGACATCTCCCGGCGCATCCGGTATCATACGGCGGTCTACTCCGATGTTG 211
DB 245 CCGGAGCGCTTCCATGAGTCAAGCAGCATCAACATATGCGCTTATCTATCGTGTG 304
QY 212 TCGTGCGGTGGTGGGCAATCGCTGTCATCTTGTATATCCGATACCAAGATGA 271
DB 305 TAGTGGGCTCTTGGAACTCTCTGTGATGATATGATATGAATATCAAAATGA 364
QY 272 AGACAGCAACCAATTATTAATTAACTGGCTTTGGAGATCTTAACTTACTTAA 331
DB 365 AGACTGCCACCAACTATCAATTTTCAACCTTGTCTGGAGATGCTTACGACTAC 424
QY 332 CCATGCCCTTTGAGATAGCGGTCTAATTGATGAATTTCTGGCTTTGGAGATGCTGT 391
DB 425 CGCTGCCCTTTGAGATGATTAATCTAGATGGAGAACTGGCCCTTTGAAATCTCT 484
QY 392 GCAAGATGATATTTCCATGATTAATTAACAATGTTACACAGATCTTCACTTGA 451
DB 485 GCAAGATGATATTTCAATGATTAATTAACAATGTTACACAGATCTTCACTTGA 544
QY 452 TGATAGCGTGGAGCCGCTACATTTGCGTGGCAACCCGCTGAAGGCTTTGACTT 511
DB 545 CCATGAGTGTAGACCGGTATCAATTTGCGTGGCAACCCGCTGAAGGCTTTGACTT 604
QY 512 CACCTTTGAAGGCAAAATCAATCAATATCTGATTTGCTGCTGTCTGATCTGTG 571
DB 605 CCCCCGAAAGGCCAAATGTCTCAATGTCTGCAATGATCTCTCTTCTCCATTTG 664
QY 572 TCTCTGCAATGATGCTTGGAGGACCAAAATGAGGAGAGAGATGATGATAGTCT 631
DB 665 TGCCCGTAAATGTTATGAGCAACCAAAATATAGGAGAGGAGTCTCTCTCTCT 718
QY 632 CTTTGACATTCAGATGATGATCTCTGATGGGAGCTCTTCAATGAAGATGCTGCT 691
DB 719 CCGTCAAGCTTCTCATCTCCACATGATGATCTGGAGAACCTGCTCTCTCTCT 775
QY 692 TCAATCTTTGCTTGTGATCTCTGCTCTCATCATCATCTGCTCAACCTGATGAT 751
DB 776 TCAATCTTTGCTTGTGATCTCTGCTCTCATCATCATCTGCTCAACCTGATGAT 835
QY 752 TGCGCTTCAAGAGGCTCGGCTCTCTTGTGGCTCCCGAGAAAGATGCAAACTGGGTA 811
DB 836 TAGACATCAAGAGTGTGGAGATGCTGTGGGCTCCAAAGAAAGAGAGAACTGGGCA 895
QY 812 GGATCACCAGACTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 871

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DB 896 GGATCACCAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 955
QY 872 ACATATTCATCTGTGTGAGGCTCTGGGAGACCTCCCAAGACAGACTCTCTTCCA 931
DB 966 ACATATTCATCTGTGTGAGGCTCTGGGAGACCTCCCAAGACAGACTCTCTTCCA 1015
QY 932 GCTATTTACTTGCATGCGCTTGAAGCTATACCAACAGTACGCTGAATCTTCTAG 991
DB 1016 CCGGCACTTCTGATGCTCTTGGGTTACCAAAACAGTGTCTGAACCTGCTTATG 1075
QY 992 CTTTCTGATGAAGAACTTCAAGCGGTCTTCCGAGCTTCTGCTTCCAGTAAGATGA 1051
DB 1076 GCTTCTGATGAAGAACTTCAAGCGGTCTTCCGAGCTTCTGCTTCCAGTAAGATGA 1135
QY 1052 GGATGAGCGGCGAGAGCACTAGCAGATCCGAATATAGTTACAGATC 1099
DB 1136 CAATCGAAGCAGCAAAACTGTGCTGGAATCCGTCAAAACACTAGGAGAC 1183

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RESULT 46
US-10-283-300-3
; Sequence 3, Application US/10283300
; Publication No. US20030103972A1
; GENERAL INFORMATION:
; APPLICANT: Memorial Sloan-Kettering Cancer Center
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF MULTIPLE SPLICE VARIANTS
; TITLE OF INVENTION: OF THE MU-OPIOID RECEPTOR GENE
; FILE REFERENCE: 830002-2000.3
; CURRENT APPLICATION NUMBER: US/10/283,300
; CURRENT FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: 09/761,962
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/743,872
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: PCT/US99/15974
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 3
; LENGTH: 1334
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-283-300-3

```

```

Query Match      37.5%; Score 432.4; DB 15; Length 1334;
Best Local Similarity 65.8%; Pred. No. 1.3e-114;
Matches 663; Conservative 0; Mismatches 336; Indels 9; Gaps 2;

```

```

QY 92 CCGGCTGGGCGGAGCCCGACAGCAACGGGCGCGGCTCGAGAGACGGGCGAGCTGGAGC 151
DB 185 CCGACCCATGCGGTCTTAACCGGAGGGGCTTGGGGAGCCAGCCTGTGCTCAGA 244
QY 152 CCGGCGACATCTCCCGGCGCATCCGGTATCATACGGGCGGTCTACTCCGATGTTG 211
DB 245 CCGGAGCGCTTTCATGATGATCAAGCAGCATCAATGAGGCTCTTATCTATGTGTG 304
QY 212 TCGTGCGGTGGTGGGCAATCGCTGTCATGTTTGTGATCATCGATACAAAGATGA 271
DB 305 TAGTGGGCTCTTGGAACTTCTGTGATGATGATGATGATGATGATGATGATGATG 364
QY 272 AGACAGCAACCAATTATTAATTTAACTGGCTTTGGAGATGCTTAACTTAACTA 331
DB 365 AGACTGCCACCAACTATCAATTTTCAACCTTGTCTGGAGATGCTTAACTTAACTA 424
QY 332 CCATGCCCTTTGAGATAGCGTCTACTGATGAATTTCTGAGCTTTTGGAGATGCTGT 391
DB 425 CGCTGCCCTTTGAGATGATTAATCTGATGAGAAAGTGGGCTTTGAAATCATCTCT 484
QY 392 GCAAGATGATATTTGATGATTTACTTACAAATGTTTCAACAGACTTCACTTGA 451
DB 485 GCAAGATGATGATCTCAATGATTAATTAACAATGTTTCAACAGATCTTCACTTGA 544

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Qy	452	TGATGAGCGTGAACCGCTCAATTCGCCGTGTGCACACCCGTGAAGGCTTTGACCTTCGGCA	511
Db	545	CCATGAGTGTGAGACCGCTCAATGTCCGTCTGTGCACACCCGTGAAGGCTTCGATATTCGGTA	604
Qy	512	CACCCCTTGAAGGCAAGATTCATCATATCTGCATCTGGCTGTGCTGCATCTGTGTGGCA	571
Db	605	CCCCCGGAAATGGCAAAATTTGTCAATGTCTGCAATGGATCCTCTCTTCTGTGCATTTGGTCC	664
Qy	572	TCTCTGCATATGTCCTTGGAGGACCAAAATGACGGGAAGAAGTGCATGTCAATGAGTCT	631
Db	665	TGCCCGTAAATGTCAATGGCAACCAAAATATCAGGCAAGGGGTCTC-----CATAGATTGCA	718
Qy	632	CCTTGACAGTTCCCAAGATGATGACATCTCTCGTGGTGGACCTCTCTCATGAAGATCTGCTCT	691
Db	719	CCCTCAGCTTCTCTCATCTCCACATGTGTACTGGAGAAACCTGTCTC---AAATCTGTGCT	775
Qy	692	TCATCTTTTGCCTTGTGTATCCCTGTCTCATCATCATCATGTCTGTCTACACCTGATGATCC	751
Db	776	TCATCTTGCCTTTCATCATGCCGGGCTTCATCATCATCATGTGTGTATGGAATGATGATCT	835
Qy	752	TGCGTTCACAAAGCGTCCGGGCTCCTTTTCTGTGCTCCCGAGAAAGATGGCAACCTGGCGTA	811
Db	836	TACAGACTAAAGTGTCCGATGTCTGTGGGCTCCAAAGAAAGGACAGAACTTGGCGCA	895
Qy	812	GGATCACCAGACTGTCTCCGTGTGTGTGTGTGAGAGTCTTGTGTCTGTCTGTGACTCCCATTC	871
Db	896	GGATCACCAGATGT	955
Qy	872	ACATATTCATCTCTGTGTGAGGCTCTGTGGGAGACCTCCCAACAGCAGCTGTCTCTCCA	931
Db	956	ACATCTATGTATCATCATCAACACATGATCACGATTCAGAAACCACTTTCAGACTGTCTT	1015
Qy	932	GCTATTACTTGTGCATCCGCTTATGGGCTATTACCAACAGTAGCGTGAATCCCATTTCTACG	991
Db	1016	CCTGGCACTTGTGATTTGCTTGGGTTTACAAAGACGTGCTGAAACCAAGTCTTTATG	1075
Qy	992	CCTTCTTGTATGAAAACCTTCAAGCGGCTTTCGGGACTTCTGCTTTCATCTGAAGATGA	1051
Db	1076	CGTTCCTGTGATGAAAACCTTCAAAACCATGTTTTATGAGAGTTCGTGACTCCCACTTCTCCA	1135
Qy	1052	GGATGGAGCGGACAGCAGCTAGACAGTCCGAAATACAGTTCAAGATC	1099
Db	1136	CAATCGAACAGCAAAACTCTGCTGAAATCGTCAAAACATGAGGAAAC	1183

RESULT 47

US-09-761-962-11

Sequence 11. Application US/09761962

Patent No. US20020077285A1

GENERAL INFORMATION:

APPLICANT: Memorial Sloan-Kettering Cancer Center

TITLE OF INVENTION: Identification and Characterization of Multiple Splice

TITLE OF INVENTION: Variants of Mu-

TITLE OF INVENTION: Opioid Receptor (MOR-1) Gene

FILE REFERENCE: 830002-2000 1

CURRENT APPLICATION NUMBER: US/09/761,962

CURRENT FILING DATE: 2001-01-17

PRIOR APPLICATION NUMBER: 09/743,872

PRIOR FILING DATE: 2001-03-13

NUMBER OF SEQ ID NOS: 46

SOFTWARE: PatentIn version 3.0

SEQ ID NO 11

LENGTH: 1365

TYPE: DNA

ORGANISM: Mus musculus

US-09-761-962-11

Query Match	37.5%	Score 432.4	DB 9	Length 1365
Best Local Similarity	65.8%	Pred. No. 1.3e-114		
Matches 663	Conservative	0	Mismatches 336	Indels 9
				Gaps 2

92 CCGGCTGGGCGGAGCCCGACAGCAACGCGAGCGCGCTCGAGGAGCGCGCAGCTTGAGCC 151

D	b		185	CCGACCCATGGCGGTCTTAACCGCAGCGGGGCTTGGCGGGAGGCACAAGCCTGTGGCCTCAGA	244
O	y		152	CCGCGCAACATCTCCCGGCCCATCCCGGTCATCATCACGGGGGTCTACTCCGTAGTTGCG	211
D	b		245	CCGGCAGCGCCCTTCATGGTACAGCCCAATCAACATCAGGCCCTCATTTCTTCGTGTGTC	304
O	y		212	TTCGGGGCTTGATGGGGAACCTGGTCAATGTTTCGTGATCATCCGATPACAAAGATGA	271
D	b		305	TAGTGGGCTCTTTGGAAACTTCGTGTCAATGATGATGATTGAAGATATACAAAATGA	364
O	y		272	AGACAGCAACCAATTTACATTTAATTAACCTGGCTTTGGCAGATGCTTAGTTACTCAA	331
D	b		365	AGATGCCACCAACATCTACATTTTCAACCTGTGCTGGCAGATGCTTAGCCACTAGCA	424
O	y		332	CCATGCCCTTTCAGAGTACGGCTCTACTTGATGAATTCCTGGCCTTTTGGGGATGTGCTGT	391
D	b		425	CGTGCCTCTTCAAGATGTTTAACTTACCCTGATGGGAACGTGGCCCTTTGGAAACATCTCT	484
O	y		392	GCAAGATATGTAATTTCCATTGATTAACATAACATGTTTCAACAGATCTTCACTCAACCA	451
D	b		485	GCAAGATGTGATCTCAATAGACTACTACAAACATGTTTCAACAGATCTTCAACCTCTGCA	544
O	y		452	TGATGACCGTGGACCGGCTACATTTGCCGTGTGGCCACCCCGTGAAAGCTTTGGACTTCCGA	511
D	b		545	CCAATGAGTATGACCGGTACATTTGCCGTGTGGCCACCCGGTCAAGCCCTGGATTTCCGTA	604
O	y		512	CACCTTGAAAGGCAAGATCATCAATATCTGCATCTGGCTGTGCTCATCTGTGGCA	571
D	b		605	CCCCCCCANAATGGCTCAATGTCTGCAACTGSAATCTCTCTCTTCTGCCAATTTGGTC	664
O	y		572	TCTGTGAATATGTCCTTTGGAGGGCCAAAGTCAAGGAAAGCTGATGTCTATGATGCT	631
D	b		665	TGCCGTAATGTTATGACACCAAAATATACAGGACAGGGGTC-----CATGAATTGCA	718
O	y		632	CCTTGACATTTCCAGATGATGACTACTCTGTGGTGGGACCTTTGATGAAGATCTGCGTCT	691
D	b		719	CCCTCAGGTTCTCATCTCCACCATGATATCTGGAGAACCTGTCTC---AAATCTGTGCT	775
O	y		692	TCATCTTTGCTTGTGTATCCCTGTCTCTCATCATCATCTGTCTGCTACACCTGATGATCC	751
D	b		776	TCATCTTCGCTTTCATCATGCGGCTCTCATCATCATCTGTGTGTTATGATGTGATGATCT	835
O	y		752	TGGGTCTCAAGAGGCTCCGGCTCCTTTCTGGCTCCGAGAGAAAGATCGAACCTGGGTA	811
D	b		836	TACACCTCAAGAGTGTCCGACTGCTGTGGGCTCAAAAGAAAGACAGGAACCTTGCGCA	895
O	y		812	GGATCACACAGACTGTCTGTGTGTGTGGGAGCTTTCGTGTCTGTGTGACTCCCATTC	871
D	b		896	GGATCACCCGGATGTGTGTGTGTGTGTGTGTGTATTTATTTGTGTGTGGACCCCATTC	955
O	y		872	ACATATTCATCTGTGTGGAGGCTCTGGGAGACACTTCCACAGCACAGCTGTCTTCCCA	931
D	b		956	ACATCTATGTTCATCATCAAGCACATGTATCAAGATTCAGAAACCATTTCCAGACTGT	1015
O	y		932	GCTATTTACTTGTGATGGCTTTAGGCTATACCAACAGATGCTGAATCCCATCTCTACG	991
D	b		1016	CTTGGCACTTGTGATTTGCTTGGGTTACACAAACAGCTGCTTAAACCCAGTTCTTTATG	1075
O	y		992	CCTTTCTTGATGAATACTTCAAGGAGTGTTCGCGGACTTCTGTCTTCCACTGAAGATGA	1051
D	b		1076	CGTTCTGTGAATGAATACTTCAAGATGTTTATGAGATTTCTGATCCCAACTTCTTCCA	1135
O	y		1052	GGATGAGACGGCAGACACTAGCAGATCCGAAATACATGTTCAAGATC	1099
D	b		1136	CAATCGAACAGCAAACTGTGCTGAATCCGTCAAAACACTTAGGGAAAC	1183

RESULT 48
US-10-283-300-11
; Sequence 11, Application US/10283300
; Publication No. US20030103972A1
; GENERAL INFORMATION:
; APPLICANT: Memorial Sloan-Kettering Cancer Center

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; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF MULTIPLE SPLICE VARIANTS
; FILE REFERENCE: 830002-2000.3
; CURRENT APPLICATION NUMBER: US/10/283,300
; PRIOR FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: 09/761,962
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/743,872
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: PCT/US99/15974
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 1365
; TYPE: DNA
; ORGANISM: Mus musculus
; US-10-283-300-11

```

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Query Match      37.5%; Score 432.4; DB 15; Length 1365;
Best Local Similarity 65.8%; Pred. No. 1.3e-114;
Matches 663; Conservative 0; Mismatches 336; Indels 9; Gaps 2;

```

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QY 92 CCGGCTGGGCGGAGCCCGACAGCAACGCGAGCGCGCTCGAGAGACGCGCAGCTGGAGC 151
DB 185 CCGACCCATGCGGCTCTTAACCGGAGCGCTTGGGGAGGACCAAGCCTGTGCCCTCAGA 244
QY 152 CCGGCGACATCTCCCGCGCATCCGGGTATATCAAGCGGCTCTACTCCGTAGTGTTCG 211
DB 245 CCGGAGCGCTTCCATGTCACAGGCATCACCATATGCCCCCTCTATCTCTATCGGTGTG 304
QY 212 TCGTGGGCTTGGTGGGCAACTCGTGTGATGTTCGTATCATCCGATACCAAAAGATGA 271
DB 305 TAGTGGGCTCTTTGGAACTTCTCGGTGATGTATGTATGTAAAGATATACCAAAATGA 364
QY 272 AGACAGCAACCAATTTAATATTTAACTTGGCTTGGCAGATCTTTAGTTACTACAA 331
DB 365 AGACTGCCACCAACTATTAATTTTCAACTTGTCTGGCAGATGCTTAGCCACTAGCA 424
QY 332 CCATGCGCTTTCAGAGTACGGTCTACTGATGCAATTTCTCGGCTTTTGGGATGTGCTGT 391
DB 425 CGCTGCCCTTTCAGAGTGTAACTATGATGGAACGTGGCTTTGGAAACATCTCT 484
QY 392 GCAAGATGATATTTCAATGATTTACTACCAATGTCACAGCATCTTCACTTGAACCA 451
DB 485 GCAAGATGATATTTCAATGATTTACTACCAATGTCACAGCATCTTCACTTGAACCA 544
QY 452 TGATGAGGTGGACCGCTTACATTTGCGGTGCGACCCCGTGAAGGCTTTGACCTTCCGCA 511
DB 545 CCATGAGGTGAGACCGCTTACATTTGCGGTGCGACCCCGTGAAGGCTTTGACCTTCCGCA 604
QY 512 CACCTTGAAGGCAAAAGATCAATATCTGATCTGCTGTGCTGCTGCTGCTGCTGCTGCA 571
DB 605 CCCCCCAAAATGCAAAATGTCATATGTCGAACTGATCTCTCTTCTGCAATGCTGTC 664
QY 572 TCTGTCAATAGTCTTGTGAGAGCAACAAAGTCAGGGAAGAGCTGATCTTGAAGTGTCT 631
DB 665 TGCCGTATATGTTATGGAACCAACAAATACAGGCAAGGGGTCTCTCTATGATTTGCA 718
QY 632 CCTTGCAATTTCCCAATATGATGATCTCTGTGTGGGACCTTCTTCAATGAAGATCTGCTGT 691
DB 719 CCGTCAAGTCTCTCATCCACATGATGATCTGGAGAACCTGCTCTCTCTCTGCTGTCT 775
QY 692 TCATCTTGGCTGATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 751
DB 776 TCATCTTGGCTGATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 835
QY 752 TGGCTTCAAGAGCGTCCGCTCTTCTGTGCTCCGAGAGAAAGATCGCAACCTGTGCTA 811
DB 836 TACAGCTCAAGAGGTCCGATGCTGTGCTGCTCCAAAGAAAGAGACAGGAACCTGTGCA 895
QY 812 GGATCAACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 871

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DB 896 GGATCAACCCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 955
QY 872 ACATATTCATCTGCTGAGGCTCTTGGGAGACACTCCACAGACAGACTGCTCTTCCA 931
DB 966 ACATCTATGATCATCAAAAGCACTGATCAGATTCAGAAACCACTTCCAGACTGTTT 1015
QY 932 GCTATTTACTTGTGATGCTGCTTGAAGCTTATACCAACAGAGCTGATATCCATTTCTTACG 991
DB 1016 CCGGCACTTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1075
QY 992 CTTTCTTATGATAAACTTCAAGCGGTGTTCGGGCACTTCTGCTTCCACTGAAGATGA 1051
DB 1076 CGTTCCTGATGAGAAACCTTCAAGAGATGTTTAAAGATTTGATCCCAACTCTTCCA 1135
QY 1052 GGATGAGCGGCAAGACATGACAGAGTCCGAAATPACAGTTACAGATC 1099
DB 1136 CAATGCAACAGCAAAACTGCTGCTGCAATCCGTCAAAACACTAGGGAAC 1183

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RESULT 49
US-10-185-083.51
; Sequence 51, Application US/10185083
; Publication No. US20030050467A1
; GENERAL INFORMATION:
; APPLICANT: Memorial Sloan Kettering Cancer Center
; APPLICANT: Pasternak, Gavril
; APPLICANT: Pan, Ying-Xian
; TITLE OF INVENTION: Multiple Splice Variants of the Mu-Opioid Receptor Gene
; FILE REFERENCE: 830002-2007.1
; CURRENT APPLICATION NUMBER: US/10/185,083
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 60/302,072
; PRIOR FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 51
; LENGTH: 1373
; TYPE: DNA
; ORGANISM: Mus Sp.
; US-10-185-083-51

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```

Query Match      37.5%; Score 432.4; DB 15; Length 1373;
Best Local Similarity 65.8%; Pred. No. 1.3e-114;
Matches 663; Conservative 0; Mismatches 336; Indels 9; Gaps 2;

```

```

QY 92 CCGGCTGGGCGGAGCCCGACAGCAACGCGAGCGCGCTCGAGAGACGCGCAGCTGGAGC 151
DB 185 CCGACCCATGCGGCTCTTAACCGGAGCGCTTGGGGAGGACCAAGCCTGTGCCCTCAGA 244
QY 152 CCGGCGACATCTCCCGCGCATCCGGGTATATCAAGCGGCTCTACTCCGTAGTGTTCG 211
DB 245 CCGGAGCGCTTCCATGTCACAGGCATCACCATATGCCCCCTCTATCTCTATCGGTGTG 304
QY 212 TCGTGGGCTTGGTGGGCAACTCGTGTGATGTTCGTATCATCCGATACCAAAAGATGA 271
DB 305 TAGTGGGCTCTTTGGAACTTCTCGGTGATGTATGTATGTAAAGATATACCAAAATGA 364
QY 272 AGACAGCAACCAATTTAATATTTAACTTGGCTTGGCAGATCTTTAGTTACTACAA 331
DB 365 AGACTGCCACCAACTATTAATTTTCAACTTGTCTGGCAGATGCTTAGCCACTAGCA 424
QY 332 CCATGCGCTTTCAGAGTACGGTCTACTGATGCAATTTCTCGGCTTTTGGGATGTGCTGT 391
DB 425 CGCTGCCCTTTCAGAGTGTAACTATGATGGAACGTGGCTTTTGGAAACATCTCTCT 484
QY 392 GCAAGATGATATTTCAATGATTTACTACCAATGTCACAGCATCTTCACTTGAACCA 451
DB 485 GCAAGATGATATTTCAATGATTTACTACCAATGTCACAGCATCTTCACTTGAACCA 544
QY 452 TGATGAGGTGGACCGCTTACATTTGCGGTGCGACCCCGTGAAGGCTTTGACCTTCCGCA 511
DB 545 CCATGAGGTGAGACCGCTTACATTTGCGGTGCGACCCCGTGAAGGCTTTGACCTTCCGCA 604

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QY 512 CACCTTGAAGGCAAAAGATCATATATCTGCATCTGCTGCTGCTCATCTGTTGGCA 571
DB 605 CCCCCGAAATGCGAAAATTTGATATGTCTGCAATCGAATCTCTCTTCTGCAATGGTC 664
QY 572 TCTGTCAATAGTCTCTTGGAGGCAACCAAGTCAAGGAGACGTGATGATTTAGTGTCT 631
DB 665 TGCCGCTATATGTTATGCAACCAACCAAAATACAGGAGGGGTC-----CATAGATTGCA 718
QY 632 CCTTGACGTCTCCCAATGATGATCTCTGCTGGAGACCTCTTCATGAAAGATCTGGCTCT 691
DB 719 CCTCAGCTTCTCTATCCACATGATGATCTGAGAGAACCTGCTC--AAATCTGTGCT 775
QY 692 TCATCTTTCCTCTGATCCCTGCTGCTGCTCATCTGCTGCTGCTGCTGCTGCTGCTGCT 751
DB 776 TCATCTGCTCTTCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 835
QY 752 TCGCTCTCAAGACGCTCGGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 811
DB 836 TACGACTCAAGAGTGTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 895
QY 812 GGATCAACCAAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 871
DB 896 GGATCAACCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 955
QY 872 ACATATTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 931
DB 956 ACATATTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1015
QY 932 GCTATTACTTCTGATCGCTTGAAGCTATACCAAGTACCTGATCCATTTCTCTAG 991
DB 1016 CTTGCACTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1075
QY 992 CTTTCTTGATGAAATCTCAAGCGGCTTTCCGGGACTTCTGCTTCTCACTGAAAGTCA 1051
DB 1076 CTTTCTTGATGAAATCTCAAGCGGCTTTCCGGGACTTCTGCTTCTCACTGAAAGTCA 1135
QY 1052 GGATGAGGCGGAGAGCACTAGACAGTCCGAATTCAGTTCAAGATC 1099
DB 1136 CAATGAAACGCAAAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1183

RESULT 50
US-10-194-595-51
; Sequence 51, Application US/10194595
; Publication No. US20030068805A1
; GENERAL INFORMATION:
; APPLICANT: Memorial Sloan Kettering Cancer Center
; APPLICANT: Pasternak, Gavril
; APPLICANT: Pan, Ying-Xian
; TITLE OF INVENTION: Multiple Splice Variants of the Mu-Opioid Receptor Gene
; FILE REFERENCE: 830002-2007.1
; CURRENT APPLICATION NUMBER: US/10/194,595
; PRIOR FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: US/09/561,523
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 60/302,072
; PRIOR FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 51
; LENGTH: 1373
; TYPE: DNA
; ORGANISM: Mus Sp.
US-10-194-595-51

Query Match 37.5%; Score 432.4; DB 15; Length 1373;
Best Local Similarity 65.8%; Pred No. 1.3e-114;
Matches 663; Conservative 0; Mismatches 336; Indels 9; Gaps 2;

QY 92 CCGGCTGGGCGGAGCCCGACAGCAACGAGCGCGGCTCGAGAGACCGGACGCTGGAGC 151
DB 185 CCGACCCATTCGGGCTCTAACCGACGGGGCTTGGGGGAGCCACAGCCTGTGCTCCAGA 244

QY 152 CCGGCAACATCTCCCGGCGCATCCGGTATCATCAAGCGGCTACTCCGATGTTGG 211
DB 245 CCGGAGCGCTTCCATGGTCAAGCATCAATCATATGACCTCTATTTCTATCTGTGG 304
QY 212 TCGTGGGCTTGGTGGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 271
DB 305 TAGTGGGCTCTTTGGAAATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 364
QY 272 AGACAGCAACCAATTTACATTTTAACCTGCTTGGCAATGCTTTAGTACTCA 331
DB 365 AGACTGCCACCAACATTTACATTTTAACCTGCTTGGCAATGCTTTAGTACTCA 424
QY 332 CCGTGGGCTTGGTGGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 391
DB 425 CCGTGGGCTTGGTGGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 484
QY 392 GCAAGATGATATTTTCAATTTTCAATTTTCAATTTTCAATTTTCAATTTTCAATTT 451
DB 485 GCAAGATGATATTTTCAATTTTCAATTTTCAATTTTCAATTTTCAATTTTCAATTT 544
QY 452 TGATGAGTGGAGCGGCTACATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 511
DB 545 CCATGAGTGGAGCGGCTACATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 604
QY 512 CACCTTGAAGGCAAAAGATCATATATCTGCATCTGCTGCTGCTCATCTGTTGGCA 571
DB 605 CCCCCGAAATGCGAAAATTTGATATGTCTGCAATCGAATCTCTCTTCTGCAATGGTC 664
QY 572 TCTGTCAATAGTCTCTTGGAGGCAACCAAGTCAAGGAGACGTGATGATTTAGTGTCT 631
DB 665 TGCCGCTATATGTTATGCAACCAACCAAAATACAGGAGGGGTC-----CATAGATTGCA 718
QY 632 CTTTCTTGATGAAATCTCAAGCGGCTTTCCGGGACTTCTGCTTCTCACTGAAAGTCA 691
DB 719 CTTTCTTGATGAAATCTCAAGCGGCTTTCCGGGACTTCTGCTTCTCACTGAAAGTCA 775
QY 692 TCATCTTTCCTCTGATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 751
DB 776 TCATCTGCTCTTCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 835
QY 752 TCGCTCTCAAGACGCTCGGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 811
DB 836 TACGACTCAAGAGTGTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 895
QY 812 GGATCAACCAAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 871
DB 896 GGATCAACCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 955
QY 872 ACATATTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 931
DB 956 ACATATTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1015
QY 932 GCTATTACTTCTGATCGCTTGAAGCTATACCAAGTACCTGATCCATTTCTCTAG 991
DB 1016 CTTGCACTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1075
QY 992 CTTTCTTGATGAAATCTCAAGCGGCTTTCCGGGACTTCTGCTTCTCACTGAAAGTCA 1051
DB 1076 CTTTCTTGATGAAATCTCAAGCGGCTTTCCGGGACTTCTGCTTCTCACTGAAAGTCA 1135
QY 1052 GGATGAGGCGGAGAGCACTAGACAGTCCGAATTCAGTTCAAGATC 1099
DB 1136 CAATGAAACGCAAAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1183

RESULT 51
US-09-761-962-1
; Sequence 1, Application US/09761962
; Patent No. US20020077285A1
; GENERAL INFORMATION:
; APPLICANT: Memorial Sloan-Kettering Cancer Center
; APPLICANT: Identification and Characterization of Multiple Splice
; TITLE OF INVENTION: Variants of Mu-

;; TITLE OF INVENTION: opioid Receptor (MOR-1) Gene
;; FILE REFERENCE: 830002-2000.1
;; CURRENT APPLICATION NUMBER: US/09/761,962
;; CURRENT FILING DATE: 2001-01-17
;; PRIOR APPLICATION NUMBER: 09/743,872
;; PRIOR FILING DATE: 2001-03-13
;; NUMBER OF SEQ ID NOS: 46
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO: 1
;; LENGTH: 1423
;; TYPE: DNA
;; ORGANISM: Mus musculus
US-09-761-962-1

Query Match 37.5%; Score 432.4; DB 9; Length 1423;
Best Local Similarity 65.8%; Pred. No. 1.3e-114;
Matches 663; Conservative 0; Mismatches 336; Indels 9; Gaps 2;

```
QY 92 CCGGCTGGGCGGAGCCGACAGCAACGGGAGCGCGCTCGGAGGACGGGAGCTGGAGC 151
DB 185 CCGACCCATGCGGTCTTAACCGGAGGGGCTGGGGAGCCAGCCTGCTCCAGCA 244
QY 152 CCGGCAACATCTCCCGGCGCATCCGGTCATCAACGGCGGTCTTACCTCGTAGTGTG 211
DB 245 CCGGAGCGCCCTTCATGTCACAGCCATCAACATATGGCCCTTATTCTATCGTGTG 304
QY 212 TCGTGGGCTTGGTGGCACTCGCTGTCATCTTGTGATCACTCGATACCAAGATGA 271
DB 305 TAGTGGGCTCTTGGAACTTCGTCGTGATGATGATGATGATGATGATGATGATGATG 364
QY 272 AGACAGCAACCAATTTATCAATATTTAACTGGCTTTGGAGAGTCTTTAGTTACTACA 331
DB 365 AGACTGCCACCAATCAATCAATTTCAACCTTGTCTGGAGATCTCTTAGCACTACCA 424
QY 332 CCATGCCCTTTGAGATGAGGTCTACTGATGATGATTTCTGCGCTTTGGAGATGCTGT 391
DB 425 CGCTGCCCTTTCAGATGTTAATCTAGTATGGAACCTGGGCTTTGGAAACATCTCTCT 484
QY 392 GCAAGATGATATTTCCATGATTTACTAATCAATGTTACCAAGCATCTTCACTTGAACA 451
DB 485 GCAAGATGATATTTCAATTAAGCTAATCAATGTTACCAAGATGTTCACTTCACTTGA 544
QY 452 TGATGAGGTGAGCCGCTACATTTGCGTGGCAACCCGCTGAAGGCTTTGGACTTCCGA 511
DB 545 CCATGATGTTAGACCGGTACATTTGCGTGGCAACCCGCTGAAGGCTTGGATTTCCGTA 604
QY 512 CACCTTGAAGGCAAGATCATCAATATCTGATCTGGCTGCTGTCTGATCTGTGGCA 571
DB 605 CCCCCGAAATGCGAAATGTCATGTCGATCTGATCTGATCTCTTCCATTTGGTGC 664
QY 572 TCTGCAATAGTCTTGGAGGACCAAGTCAAGGGAAGAGTGGATGTCATTGAGTGT 631
DB 665 TGCCGTATATGTTATGAGCAACACAAATACAGGAGAGGCTC-----CATAGATTGCA 718
QY 632 CTTGCACTTCCAGATGATGATCTCTGCTGGGACCTCTTCAATGAAGATCTGCGTCT 691
DB 719 CCTTCACGTTCTCTCATCCCAATGATGATGAGGAACCTGCTC---AAATCTGTGCT 775
QY 692 TCACTTTTGGCTTGGTATCTCTGCTCATCATCATGTCGCTCAACCTGATGATCC 751
DB 776 TCACTTTTGGCTTGGTATCTCTGCTCATCATCATGTCGCTCAACCTGATGATGATCT 835
QY 752 TGCGCTCAAGAGCGTCCGCTCTTCTGCTGCTCCGAGAGAAAGATGCAACCTGGGTA 811
DB 836 TACGACTCAAGAGTCTCCGATGCTGCTGGGCTCCAAAGAAAGACAGAACTTGGGCA 895
QY 812 GGATTCACCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 871
DB 896 GGATTCACCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 955
QY 872 ACAATTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 931
DB 956 ACATCTATGTCATCAAAAGCACTGATCAGATTCAGAAACCACTTTCAGACTGTCTT 1015
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QY 932 GCTATTAATTTGATGCTCTTGAAGCTTAAAGCTTAAACCAAGATGCTGAATCTCTACG 991
DB 1016 CCGGCACTTCTGATGCTCTTGAAGCTTAAAGCTTAAACCAAGATGCTGAATCTCTTATG 1075
QY 992 CTTTCTTGAATGAAGAACTTCAAGGCTGTTCCGGGACTTCTGCTTTCACCTGAAGATGA 1051
DB 1076 GCTTCTGATGAAGAACTTCAAGGCTGTTTGAAGGCTTCTGATCTTCCCACTTCTTCA 1135
QY 1052 GGATGAGCGGCGAGAGCACTAGCAGAGTCCGAAATTAAGTTACAGATC 1099
DB 1136 CAATCGAAACAGCAAAACTGCTGCTGATTCGTCAAAACACTAGGGAAC 1183
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RESULT 52
US-10-283-300-1
; Sequence 1, Application US/10283300
; Publication No. US20030103972A1
; GENERAL INFORMATION:

;; APPLICANT: Memorial Sloan-Kettering Cancer Center
;; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF MULTIPLE SPLICE VARIANTS
;; FILE REFERENCE: OF THE MU-OPLOID RECEPTOR GENE
;; CURRENT APPLICATION NUMBER: US/10/283,300
;; PRIOR FILING DATE: 2002-10-29
;; PRIOR APPLICATION NUMBER: 09/761,962
;; PRIOR FILING DATE: 2001-01-17
;; PRIOR APPLICATION NUMBER: 09/743,872
;; PRIOR FILING DATE: 2001-01-16
;; PRIOR APPLICATION NUMBER: PCT/US99/15974
;; PRIOR FILING DATE: 1999-07-15
;; NUMBER OF SEQ ID NOS: 46
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO: 1
;; LENGTH: 1423
;; TYPE: DNA
;; ORGANISM: Mus musculus
US-10-283-300-1

Query Match 37.5%; Score 432.4; DB 15; Length 1423;
Best Local Similarity 65.8%; Pred. No. 1.3e-114;
Matches 663; Conservative 0; Mismatches 336; Indels 9; Gaps 2;

```
QY 92 CCGGCTGGGCGGAGCCGACAGCAACGGGAGCGCGCTCGGAGGACGGGAGCTGGAGC 151
DB 185 CCGACCCATGCGGTCTTAACCGGAGGGGCTGGGGAGCCAGCCTGCTCCAGCA 244
QY 152 CCGGCAACATCTCCCGGCGCATCCGGTCATCAACGGCGGTCTTACCTCGTAGTGTG 211
DB 245 CCGGAGCGCCCTTCATGTCACAGCCATCAACATATGGCCCTTATTCTATCGTGTG 304
QY 212 TCGTGGGCTTGGTGGCACTCGCTGTCATCTTGTGATCACTCGATACCAAGATGA 271
DB 305 TAGTGGGCTCTTGGAACTTCTGCTGATGATGATGATGATGATGATGATGATGATG 364
QY 272 AGACAGCAACCAATTTATCAATATTTAACTGGCTTTGGAGAGTCTTTAGTTACTACA 331
DB 365 AGACTGCCACCAATCAATCAATTTCAACCTTGTCTGGAGATCTCTTAGCACTACCA 424
QY 332 CCATGCCCTTTGAGATGAGGTCTACTGATGATGATTTCTGCGCTTTGGAGATGCTGT 391
DB 425 CGCTGCCCTTTCAGATGTTAATCTAGTATGGAACGTTGGGCTTGGAAACATCTCTCT 484
QY 392 GCAAGATGATATTTCCATGATTTACTAATCAATGTTACCAAGATGTTCACTTGAACA 451
DB 485 GCAAGATGATGATCTCAATTAAGCTACTACCAATGTTCAACAGTATCTTCAACCTTGA 544
QY 452 TGATGAGCGGTGAGCGCTCATTTGCGTGGGACCCGCTGAAGGCTTTGGAGTTCGCA 511
DB 545 CCAATGATGATGAGCGCTCATTTGCGTGGGACCCGCTGAAGGCTTGGAGTTCGCA 604
QY 512 CACCTTGAAGGCAAGATCATCAATATCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 571
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Db      605 CCCCCGAATGCCAAATTTGTAATGTCTGCAACTGATCCTCTTCTGCAATTGTC 664
Qy      572 TCTTGCAATAGTCTTGTGAGGACCAAGTCAAGGAAACGTCCATGTCATTGAGTGT 631
Db      665 TCCCGGTAATGTTCAATGCGAACCAAAATACAGGAGGGGTC-----CATAGATTGA 718
Qy      632 CTTTCAGTTCCTCAGTGTGACTACTCTGTTGGAGACTCTTCATGAAAGATGCGGTCT 691
Db      719 CCTCAGCTTCTCTCATCCACATGTAATGGAAGAACTGCTC---AAATCTGTGTCT 775
Qy      692 TCATCTTTGCTCTGATCCTGTCTCTCATCATCTGTCTGTAACCTGATGATCC 751
Db      776 TCATCTTGCGCTTCATCATGCGGTCCTCATCATCTGTGTATGAGACTGATGATCT 835
Qy      752 TGGCTCTCAAGAGCTCCGCTCTTCTGCTCCGAGAGAAAGATGCGCACTGCGTA 811
Db      836 TACGACTCAAGAGTGTCCGACGATGTCGGGCTCCAAAGAAAGACAGAACTGCGCA 895
Qy      812 GGATCAGCAGATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 871
Db      896 GGATCAGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 955
Qy      872 ACATATTCATCTGTGTGAGGCTCTGGGAGACCTCCCAAGACAGCTGCTCTCTCA 931
Db      956 ACATCTATGTCATCATCAAAAGCATGATCAGATTCAGAAACACTTCCAGACTGTT 1015
Qy      932 GCTATTACTCTTGCAATGCTTGAAGCTATACCAAGATGCTGATCCATCTCTACG 991
Db      1016 CTGGACCTTCTGCAATGCTGCTGGGTTCACAAACAGCTGCAACCGATCTTATG 1075
Qy      992 CTTTCTTGATGAAACTTCAAGCGGTGTTCCGGGACTTCTGCTTTCATGAAAGATG 1051
Db      1076 CTTTCTTGATGAAACTTCAAGCGGTGTTCCGGGACTTCTGCTTTCATGAAAGATG 1135
Qy      1052 GGATGAGCGGAGAGCACTAGCAGATCCGAATATACAGTTTCAGATC 1099
Db      1136 CAATCGAACAGCAAAACTCTGCTCGATCCGTCAAAACACTAGGGAC 1183

RESULT 53
US-10-185-083-15
; Sequence 15, Application US/10185083
; Publication No. US20030050467A1
; GENERAL INFORMATION:
; APPLICANT: Memorial Sloan Kettering Cancer Center
; APPLICANT: Pasternak, Gavril
; APPLICANT: Pan, Ying-Xian
; TITLE OF INVENTION: Multiple Splice Variants of the Mu-Opioid Receptor Gene
; FILE REFERENCE: 830002-2007.1
; CURRENT APPLICATION NUMBER: US/10/185,083
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 60/302,072
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1.
; SEQ ID NO: 15
; LENGTH: 1440
; TYPE: DNA
; ORGANISM: Mus Sp.
US-10-185-083-15

```

Query Match 37.5%; Score 432.4; DB 15; Length 1440;

Best Local Similarity 65.8%; Pred. No. 13e-114; Matches 663; Conservative 0; Mismatches 336; Indels 9; Gaps 2;

```

Qy      92 CCGAGCTGGGCGGAGCCGACAGCAAGCGAGCGGCTCGAGAGAGCGAGCTGAGAC 151
Db      348 CCGAGCCATGCGCTCTTAACCGCAGGGGCTTGGGAGAGCCAGCCTGTGCTCTCAGA 407
Qy      152 CCGGCAACATCTCCCGGCGCATCCGGTATATATACAGCGGCTTACTCCGTAGTGTTCG 211
Db      408 CCGGCAACCTTCTCATGTGTACAGAGCATACATCATGAGCCCTTATCTATCTGTGTG 467

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Qy      212 TGTGGGCTTGTGGGCAACTCGTGTGATGTTGATCATCCGATACAGAAAGATGA 271
Db      468 TAGTGGGCTCTTTGGAACTTCTGTGATATATGATTTAGATATACCAAAATGA 527
Qy      272 AGACAGCAACCAATTATATATTTAACTGTGGCTTTGGCAGATGCTTTAGTACTACA 331
Db      528 AGATGCGACCAACATATATTTTCAACCTTGTCTGGCAGATGCTTTAGCACTAGCA 587
Qy      332 CCATCCCTTTTCAAGTACAGGCTCTATGATGAATTTCTGGGCTTTTGGGAGTGTCT 391
Db      588 CGCTCCCTTTTCAAGTATTAATCTATGATGGAACGAGGCTTTGGAAATCTCTCT 647
Qy      392 GCAAGATGTAATTTTCAATGATTTACTAACAATGTTCAACGATGTTCACTTCACTTGA 451
Db      648 GCAAGATGTAATTTTCAATGATTTACTAACAATGTTCAACGATGTTCACTTCACTTGA 707
Qy      452 TGATAGGCTGAGCCGCTACATATGCTGATGCTGATGCTGCTGCTGCTGCTGCTGCT 511
Db      708 CCATGATGTAAGCCGCTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 767
Qy      512 CACCTTGAAGCAAAATCATCAATATCTGATCTGCTGCTGCTGCTGCTGCTGCTGCT 571
Db      768 CCCCCGAAATGCCAAATTTGTCATGTCGTCATCTGATCTCTTCTGCAATGTGTC 827
Qy      572 TCTTGCAATAGTCTTGGAGGACCAAGTCAAGGAAAGAGTGTGATGATGATGATGAT 631
Db      828 TCCCGTATATGTTCAATGCGAACACAAATATACAGGAGGGGTC-----CATAGATTGA 881
Qy      632 CTTTCAGTTCCTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 691
Db      882 CCTCAGCTTCTCTATCCACATGATGATGATGATGATGATGATGATGATGATGATGATG 938
Qy      692 TCATTTTTCCTTGTGATATCCCTGCTCATCATCATGCTGTCTGTAACCTGATGATCC 751
Db      939 TCATTTTTCCTTGTGATATCCCTGCTCATCATCATGCTGTGTATGATGATGATGATCT 998
Qy      752 TGGCTCTAAGAGGCTCCGGGCTCTTCTGCTCCGAGAGAAAGATGCGAACCTGCGTA 811
Db      999 TACGACTCAAGAGTGTCCGATGCTGTGGGCTCCAAAGAAAGACAGAACTGCGCA 1058
Qy      812 GGATCAGCAGATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 871
Db      1059 GGATCAGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1118
Qy      872 ACATATTCATCTGTGTGAGGCTCTGGGAGACCTCCCAAGACAGCTGCTCTCTCA 931
Db      1119 ACATCTATGTCATCATCAAGACATGATCAGATTCAGAAACACTTCCAGACTGTT 1178
Qy      932 GCTATTACTTCTGCAATGCTTGAAGCTTATGATGATGATGATGATGATGATGATGATG 991
Db      1179 CTTGCACTTCTGCAATGCTTGAAGCTTATGATGATGATGATGATGATGATGATGATGATG 1238
Qy      992 CTTTCTTGATGAAACTTCAAGCGGTGTTCCGGGACTTCTGCTTTCATGAAAGATG 1051
Db      1239 CTTTCTTGATGAAACTTCAAGCGGTGTTCCGGGACTTCTGCTTTCATGAAAGATG 1298
Qy      1052 GGATGAGCGGAGAGCACTAGCAGATCCGAATATACAGTTTCAGATC 1099
Db      1299 CAATCGAACAGCAAAACTCTGCTCGAATCCGTCAAAACACTAGGGAC 1346

```

RESULT 54

US-10-194-595-15

; Sequence 15, Application US/10194595

; Publication No. US20030068805A1

; GENERAL INFORMATION:

; APPLICANT: Memorial Sloan Kettering Cancer Center

; APPLICANT: Pasternak, Gavril

; APPLICANT: Pan, Ying-Xian

; TITLE OF INVENTION: Multiple Splice Variants of the Mu-Opioid Receptor Gene

; FILE REFERENCE: 830002-2007.1

; CURRENT APPLICATION NUMBER: US/10/194,595

; CURRENT FILING DATE: 2002-07-11

PRIOR APPLICATION NUMBER: US/09/561,523
PRIOR FILING DATE: 2002-07-03
PRIOR APPLICATION NUMBER: 60/302,072
PRIOR FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn version 3.1
SEQ ID NO 15
LENGTH: 1440
TYPE: DNA
ORGANISM: Mus Sp.
US-10-194-595-15

Query Match 37.5%; Score 432.4; DB 15; Length 1440;
Best Local Similarity 65.8%; Pred. No. 1.3e-114;
Matches 663; Conservative 0; Mismatches 336; Indels 9; Gaps 2;

QY 92 CCGGCTGGGCGGAGCCGAGCAGCAAGCAGCGCGCGGCTCGAGAGACGCGCAGCTGGAGC 151
DB 348 CCGAGCCATGCGGTCTTAACCGGCGGGCTTGGCGGAGCAGCAGCTGTGCTCCAGCA 407
QY 152 CCGGCGCATCTCCCGGCGCATCCGCGTATCATCAGCGCGGTCTTACTCCGAGTGTG 211
DB 408 CCGGCGAGCCCTTCCATGTCACAGCCATCACAATGAGCCCTTATCTTATCGTGTG 467
QY 212 TCGTGGGCTTGGTGGCACTGCGTGTGATGTCATCCGATCACAAGATGA 271
DB 468 TAGTGGGCTCTTGGAACTTCTGTGATGTATGTATGTATGATATACCAAAATGA 527
QY 272 AGACGCAACCAACATTTACATATTTACCTGCTTGGCAGATGCTTACTACAA 331
DB 528 AGACTGCCACCAACATCTACATTTTCAACCTTGTCTGCGAGATGCTTACGACATAGCA 587
QY 332 CCATGCGCTTTAGAGTACGCTCTGATGATGATTTCTGGGCTTTGGGAGTGTGCT 391
DB 588 CGCTGCGCTTTAGAGTGTAACTGATGATGAGAACTGGGCTTTGGAAACATCTCT 647
QY 392 GCAAGATGATATTTCCATTTGATTTACTACAGATGTCACAGATCTTCACTTGAACCA 451
DB 648 GCAAGATGATGATTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 707
QY 452 TGATAGGCTGAGCGGCTACATTTGCGGTGCGCAACCGGCTGAGGCTTTGAGCTTCCGCA 511
DB 708 CCATAGGTGATACCGCTACATTTGCGGTGCGCAACCGGCTGAGGCTTTGAGCTTCCGCA 767
QY 512 CACCTTGAAGGCAAGATCATCAATTCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 571
DB 768 CCCCCGAAATGCCAAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 827
QY 572 TCTGTGCAATGCTCTTGAAGGCAACAAAGTCAGGAAAGACGTCGATGCTATGAGTGTCT 631
DB 828 TGCCGCTATGTTTCAATGCAACCAAAATACAGGCAAGGCTGCTGCTGCTGCTGCTGCT 881
QY 632 CCTTGCATTTCCCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 691
DB 882 CCTTGCATTTCCCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 938
QY 692 TCATTTTGGCTTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 751
DB 939 TCATTTTGGCTTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 998
QY 752 TGCGTCTCAAGAGCTGCGGCTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 811
DB 999 TACGCTCAAGAGTGTGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1058
QY 812 GGATACCAAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 871
DB 1059 GGATACCAAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1118
QY 872 ACATATTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 931
DB 1119 ACATATTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1178
QY 932 GCATTTACTTCTGCTGCTGCTTGAAGCTTATACCAACAGTAGCTGATTCATCTCTACG 991

DB 1179 CCGGCACTTCTGATGCTGCTTGGTATACAAACAGCTGCTGAACCCAGTCTTTATG 1238
QY 992 CTTTCTTGAAGAAACTTCAAGGCTGTTTCCGAGCTTCTGCTTCCAGTGAAGATGA 1051
DB 1239 GCTTCTGATGAAACTTCAAGGCTGTTTGAAGGCTTCTGATCCCACTTCTCTCA 1298
QY 1052 GGATGAGCGGCGAGAGCACTAGCAGATGCTCGAAATATACGTTCAAGATC 1099
DB 1299 CAATGCAACAGCAAAACTTGTCTGAAATCCGTCAAAACACTAGGAAAC 1346

RESULT 55
US-10-185-083-17

Sequence 17, Application US/10185083
Publication No. US2003050467A1
GENERAL INFORMATION:
APPLICANT: Memorial Sloan Kettering Cancer Center
APPLICANT: Pasternak, Gavril
APPLICANT: Pan, Ying-Xian
TITLE OF INVENTION: Multiple Splice Variants of the Mu-Opioid Receptor Gene
FILE REFERENCE: 830002-2007.1
CURRENT FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: 60/302,072
PRIOR FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn version 3.1
SEQ ID NO 17
LENGTH: 1569
TYPE: DNA
ORGANISM: Mus Sp.
US-10-185-083-17

Query Match 37.5%; Score 432.4; DB 15; Length 1569;
Best Local Similarity 65.8%; Pred. No. 1.4e-114;
Matches 663; Conservative 0; Mismatches 336; Indels 9; Gaps 2;

QY 92 CCGGCTGGGCGGAGCCGAGCAGCAAGCAGCGCGCGGCTCGAGAGACGCGCAGCTGGAGC 151
DB 477 CCGAGCCATGCGGTCTTAACCGGCGGGCTTGGCGGAGCAGCAGCTGTGCTCCAGCA 536
QY 152 CCGGCGCATCTCCCGGCGCATCCGCGTATCATCAGCGCGGTCTTACTCCGAGTGTG 211
DB 537 CCGGCGAGCCCTTCCATGTCACAGCCATCACAATGAGCCCTTATCTTATCGTGTG 596
QY 212 TCGTGGGCTTGGTGGCACTGCGTGTGATGTCATGTCATGTCATGTCATGTCATGTCATG 271
DB 597 TAGTGGGCTCTTGGAACTTCTGTGATGTATGTATGTATGATATACCAAAATGA 656
QY 272 AGACGCAACCAACATTTACATTTTAACTGCTTGGGAGATGCTTATGATTTACTTACAA 331
DB 657 AGACTGCCACCAACATCTACATTTTCAACCTTGTCTGCGAGATGCTTACGACATAGCA 716
QY 332 CCATGCGCTTTAGAGTACGCTCTGATGATGATTTCTGGGCTTTGGGAGTGTGCTGT 391
DB 717 CGTGGCTTTAGAGTGTAACTTCTGATGATGAGAACTGCGCTTGTGAAACATCTCT 776
QY 392 GCAAGATGATATTTCCATGATTTACTACAAAGTTCACAGACATCTTCACTTGAACCA 451
DB 777 GCAAGATGATGATTTCAATGATTTACTACAAAGTTCACAGACATCTTCACTTGAACCA 836
QY 452 TGATAGCGGAGCGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 511
DB 837 CAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 896
QY 512 CACCTTGAAGGCAAGATCATCAATTCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 571
DB 897 CCCCCGAAATGCCAAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 956
QY 572 TCTGTGCAATGCTCTTGAAGGCAACAAAGTCAGGAAAGACGTCGATGCTATGATGATGCT 631
DB 957 TGCCGCTATGTTTCAATGCAACCAAAATACAGGCAAGGCTGCTGCTGCTGCTGCTGCTGCT 1010

Qy	632	CCTTGCACTTCCCAAGATAGTACTCTCGTGGGAACTCTTCAATGAAGACTGAGTCT	691
Db	1011	CCCTCAGCTTCTTCATCCCACTGACATGATGGAAGAACTGCTC---AAATCTGTGCT	106
Qy	692	TCATCTTGTGCTTCGTGATGCCCTGCTCATCATCATGCTCTGTCAACCCGTGATGCC	751
Db	1068	TCATCTTGCGCTTTCATCATGCCGGTCTTCATCATCATGTGTGTATGAGCATGATGATCT	112
Qy	752	TGCGCTCAAGAAGGCTCCGGGCTCTTTCGTGCTCCCGAAGAAAGATGGCAACCTGGCTA	811
Db	1128	TACGACTCAAGAAGTCCGCAATGCTGTGGGCTCCAAAAGAAAGACAGAACTGGCGA	118
Qy	812	GGATCACCAGACTGTGCTCGTGGTGTGTGGACATGCTCGCTGCTGCTGACTCCATTC	871
Db	1188	GGATCACCAGGATGGTGTGCTGTGTGTGTGTGTGTGTATTTATGTCTGTGCTGAGCCCCATCC	124
Qy	872	ACATATTCATCTGTGTGAGGCTCTGGGGAGCACTCCACAGCAGCTGCTCTCTCCA	931
Db	1248	ACATCTATGTATCATCAAAAGACATGATCAACATTCCAAGAAACCACTTCCAGACTGTTT	130
Qy	932	GCTATTACTTCGTCATCGCTTAGGCTATACAAAGATGAGCTGATGCCATCTCTACG	991
Db	1308	CCTGGCACTTCGTGCAATTGCTCTGGGTTACAAACAGCTGCTGAACCAAGTCTTTTAG	136
Qy	992	CCTTTCCTGATGAAAACTTCAAGCGGTGTTTCCGGGACTTCTGCTTTCATCTGAAGATGA	105
Db	1368	CGTTCCTGGATGAAAACTTCAAAACATGTTTATGAGAGCTTCGACATCCCACTTCTCCA	142
Qy	1052	GGATGAGACGGCAGAGCACTAGCAAGTCCGAATAACAGTTCCAGATC	1099
Db	1428	CAATGAACAGCAAACTCTGCTCGAATCCGTCACAAAACCTGAGGAACT	1475

SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 16
 ; LENGTH: 1610
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 US-09-761-962-16

Query Match 37.5%; Score 432.4; DB 9; Length 1610;
 Best Local Similarity 65.8%; Pred. No. 1.4e-114;
 Matches 663; Conservative 0; Mismatches 336; Indels 9; Gaps 2;

```

QY 92 CCGGCTGGGCGGAGCCCGACACGAGCGGAGCGGAGGAGCGGAGCGGAGGAGC 151
DB 401 CCGACCCATCGGCTCTTAACCGGACCGGGCTGGCGGAGGAGCGGAGCGGAGGAGC 460
QY 152 CCGGCGACATCTCCCGGCGCATCCGGGATCATCAAGGCGGATCTACTCCGATGTTG 211
DB 461 CCGGCGAGCCCTTCACATGCTCACAGCCATCACATGAGCCCTCTATCTATCTGTTG 520
QY 212 TCGTGGGCTTGGGCGACCTGGTGCATGTTGTGATCTACCGATACAAAGATGA 271
DB 521 TAGTGGGCTCTTGGAAATCTTCGTGCTATGATGATGATGATGATGATGATGATGAT 580
QY 272 AGACAGCAACCAATTTTACATATTTTAACTGGCTTGGAGAGATCTTTAGTTACTACA 331
DB 581 AGACGCGCAACCAATTTTACATATTTTAACTGGCTTGGAGAGATCTTTAGTTACTACA 640
QY 332 CCATGCGCTTTAGAGTACGCTTACTGATGATGATGATGATGATGATGATGATGATG 391
DB 641 CCGTCCCTTTAGAGTACGCTTACTGATGATGATGATGATGATGATGATGATGATG 700
QY 392 GCAAGATGATGATTTTCAATGATTTACTAATGATGATGATGATGATGATGATGATGAT 451
DB 701 GCAAGATGATGATTTTCAATGATTTTACTAATGATGATGATGATGATGATGATGATGAT 760
QY 452 TGATGAGCGTGGACCGCTACATTTGCGTGGCCACCGGCTGAGGCTTGGAGCTTCCGA 511
DB 761 CCATGAGTGTAGACCGCTACATTTGCGTGGCCACCGGCTGAGGCTTGGAGCTTCCGA 820
QY 512 CACCTTGAAGGCAAGATCATATATTCGATCTGGCTGCTGCTGCTGCTGCTGCTGCTG 571
DB 821 CCCCCGAAATGCAAAATTTGTCATATGTCGACATGATCTCTCTCTGCTGCTGCTGCT 880
QY 572 TCTGTCAATAGTCTTGGAGGACCAAGTACAGGAAAGAGTGCATGATGATGATGATG 631
DB 881 TGCCGTATATGTTCAATGACACCAAAATACAGGAGGAGGCTC-----CATAGTTGCA 934
QY 632 CTTTGACGTTCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 691
DB 935 CCGTCAAGTCTCTCATCCACATGATGATGATGATGATGATGATGATGATGATGATGAT 991
QY 692 TCAATTTGGCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 751
DB 992 TCAATTTGGCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1051
QY 752 TGCGCTCAAGAGCGCTCGGCTCTTTCGAGCTCCGAGAGAAAGATGCAACCTGGGTA 811
DB 1052 TACGACTAAGAGTCTCCGATGCTGTGGGCTCCAAAGAAAGAGAGAGAGAGAGAGAG 1111
QY 812 GGATACCAAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 871
DB 1112 GGATACCAAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1171
QY 872 ACATATTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 931
DB 1172 ACATATTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1231
QY 932 GCTATTTACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 991
DB 1232 CTTGCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1291
QY 992 CTTTCTTGTATGAAATCTCAAGCGGCTGCTTCCGGGACTTCTGCTTCCACTGAAATGA 1051

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DB 1292 CTTTCTGATGAAATCTTCAACGATGTTTATAGAGTCTTGATCCCACTTCTTCCA 1351
QY 1052 GGATGAGCGGCGAGAGCATGACAGAGTCCGAAATACAGTTTCAAGATC 1099
DB 1352 CAATGCAACACCAAAATCTGCTGCAATCCGTCAAAACACTAGGGAAC 1399

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RESULT 58
 US-10-283-300-16
 ; Sequence 16, Application US/10283300
 ; Publication No. US20030103972A1
 ; GENERAL INFORMATION:

APPLICANT: Memorial Sloan-Kettering Cancer Center
 TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF MULTIPLE SPLICE VARIANTS
 FILE REFERENCE: 830002-2000.3
 CURRENT APPLICATION NUMBER: US/10/283.300
 PRIOR FILING DATE: 2002-10-29
 PRIOR APPLICATION NUMBER: 09/761,962
 PRIOR FILING DATE: 2001-01-17
 PRIOR APPLICATION NUMBER: 09/743,872
 PRIOR FILING DATE: 2001-01-16
 PRIOR APPLICATION NUMBER: PCT/US99/15974
 PRIOR FILING DATE: 1999-07-15
 NUMBER OF SEQ ID NOS: 46
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 16
 ; LENGTH: 1610
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 US-10-283-300-16

Query Match 37.5%; Score 432.4; DB 15; Length 1610;
 Best Local Similarity 65.8%; Pred. No. 1.4e-114;
 Matches 663; Conservative 0; Mismatches 336; Indels 9; Gaps 2;

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QY 92 CCGGCTGGGCGGAGCCCGACACGAGCGGAGCGGAGGAGCGGAGCGGAGGAGC 151
DB 401 CCGACCCATCGGCTCTTAACCGGACCGGGCTGGCGGAGGAGCGGAGCGGAGGAGC 460
QY 152 CCGGCGACATCTCCCGGCGCATCCGGGATCATCAAGGCGGATCTACTCCGATGTTG 211
DB 461 CCGGCGAGCCCTTCACATGCTCACAGCCATCACATGAGCCCTCTATCTATCTGTTG 520
QY 212 TCGTGGGCTTGGGCGACCTGGTGCATGTTGTGATCTACCGATACAAAGATGA 271
DB 521 TAGTGGGCTCTTGGAAATCTTCGTGCTATGATGATGATGATGATGATGATGATGATG 580
QY 272 AGACAGCAACCAATTTTACATATTTTAACTGGCTTGGAGAGATCTTTAGTTACTACA 331
DB 581 AGACGCGCAACCAATTTTACATATTTTAACTGGCTTGGAGAGATCTTTAGTTACTACA 640
QY 332 CCATGCGCTTTAGAGTACGCTTACTGATGATGATGATGATGATGATGATGATGATG 391
DB 641 CCGTCCCTTTAGAGTACGCTTACTGATGATGATGATGATGATGATGATGATGATG 700
QY 392 GCAAGATGATGATTTTCAATGATTTTACTAATGATGATGATGATGATGATGATGATG 451
DB 701 GCAAGATGATGATTTTCAATGATTTTACTAATGATGATGATGATGATGATGATGATG 760
QY 452 TGATGAGCGTGGACCGCTACATTTGCGTGGCCACCGGCTGAGGCTTGGAGGATGCTGT 511
DB 761 CCATGAGTGTAGACCGCTACATTTGCGTGGCCACCGGCTGAGGCTTGGAGGATGCTGT 820
QY 512 CACCTTGAAGGCAAGATCATATATTCGATCTGGCTGCTGCTGCTGCTGCTGCTGCTG 571
DB 821 CCCCCGAAATGCAAAATTTGTCATATGTCGACATGATCTCTCTCTGCTGCTGCTGCT 880
QY 572 TCTGTCAATAGTCTTGGAGGACCAAAATGTCAGGAAAGAGTGCATGATGATGATG 631
DB 881 TGCCGTATATGTTCAATGACACCAAAATACAGGAGGAGGCTC-----CATAGTTGCA 934
QY 632 CTTTGACGTTCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 691

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[illegible]

RESULT 59
US-10-185

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Sequence 16 Application US/10185063
Publication No. US20030050467A1
GENERAL INFORMATION:
APPLICANT: Memorial Sloan Kettering Cancer Center
APPLICANT: Pasternak, Gavril
APPLICANT: Pan, Yang-Xian
TITLE OF INVENTION: Multiple Splice Variants of the Mu-Opioid Receptor Gene
FILE REFERENCE: 830002-2007.1
CURRENT APPLICATION NUMBER: US/10/185,083
CURRENT FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: 60/302,072
PRIOR FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn version 3.1
SEQ ID NO 16
LENGTH: 1614
TYPE: DNA
ORGANISM: Mus Sp.
US-10-185-083-16

```

Query Match	37.5%	Score 432.4;	DB 15;	Length 1614;
Best Local Similarity	65.8%;	Pred. No. 1.4e-114;		
Matches 663;	Conservative 0;	Mismatches 336;	Indels 9;	Gaps 2

Qy	92	CCGGCTGGGGCGAGGCCGACAGCAACGGCAGGGCGCGCTCGAGAGACAGCGCGAGCTGGAGC	151
Db	522	CCGACCCATGCGGCTCTTAACCGCAGCGGGCTTGGCGGGAGCCACAGCCTGTGCTTCAAGA	581
Qy	152	CCGCGCACATCTCCCCCGGCATCCCGGTATCATCAGCGAGGTCTACTCCGTAGTTCG	211
Db	582	CCGGCAGGCCCTTCATAGTCAACAGCATCATACATATGCCCCCTCTATTTCTATGTGTGTG	641
Qy	212	TCTGTGGGCTTGGTGGCAACTGCGTGTGTCATGTTGCTGATCATCCGATACACAAAGATGA	271
Db	642	TAGTGGGCTCTTTTGGAACTTCTCGTGCATGATGATGATTGTAAGATATACCAAAATGA	701
Qy	272	AGACAGCAACCAACATTTACATATTTAAACCTGGCTTGGCAACATGCTTATAGTATCTACAA	331
Db	702	AGACTGCCAACCAACATCTACATTTTTCACCTTGTCTGTGGCAATGCTTATAGCCACTACGA	761

OY	332	CCAGGCCCTTTCAAGAGTACGGCTACTGACTGAGAAATTCCTGGCCCTTTGGGAGTGGCTGT	391
Db	762	CGCTGCCCTTTCAAGAGTGTAACTAACTGATGGAGAGGTGGCCCTTTGGAAACAATCTCTCT	821
OY	392	GCAAGATAGTAATTTCCATTGATTAACTAACCAATGTTCCACGACATCTTCACTTGCACCA	451
Db	822	GCAAGATGTGATCTCAATAGACTACTAACCAATGTTTCAACCAATATCTTCAACCTCTGCA	881
OY	452	TGATGAGCGTGGACCCGCTACATTTGCGGTGTGCCACCCCGTGAAGGCTTTGGACTTCGGCA	511
Db	882	CCATGAGGTGTAGACCGCTACATTTGCGGTGTGCCACCCCGTGAAGGCTTCGATTTTCCTGA	941
OY	512	CACCCCTTGAAGGCAAAAGTATCATCAATATCTGATCTGGCTGTGCGTATCTGTGTGGCA	571
Db	942	CCCCCCGAATATCCAAATTTGTCAATGTCTTGCAACTGGATCTCTCTTTCTGCAATTTGGTC	1001
OY	572	TCCTGTCAATATGTCCTTGGAGGCAACCAAGTCAGAGGAAGAGTGCATGTCATTGAGTGTCT	631
Db	1002	TGCCCGTAATGTTTATGTGCAACCAACCAAAATACAGGAGGGGTCTC-----CATTAATGTCA	1051
OY	632	CCTTGCAGTTTCCCAAGATGATGACTACTCTCTGTGTGGACCTTTTCATGAAGATCTGCGTCT	691
Db	1056	CCCCACGTTCTCTCATCTCCACCACTGGTAAGTGGGAAACTGTCTC---AAAATCTGTGTCT	1112
OY	692	TCATCTTTGCGCTGTGATGCCCTGTCCCTCATCATCATCTGTGCTGATCACCCGTATGATCC	751
Db	1113	TCATCTTGGCTTTATCATATGCGGCTCTCATCATCATCTGTGTGTTATGGACTGATGATCT	1172
OY	752	TGCGTCTCAAGAGCGTCCGGCTCTCTTTCTGTGCTCCGAGAGAAAGATGCAACCTGCGTA	811
Db	1173	TACGACTCAAGAGTGTCCGCAATGCTGTGTGCGGCTCCAAAGAAAGAGCAAGAACTGTGGCA	1232
OY	812	GGATCACCAAGCTGTCTGTGTGTGTGGCAGTCTTGTGTCTGTGCACTCCCATTC	871
Db	1233	GGATCACCCGGATGT	1292
OY	872	ACATATTCATCTGTGTGAGGCTGTGGGAGACCTCCACAGCAGACAGTCTCTCTCCA	931
Db	1293	ACATCTATGTATCATCAAAAGCACTGATCAGATTTCCAGAAACCACTTTCCAGACTGTT	1351
OY	932	GCTATTAATCTTGCATGCGCTTAGGCTAATACCAACAGTAGCGCTGAATCCATTTCTACG	991
Db	1353	CTGTGCACTTGTGATTTGCTTGGGTTAACCAACAGGTGCTGAACCCAGTCTTTATG	1412
OY	992	CCTTTCTTGAAGAACTTCAAGCGGTGTTCCGGGACTTCTGCTTTCACCTGAAGATGA	1051
Db	1413	CGTTCCTGTGATGAAACCTTCAACAGATGTTTAAAGAGTCTTGATCTCCCACTTCTTCCA	1472
OY	1052	GGATGAGCGGCAAGAGCACTAGCAGAGATCGGAAATACAGTTCAAGATC	1099
Db	1473	CAATGAAACGCAAACTGTGCTGAATTCGTCACCAACACTAGGGAAC	1520

RESULT 60
US-10-194-595-16

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? Sequence 16, Application US/10194595
? Publication No. US20030068805A1
?
? GENERAL INFORMATION:
? APPLICANT: Memorial Sloan Kettering Cancer Center
? APPLICANT: Pasternak, Gavril
? APPLICANT: Pan, Ying-Xian
? TITLE OF INVENTION: Multiple Splice Variants of the Mu-Opioid Receptor Gene
? FILE REFERENCE: 830002-2007.1
?
? CURRENT APPLICATION NUMBER: US/10/194,595
? CURRENT FILING DATE: 2002-07-11
?
? PRIOR APPLICATION NUMBER: US/09/561,523
? PRIOR FILING DATE: 2002-07-03
? PRIOR APPLICATION NUMBER: 60/302,072
? PRIOR FILING DATE: 2001-06-29
?
? NUMBER OF SEQ ID NOS: 53
?
? SOFTWARE: PatentIn version 3.1
?
? SEQ ID NO 16

```


Db	776	TCATCTTGGCCTTATCAATGCGCGGCTCCATCATCATCTGTGTGTTATGACATGAAGATCT	835
Qy	752	TGCGCTCAAGAGCGTCCGGGCTCCTTTCTGAGCTCCGAGAGAAAGATCGCAACTGGCGTA	811
Db	836	TACGACTCAAGAGTGTCCGCAATGCTGTGCGGGCTCCAAAGAAAAGSACGAAACCTGGCGCA	895
Qy	812	GGATTAACCAAGACTGGTCTCTGGTGTGTGTGTGGCAGTCTTGTGTGTCTGTCTGGACTCCCATTC	871
Db	896	GGATCAACCCGGAATGGTGTGTGGTGTGTCGGCTGTATTTATGTCTGTCTGGAACCCCATTC	955
Qy	872	ACATATTCATCCGTGGTGGAGGCTCTGGGGGAGCACTCCCAACGACAGTGTCTCTCA	931
Db	956	ACATTTATGTCTATCTCAAGACTGAATCAAGATTCAGAAACCATTTTCCAGACTGTTT	1015
Qy	932	GCTATTACTTGTGCATCGCTTATGGCTATACCAACAGTAGCTGTAATCCCATTTCTTACG	991
Db	1016	CCTGGCACTTCTGCATTTGCTCTTGGGTTACAAACAGCTGCCTGAACCCAGTTCTTTATG	1075
Qy	992	CCTTTCCTTGATGAATACTTCAAGCGGTGTTCCGGACTTCTGCTTCCACTGAAGATGA	1051
Db	1076	CGTTCCTGGATGAATACTTCAACAGATGTTTAAAGAGATTCTGCATCCCACTTCTCTCA	1135
Qy	1052	GGATGAGACGGCAGACACTAGACAGATGCCAAATACAGTTCAAGATC	1099
Db	1136	CAATGAAACAGCAAAACCTGTGCTGAATCTCCGCAAAACACTAGGGGAAC	1183

RESULT 62
US-10-194

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Sequence 24 Application US/10194595
Publication No. US2003006805A1
GENERAL INFORMATION:
APPLICANT: Memorial Sloan Kettering Cancer Center
APPLICANT: Pasternak, Gavril
APPLICANT: Pan, Ying-Xian
TITLE OF INVENTION: Multiple Splice Variants of the Mu-Opioid Receptor Gene
FILE REFERENCE: 830002-2007.1
CURRENT APPLICATION NUMBER: US/10/194,595
CURRENT FILING DATE: 2002-07-11
PRIOR APPLICATION NUMBER: US/09/561,523
PRIOR FILING DATE: 2002-07-03
PRIOR APPLICATION NUMBER: 60/302,072
PRIOR FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn version 3.1
SEQ ID NO 24
LENGTH: 1695
TYPE: DNA
ORGANISM: Mus sp.
US-10-194-595-24

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Query Match	37.5%	Score 432.4;	DB 15;	Length 1695;
Best Local Similarity	65.8%	Pred. No. 1.4e-114;		
Matches 663; Conservative	0;	Mismatches 336;	Indels 9;	Gaps 2

Oy	92	CCGGGTGGGGCCGAGGCCGACAGCAACGGAGGGCCGGCTCGGAGGACGGCAGCTGGAGGC	151
Db	185	CCGACCACATGGCGGTCTTAACGGCAAGGGGCTTGGGGAGAGCCACAGCTGTGGCTTCAGAA	244
Oy	152	CCGGGCACATCTCCCGGCGATCCGGGTATCATCAAGGGGTCTACTCCGTAGTGGTTCC	211
Db	245	CCGGGAGCCCTTTCATGTGCACAGGCATCACCATCATGGCCCTCTATTCTATCCGTGGTGG	304
Oy	212	TCGTGGGCTTGTGGGCAACTCGTGTGATGTTGATCATCCGATGCACAAAGATGA	271
Db	305	TAGTGGGCTCTTTGGAAACTTCCGTGTCATGTATGTGATGTAGATATACCAAAATGA	364
Oy	272	AGACGCAACCAACATTAATTAATTAACCTGGCTTGGCAATGCTTTAGTTACTACAA	331
Db	365	AGACTGCCACCAACATCTACATTTTCAACCTGTGCTCTGGCAATGGCTTAGCCACATAGCA	424
Oy	332	CCATGCCCTTTCAGAGTACGGTCTACTTGGATGAATTCCTGGCCCTTTTGGGGAATGTGCTGT	391

Db	425	CGCTGCCCTTTCAGAGTGTAACTACCTGATGGAAACGTGGCCCTTTGGAAACATCTCT	484
Oy	392	GCAAGATAGTAATTTCCATGTATTCTACACACATGTTCCACGACATCTTCACTTGACCA	451
Db	485	GCAAGATCGTAGTCTCAATAGACTACTACACATGTTCCACGATCTTCACTCCCTCGCA	544
Oy	452	TGATGAGGCTGGACCGCTACATTTGCCGTGTGCCACCCCGTGAAGGCTTTGGACTTCCGCA	511
Db	545	CCATGAGGTGAGACCGCTACATTTGCCGTGTGCCACCCCGGTCAAGGCCCTGGAAATTTCCGTA	604
Oy	512	CACCCCTGAAGGCAAAAGATTCATCAATATCTGGCATCTGGCTGTGCTCATCTGTTGGCA	571
Db	605	CCCCCGGAAATGCGAAATTTGTCAATGTCTGCAATCTGATCCTCTTCTTGCCATTTGGTC	664
Oy	572	TCTCTGCAATAGTCCCTTGGAGGCAACCAAGTCAGGGAAGACGTGCATGTCAATTGAAGTCT	631
Db	665	TGCCCGTATGTTCATGCGACACCAAAATATACAGGAGGGGTCT-----CATAGATTGCA	718
Oy	632	CTTTGCAATTCCTCCAGATGATGACTACTCTGTGTGGACCTTTTCATGAAGATTTGGCTCT	691
Db	719	CCCTCACGTTCTCTCATCCCACTGTGATCTGGGAAACCTGTGCTC---AAATCTGTGTCT	775
Oy	692	TCATCTTTGCCCTGTGTGATCCCTGTCCATCATATGATGTCTMGCTACACCTGATGATCC	751
Db	776	TCATCTTGCCCTTATCATACGCCGCTCTCATATCACTGTGTATTGAGACTGATATATCT	835
Oy	752	TGCGTCTCAAGAGCGTCCGCGCTCTTTTGTGCTCCGAGAGAAAGATTCGCAACTTGCCTA	811
Db	836	TACGACTCAAGAGTGTCCGCATGCTGTGGCGCTCCAAAGAAAGACAGAAACGTGCGCA	895
Oy	812	GGATTCACCAACTGGTCTGTGTGTGTGTGGCAGTCTTGTGCTGTGTGCTGATCCCATTC	871
Db	896	GGATCACCCGGATGGTGTGTGTGTGTCGTGTGCTGTATTATTTGTCTGTGACCCCCATCC	955
Oy	872	ACATATTCATCTGTGTGAGGCTCTGTGGGAGACCTCCACAGCACAGCTGCTCTCCCA	931
Db	956	ACATCTATGTATCATCAAAAGACTGTATCAAGATTCAGAAACCACTTTCAGACTGTTT	101
Oy	932	GCTATTACTTGTGCATCGCTTGAAGCTATACCAACAGTAGAGCTGATCCATTTCTCTACG	991
Db	1016	CTTGGCACTTGTGATTTGCTTGTGGTTACCAAAACAGCTGCTGAACCAAGTTCTTTATG	107
Oy	992	CCTTTCTTGTGAATAACTTCAAGCGGTGTTCCGGGACTTGTGCTTTCATCTGAAGATGA	105
Db	1076	CGTTCTGTGATGAATAACTTCAACGATGTTTAAAGAGTTTGTGATCCCAACTTCTCCG	113
Oy	1052	GGATGAGCGGCAAGCACTAGCAGAGTCCGAAATACACTTCAAGATC	1099
Db	1136	CAATTCGACAGCAAAACTCTGTCTCAATTCGGTCAAAACACTTGGGAAAC	1183

RESULT 63

US-09-761-962-9
; Sequence 9, Application US/09761962
; Patent No. US20020077285A1

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? ORGANISM: Mus musculus
? APPLICANT: Memorial Sloan-Kettering Cancer Center
? TITLE OF INVENTION: Identification and Characterization of Multiple Splice
? TITLE OF INVENTION: Variants of Mu-
? TITLE OF INVENTION: opioid Receptor (MOR-1) Gene
? FILE REFERENCE: 830002-2000.1
? CURRENT APPLICATION NUMBER: US/09/761,962
? CURRENT FILING DATE: 2001-01-17
? PRIOR APPLICATION NUMBER: 09/743,872
? PRIOR FILING DATE: 2001-03-13
? NUMBER OF SEQ ID NOS: 46
? SOFTWARE: PatentIn version 3.0
? SEQ ID NO 9
? LENGTH: 1729
? TYPE: DNA
? ORGANISM: Mus musculus
US-09-761-962-9

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Query Match 37.5%; Score 432.4; DB 9; Length 1729;
 Best Local Similarity 65.8%; Pred. No. 1.4e-114;
 Matches 663; Conservative 0; Mismatches 336; Indels 9; Gaps 2;

```

QY 92 CCGGCTGGGCGGAGCCCGACAGCAACGCGAGCGCGCTCGAGAGACGCGCAGCTGGAGC 151
DB 185 CCGAGCCCAATGGCGGCTCTAAACGCGAGGCGTTGGCGGAGGACAGACGCTGTGCTCAGAG 244
QY 152 CCGGCGCAATCTCCCCCGGCGATCCGGGTCTATCAACGGCGGTCTTACTCCGAGTGTTCG 211
DB 245 CCGGAGCGCTTTCAGATGTCACAGCCATCACATATGCCCCCTTATTTCTTACCGGTGTG 304
QY 212 TCGTGGGCTTGGTGGGCAACTCGTGTGATGTTGTGATCTATCCGATACACAAGATGA 271
DB 305 TAGTGGGCTCTTTGGAAAATTCCGTGTATGTATGTATTTAAGATATACAAAATGA 364
QY 272 AGACAGCAACCAATTTACATATTTAACTGGCTTTGGCAGATCTTTAGTTACTTACAA 331
DB 365 AGACTGCCACCAACTTACATTTTCAACCTTGTCTGGCAGATGCTTACGCACTAGCA 424
QY 332 CCATGCCCTTTCAAGTACGGTCTACTTATGATAATTCCTGGCTTTTGGGAGTGTCTGT 391
DB 425 CGCTGCCCTTTCAAGTGTAACTTACCTGATGGAAAGTGGCCCTTGGAAAATCTCTCT 484
QY 392 GCAAGATAGTAAATTTCCATTGATTAATACTAACAATGTTCAACGACATCTTACCTTGA 451
DB 485 GCAAGATGATGATCTCAATAGCTACTACACATGTTTACCGATATCTTTCACCTCTGCA 544
QY 452 TGATAGCGGTGAGCGGTACATTTGCGGTGCGACCCCGTGAAGGCTTTTGAATTCGCA 511
DB 545 CCATAGAGTGTAGACCGGTACATTTGCGGTGCGACCCCGTGAAGGCTTGGATTTCCGTA 604
QY 512 CACCTTTGAAGCAAGATCAATCAATATCTGATCTGTGTCTGATCTGTGTGCA 571
DB 605 CCCCCGAAATGCAAAATGTCAATGTCTGCACTGGAATCTCTCTTCTGTGCAATGTGTC 664
QY 572 TCTCTGAATAGTCTTGGAGGACCAAAAGTCAAGGAAAGACGTGATGTCATTAGTGTCT 631
DB 665 TGCCGTGATGTTTCAATGCAACCAAAAATACAGGCAAGGCTC-----CATAGTTGCA 718
QY 632 CTTTGCAATAGTCTTGGAGGACCAAAAGTCAAGGAAAGACGTGATGTCATTAGTGTCT 691
DB 719 CCCTGACGTTCTCTCATCCCATGATGTAATGGGAAACCTGTCTC---AAAATCTGTGCT 775
QY 692 TCATCTTGGCTTCCGATGATGCTGCTGCTCATCATCATGCTGCTGCTGCTGCTGCTGCT 751
DB 776 TCATCTTGGCTTCCGATGATGCTGCTGCTCATCATCATGCTGCTGCTGCTGCTGCTGCT 835
QY 752 TGCGTCTGAAGAGCTCCGGCTCTTCTGGCTCCGAGAGAAAGATGCAACCTGCGTA 811
DB 836 TACGACTCAAGAGTGTCCGCAATGCTGTGGGCTCCAAAGAAAAGACAGAAACCTGCCA 895
QY 812 GGATCAACCAAGCTGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 871
DB 896 GGATCAACCAAGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 955
QY 872 ACATATTAATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 931
DB 956 ACATATTAATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1015
QY 932 GCTATTAATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 991
DB 1016 CCGTGCACCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1075
QY 992 CTTTCTTGATGAAAATTCAAGCGGTGTTCGCGGACTTGTCTTTCACCTGGAAGATGA 1051
DB 1076 CGTTCCTGATGAAAATTCAAGCGGTGTTCGCGGACTTGTCTTTCACCTGGAAGATGA 1099
QY 1052 GGATGAGCGGAGAGCACTAGCAGAGTCCGAAATACAGTTTCAAGATC 1099
DB 1136 CAATGGAACGCAAAATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1183

```

RESULT 64
 US-10-283-300-9
 ; Sequence 9, Application US/10283300
 ; Publication No. US20030103972A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Memorial Sloan-Kettering Cancer Center
 ; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF MULTIPLE SPLICING VARIANTS
 ; FILE REFERENCE: 830002-2000.3
 ; CURRENT APPLICATION NUMBER: US/10/283.300
 ; PRIOR FILING DATE: 2002-10-29
 ; PRIOR APPLICATION NUMBER: 09/761,962
 ; PRIOR FILING DATE: 2001-01-17
 ; PRIOR APPLICATION NUMBER: 09/743,872
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: PCT/US99/15974
 ; PRIOR FILING DATE: 1999-07-15
 ; NUMBER OF SEQ ID NOS: 46
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 9
 ; LENGTH: 1729
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 US-10-283-300-9

Query Match 37.5%; Score 432.4; DB 15; Length 1729;
 Best Local Similarity 65.8%; Pred. No. 1.4e-114;
 Matches 663; Conservative 0; Mismatches 336; Indels 9; Gaps 2;

```

QY 92 CCGGCTGGGCGGAGCCCGACAGCAACGCGAGCGCGCTCGAGAGACGCGCAGCTGGAGC 151
DB 185 CCGAGCCCAATGGCGGCTCTAAACGCGAGGCGTTGGCGGAGGACAGACGCTGTGCTCAGAG 244
QY 152 CCGGCGCAATCTCCCCCGGCGATCCGGGTCTATCAACGGCGGTCTTACTCCGAGTGTTCG 211
DB 245 CCGGAGCGCTTTCAGATGTCACAGCCATCACATATGCCCCCTTATTTCTTACCGGTGTG 304
QY 212 TCGTGGGCTTGGTGGGCAACTCGTGTGATGTTGTGATCTATCCGATACACAAGATGA 271
DB 305 TAGTGGGCTCTTTGGAAAATTCCGTGTATGTATGTATTTAAGATATACAAAATGA 364
QY 272 AGACAGCAACCAATTTACATATTTAACTGGCTTTTGGCAGATCTTTAGTTACTTACAA 331
DB 365 AGATGAGTGTAGTCTCAATAGCTACTACACATGTTTACAGATATCTTTCACCTCTGCA 424
QY 332 CCATGCCCTTTCAAGTACGGTCTACTTGTATGAATTCCTGGCTTTTGGGAGTGTCTGT 391
DB 425 CGCTGCCCTTTCAAGTGTAACTTACCTGATGGGAAAGTGGCCCTTGGAAAATCTCTCT 484
QY 392 GCAAGATAGTAAATTTCCATTGATTAATACTAACAATGTTCAACGACATCTTCACTTGA 451
DB 485 GCAAGATGATGATCTCAATAGCTACTACACATGTTTCAAGATATCTTTCACCTCTGCA 544
QY 452 TGATAGCGGTGAGCGGTACATTTGCGGTGTGCAACCCCGTGAAGGCTTTGGAATTCGCA 511
DB 545 CCATGAGATGATGAGACCGGTACATTTGCGGTGTGCAACCCCGTGAAGGCTTGGATTTCCGTA 604
QY 512 CACCTTTGAAGCAAGATCAATATCTGATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 571
DB 605 CCCCCGAAATGCAAAATGTCAATGTCTGCAACTGGAATCTCTTCTTCCGCAATGTGTC 664
QY 572 TCTGTGAATAGTCTTGGAGGACCAAAAGTCAAGGAAAGACGTGATGTAATGATGCT 631
DB 665 TGCCGTGATGTTTATGGAACAACAAAATACAGGAGGAGGCTC-----CATAGATTGCA 718
QY 632 CTTTGCAATAGTCTTGGAGGACCAAAAGTCAAGGAAAGACGTGATGTAATGATGCT 691
DB 719 CCCTGATGTTTATGGAACAACAAAATACAGGAGGAGGCTC-----CATAGATTGCA 775
QY 692 TCATCTTGGCTTCCGATGATGCTGCTGCTCATCATCATGCTGCTGCTGCTGCTGCTGCT 751
DB 776 TCATCTTGGCTTCCGATGATGCTGCTGCTCATCATCATGCTGCTGCTGCTGCTGCTGCT 835

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Best Local Similarity 65.8%; Pred. No. 1.6e-114;
Matches 663; Conservative 0; Mismatches 336; Indels 9; Gaps 2,

QY	92	CCGGGTGGGGCCGAGGCCACAGGCAACGGAGAGCGCGCTCCGAGAGACCGGACGCTGGAC	151
Db	185	CCGACCCATGCGGCTCTTAACCGGACGGGGGCTTGGGGGAGGCCACAGCCTTGCTCCAGA	244
QY	152	CCGCGCAATCTCCCCGCGCATCCCCGCTCATCAAGCGGGCTCTACTCCGTAAGTTTCG	211
Db	245	CCGGAGGCGCTTCATGGTCAACAGGCATCCATCATGGCCCTCTATTCTATCGGTGG	304
QY	212	TCGTGGGCTTGGTGGGCACTCGCTGGTCAATGTTGTTGATCATCCGATACACAAAGATGA	271
Db	305	TAGTGGGCGCTCTTTGGAAACCTTCGGTCACTGATGTGATGTGAAGATATACCAAAATGA	364
QY	272	AGACGAGCAACAAACATTAACATTTAACCTGGGCTTTGGGAGANAGCTTTTATGTTACTACA	331
Db	365	AGACTGCCAACAAACATCTACATTTTCAACCTTGGCTCTGGCAAGATGCTTAAAGCACTAGCA	424
QY	332	CCATGCCCTTTCAGAGTACGGGTCTACTTGATGAATTCCTGGCGCTTTCGGGGATGTGCTGT	391
Db	425	CGTGCCCTTTCAGAGTGTTAATCACTGATGGAAAGTGGCGCTTTCGGAAACATCTCTCT	484
QY	392	GCAAGATATGTAATTTCCATGTATTAATCAACATGTTCAACGCACTTTCACTTCACTGACCA	451
Db	485	GCAAGATGTGATCTCAATAGACTCTACACATGTTTCAACGATTTCAACGATCTTCAACCTCTGCA	544
QY	452	TGATAGGCGTGAACCGGTACATATGCGAGTGGCACCCGGTGAAGGCTTTCGACTCCGCA	511
Db	545	CCATAGATGTAGACCGGCTCAATGCTGGCTGCGCACCCGGTCAAGGCCCTTGATTTCCGTA	604
QY	512	CACCTTGAAGCAAAAGATCATCAATATCTGCATCTGGCTGTGTCATCTGTTGGCA	571
Db	605	CCCCCGGAAATGGCAAAATGTGCATGTCTGGCACTGGATCCTCTCTCTGCGCAATTGGTC	664
QY	572	TCTCTGCATATGCTCTTGAAGGCACCAAGTACGGGAAGCGTGCATGTCTATGATGTCT	631
Db	665	TGCCGTAATGTTCAATGGCAACCAAAATAAGGCAAGGGGTCT-----CATAGATTGCA	718
QY	632	CCTTGCAATTCACCAAGATGATGACTACTCCTGGTGGGACCTCTTCAATGAAGATCTGCTCT	691
Db	719	CCCTCAAGTTCCTCATATCCCAATGTGTACTGGGAAACCTGCTC---AAATCTGTGCT	775
QY	692	TCATCTTTCGCTCGTATCCCTGTCTCATCATCATCATGCTGTGCTACACCTGATGATCC	751
Db	776	TCATCTTTCGCTCTCATATGCGGCTCTCATCATCATCATGCTGTGATGGAATGATGATCT	835
QY	752	TGCGTCTCAAGAGCGTCCGGGCTCTTTCGGGTCCCCGAGAAAGATGGCAACTTGGCTA	811
Db	836	TACGACTCAAGAGTGTCCGCAATGCTGTGGGCTCTCAAGAAAGAAAGCAAGAACTTGGCA	895
QY	812	GGATCAACAGACTGGTCTCTGGTGTGTGTGGGCAAGTCTTGTGCTGTGCTGACTCCCATTC	871
Db	896	GGATCAACCGGATGCTGT	955
QY	872	ACATATTCATCTGTGTGAAGGCTCTTGGGAGACCTCCCAACGACAGCTGCTCTTCCCA	931
Db	956	ACATCTATGTATCATCTCAAGACCTGAATCCAGATTCAGAAACCACTTTCAGACTGTTT	1015
QY	932	GCATATTAATTCAGCATGGCTTTAGGCTTATCCAAAGTAAGCTGAATCCATTCCTATAG	991
Db	1016	CTGGGACTTCTGCATTCCTTGGGTATACAAAGAGCTGCTGAAACCAAGTTCTTATATG	1075
QY	992	CCTTTCTTGATGAAGAACTTCAAGCGGTATTTCCGGGACTTCTGCTTTCACATGAAGATGA	1051
Db	1076	CGTTCTCGATGAAGAACTTCAAGATGTATTTAAGAGATTTCTGATATCCCACTTCTCTCA	1135
QY	1052	GGATGAGCGGCGACGACACTAGACAGATGCCAATATCAATTCAGATC	1099
Db	1136	CAATTCGAACAGCAAACTCTGTCTCAATTCGGTCAAAACACTAGAGGATC	1183

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US-10-185-083-23
/ Sequence 23, Application US/10185083
/ Publication No. US20030050467A1
/ GENERAL INFORMATION:
/ APPLICANT: Memorial Sloan Kettering Cancer Center
/ APPLICANT: Pasternak, Gavrill
/ APPLICANT: Pan, Ying-Xian
/ TITLE OF INVENTION: Multiple Splice Variants of the Mu-Opioid Receptor Gene
/ FILE REFERENCE: 830002-2007.1
/ CURRENT APPLICATION NUMBER: US/10/185,083
/ CURRENT FILING DATE: 2002-06-28
/ PRIOR APPLICATION NUMBER: 60/302,072
/ PRIOR FILING DATE: 2001-06-29
/ NUMBER OF SEQ ID NOS: 53
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 23
/ LENGTH: 2588
/ TYPE: DNA
/ ORGANISM: Mus Sp.
US-10-185-083-23

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Qy	812	GGATACACAGACTGGTCCGTGGAGGGGAGGAGCACTTGTGTGTGCTGACACTCCATTCC	871
Db	886	GGATCACCCGGAGTGGTGGCTGGGGTCGGCGGCTGTAATTATGTCTGTGGACCCCCATCC	955
Qy	872	ACATATTGATCCTGTGTGAGGCTCTGGGGAGCACCCTCCACAGCAGACGTGCTCTTCCA	931
Db	956	ACATCTATGTATCATCATCAAGCAGCTGATCAAGATCCAGAAACCACTTCCAGACTGTT	1015
Qy	932	GCATATTATTTCTGCACTGCCCTTAAGGCTATACCAAGTAGGCTGAATCCCATTTCTTAGG	991
Db	1016	CCTGGCACTTCTGCATTCCTCTTGGGTTACACAAAGACGCTCGTAACCCAGTTCTTTATVG	1075
Qy	992	CCTTTCTTGATGAAAACTTCAAGCCGATGTTTCCGGACTTCTGCTTCCACTGAGAAATGA	1051
Db	1076	CGTTCCTGAGTGAATAAATTCCAACGATGTTTAAAGAGATTTCGATCCCAACTTCTCTCA	1135
Qy	1052	GGATGAGACGGCAGACACTAGCAGAGTCCGAAATATCACTTCAGAGATC	1099
Db	1136	CAATGAACAGCAAAACTCTGCTGCAGAAATCCGTCAGAAACACTAAGGAAAC	1183

	RESULT	68	
US-10-194-595-23	/ Sequence 23, Application US/10194595		
	/ Publication No. US20030068805A1		
	/ GENERAL INFORMATION:		
	/ APPLICANT: Memorial Sloan Kettering Cancer Center		
	/ APPLICANT: Pasternak, Gavril		
	/ APPLICANT: Pan, Ying-Xian		
	/ TITLE OF INVENTION: Multiple Splice Variants of the Mu-Opioid Receptor Gene		
	/ FILE REFERENCE: 830002-2007.1		
	/ CURRENT APPLICATION NUMBER: US/10/194,595		
	/ CURRENT FILING DATE: 2002-07-11		
	/ PRIOR APPLICATION NUMBER: US/09/561,523		
	/ PRIOR FILING DATE: 2002-07-03		
	/ PRIOR APPLICATION NUMBER: 60/302,072		
	/ PRIOR FILING DATE: 2001-06-29		
	/ NUMBER OF SEQ ID NOS: 53		
	/ SOFTWARE: PatentIn version 3.1		
	/ SEQ ID NO: 23		
	/ LENGTH: 2588		
	/ TYPE: DNA		
	/ ORGANISM: Mus Sp.		
US-10-194-595-23			
Query Match	37.5%	Score 432.4;	DB 15; Length 2588;
Best Local Similarity	65.8%;	Pred. No. 1.8e-114;	
Matches 663; Conservative	0;	Mismatches 336;	Indels 9; Gaps 2;
Oy	92	CCGGGTGAGCGAGGCCGACAGCAACGGCAGGCGCCGCTCGAGAGACGCAGAGCTGAGC	151
Db	185	CCGACCATTGGGTCTTAACCGCACGGGGCTTGGCGGAGCCACAGCCTTGCCCTCAGA	244
Oy	152	CCGGGCATCTCCCCGGCCATCCCGCATCATCATCACGGCGGATCTACTCGTAGTTTCG	211
Db	245	CCGGAGCCCTTCATGTGTACAAGCCATCACCATCATGAGCCCTGTATTCTATCGTGTG	304
Oy	212	TCTGTGGCTTGGTGGGCACTCGCTGTGCATGTTCTGTGATCATCCGATACCAAAAGATGA	271
Db	305	TATGTGGGCTCTTTGGAAACTTCCGTGTCACTGATGATGATTTGTAAGATATACAAAATGA	364
Oy	272	AGACGACCAACCACTTATCATATTTAACCTGGCTTGGCAGATGCTTATGTTACTACA	331
Db	365	AGACTGCAACCAATCTACATTTTCAACCTTGCTCTGTGGAGATGCCCTTAGCCACTAGCA	424
Oy	332	CCATGCCCTTTCAGAGTACGGTCTACTGATGAATTTCCGTGCGCTTTTGGGATGTCTGT	391
Db	425	CGGTGCCCTTTCAGAGTGTATACTACCTGATGGGAAGTGGGCCCTTGGAAACATCTCT	484
Oy	392	GCAAGATAGTATTTCATTTGATTATCTACCAACATGTTTACACGACCTTTCACTTGACCA	451
Db	485	GCAAGATGTATCTCAATAGACTACTACCAACATTTTCAACAGATATCTTCAACCTCTGCA	544

QY	452	IGATGAGGTGAGACCGCTACATATGCGGTGGACACCCGTAAGGCTTTGGACTTCCGA	511
Db	545	CCATGAGTGTAGACCGCTACATATGCGGTGGACACCCGTAAGGCTTTGGACTTCCGA	604
QY	512	CACCCCTTAAAGCAAAAGATTCATCATATCTGCATCTGGCTGTCTGCATCTGTTGGCA	571
Db	605	CCCCCGCAAAATGCAAAATGTGTCAATGTCTGGAATGGATCCTCTCTTCTGCACTTGGTC	664
QY	572	TCTCTGCATATGTCCTTGGAGGCACCAAAATGCAAGGAAAGACGTGCATGTCAATGATGCT	631
Db	665	TGCCCGTATGTTCATGAGCAACCAAAATTCAGGCAAGGAGTC-----CATAGATTCGA	718
QY	632	CCTTGAGCTTCCAGATGATGATGACTACTCTGTGGAGACCTCTTCATGAAAGATCTGAGTCT	691
Db	719	CCCTCAGCTTCTCTCATCTCCACATGTAAGTGGAGAACTGTCTC--AAATCTGTGTCT	775
QY	692	TCATCTTGTGCTTGTGATATCCCTGTCTCATCATCATGCTGTGCTACACCTGATATCC	751
Db	776	TCATCTTGTGCTTGTGATATCCCTGTCTCATCATCATGCTGTGCTACACCTGATATCC	835
QY	752	TGCGTCTTAAAGAGCGTCCGGCTCCTTTCTGGCTCCCGAGAGAAAGATGGCAACTTGGCTA	811
Db	836	TACAGCTTAAAGAGTGTCCGATGCTGTGGCTCCAAAGAAAGAGCAAGAACTTGGCTA	895
QY	812	GGATCACAGACTGGTCTGTGATGATGAGTGTGAGTCTTGTGCTGTGATCTCCATTC	871
Db	896	GGATCACAGACTGGTCTGTGATGATGAGTGTGAGTCTTGTGCTGTGATCTCCATTC	955
QY	872	ACATATTCATCTGTGTGAGGCTCTGTGGAGACACTCCACAGCACAGCTGCTCTTCCCA	931
Db	956	ACATCTATGTATCATCAAAAGCACTGATCAAGATTCAGAAACCTTTCAGACTGTTT	1015
QY	932	GCTATTAATTCGTGATGCGCTTAAAGCTATTAACACAGTAGAGCTGATCCATTCCTAG	991
Db	1016	CTTGCACTTGTGATGCGCTTAAAGCTATTAACACAGTAGAGCTGATCCATTCCTAG	1075
QY	992	CTTTCTTGTATGAAAACCTTCAAGCGTGTTCCTGGACCTTGTGCTTTCACATGAAATGA	1051
Db	1076	CGTTCTGTGATGAAAACCTTCAAGCGTGTTCCTGGACCTTGTGCTTTCACATGAAATGA	1135
QY	1052	GGATGAGCGGCAAGCACTAGCAGAGTCCGAATACATTCAGATC	1099
Db	1136	CAATTCGACAGCAAACTGTCTGAAATCCGTCAAAACATCTAGGGAAC	1183

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RESULT 69
US-09-826-509-546
; Sequence 546, Application US/09826509
; Publication No. US20030204073A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinema, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: NO. US20030204073A1-Endogenous, Constitutively Activated Known G
; TITLE OF INVENTION: Protein-Coupled Receptors
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 546
; LENGTH: 1182
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-826-509-546

Query Match      37.4%; Score 431.6; DB 11; Length 1182;
Best Local Similarity 66.1%; Pred. No. 2e-114;
Matches 658; Conservative 0; Mismatches 329; Indels 9; Gaps 2;

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OY	92	CCGGCTGGGCGCAGCCCGACAGCAAGGAGCGCGGCTCGAGAGACGGCGACCTGGAGC	151
Db	125	CCGACCCATGCGGTCCGAACCGCACCAACTGGGCGGAGAGACAGCTGTGCCCTCCGA	184
OY	152	CCGCGCAACATCTCCCGGCGATCCGGGTATCATCACGGCGGTCTACTCGTGAATGTTCG	211
Db	185	CCGGCAGTCCCTTCATGATCAACGGCGATCAAGATCAATGGCCCTCTACTCATGTGTGCG	244
OY	212	TGCTGGGCTTGGGGGCACTCGTGGTATAGTGTGGATCATCGATACAGAAAGATGA	271
Db	245	TGCTGGGCTCTTGGAACTTCTGTGTATGTATGTGATTTGTCAAGTACCAAGATTGA	304
OY	272	AGACGACCAACCAATTTACATATTTAACTGTGGCTTTGGCAGATGCTTTAGTTACAA	331
Db	305	AGACTGCCACCAACATCTACATTTTCAACTTGTCTGGGAGATGCTTAGCACCAGTA	364
OY	332	CCATGCGCTTGTAGAGTACGTCTACTTGAATATTCCTGGCCCTTTGGGAGATGTCTGT	391
Db	365	CCCTGCCCTTCCAGAGTGAATTACTTAATGGAAACATGGCCATTGGAAACCATCTCTT	424
OY	392	GCAAGATAGTAATTTTCATTTGATTACTTACAAACATGTTCAACAGCATTTTCACTTGACA	451
Db	425	GCAATATAGTATCTCCATAGATTACTTATACATGTTCAACAGCATTTTCACTTGACA	484
OY	452	TGATAGCGGTGACCGGTCAATTTGGGTGGCCACCCCGTAGAGGCTTTGAACTTCCGA	511
Db	485	CCATAGGTGTATGATACATATGCACTGCGCACCCCTGTCAAGGCTTAGATTTCCGTA	544
OY	512	CACCTTGAAGCAAAAGATCATCAATATCTGCATCTGGCTGTCTGTGATCTGTTGGCA	571
Db	545	CTCCCCGAAATGCCAAAATTTATCAATGTCTGCACATGTGATCTCTCTTGACCATTTGGTC	604
OY	572	TCTCTGCAATTACTCTTGAGAGGCAACCAAGTACAGGAAAGCGATATGTCATTGAATGCT	631
Db	605	TTCCTGTATGTTCAATGCTTACAAACAAATPACAGGAAAG-----TTCATATGATTTGA	658
OY	632	CCTTGACGTTCCAGATGATGACTACTCCGTGTGGAGCTCTTTATGAAAGATCTGCGTCT	691
Db	659	CACTTAACTTCTCTCATCCACCTGTGTACTGGGAAAACCTCG--TGAAGATCTGTGTTT	715
OY	682	TCATCTTTGGCTTGTGATCCCTGTCTCTATCATATGCTGTCTACACCTGTATATCTC	751
Db	716	TCATCTTGCCTTCAATTATGCCAGTCTCATATTAACGTGTCTATGATCTGATATCTT	775
OY	752	TGCGTCTCAAGACGCTCGGCTCTTTCTGGCTCCCGAGAGAAAGATTCGCAACTTGCATA	811
Db	776	TGCGCTCAAGAGTGTCCGCATGCTCTTGGCTCCAAAAGAAAAGACAGAAATCTTCGAA	835
OY	812	GGATACACAGACTGTCTCTGTGTGTGTGTGGCAGTCTTGTGTCTGTCTGTGACTCCCATTC	871
Db	836	GGATCAAGAGATGT	895
OY	872	ACATATTCATCTGTGTGAGGCTCTGGGGAGACCTCCACAGCAGCTGTCTTCTCA	931
Db	896	ACATTTAGTATCATTTAAAGCTTGTGTATCAATCCCAAGAACTAAGTTCCAGATCTT	955
OY	932	GCTATTACTTCTGTGATGCGCTTAGGCTATACCAACAGTAGCTGAATCCCATTTCTAG	991
Db	956	CTTGGACCTTGTGATGTCTTAGGTTACAAACAGCTGCTCAACCCAGTCTTTTAG	1011
OY	992	CCTTTCTTGATGAAATCTCAAGCGGTGTTTCCGGGACTTGTGCTTTCACATGAAGATGA	1051
Db	1016	CATTTCTGATGAAATCTCAACAGATGTTCAAGAGTCTGTATCCCACTCTTCA	1071
OY	1052	GGATGAGCGGCGACGACATAGACAGTCCGAAT	1087
Db	1076	ACATTGACCAACAAATCTCACTGAAATTCGTCAG	1111

```

/ Publication No. US20030204073A1
/ GENERAL INFORMATION:
/ APPLICANT: Lehmann-Brunisma, Karin
/ APPLICANT: Liaw, Chen W.
/ APPLICANT: Lin, I-Lin
/ TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G
/ TITLE OF INVENTION: Protein-Coupled Receptors
/ FILE REFERENCE: AREN-207
/ CURRENT APPLICATION NUMBER: US/09/826,509
/ CURRENT FILING DATE: 2001-04-05
/ PRIOR APPLICATION NUMBER: 60/195,747
/ PRIOR FILING DATE: 2000-04-07
/ PRIOR APPLICATION NUMBER: 09/170,496
/ PRIOR FILING DATE: 1998-10-13
/ NUMBER OF SEQ ID NOS: 589
/ SOFTWARE: PatentIn Version 2.1
/ SEQ ID NO 544
/ LENGTH: 1203
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-826-509-544

Query Match      37.4%      Score 431.6; DB 11; Length 1203;
      Bseq Local Similarity 66.1%; Pred. No. 2.1e-114;
Matches 658; Conservative 0; Mismatches 329; Indels 9; Gaps 2;

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RESULT 70
US-09-826-509-544
; Sequence 544, Application US/09826509

Query Match	37.4%	Score 431.6	DB 11	Length 1203
Best Local Similarity	66.1%	Pred. No. 2.1e-114		
Matches	658	Conservative	0	Mismatches 329; Indels 9; Gaps 2
QY	CCGGCTGGGGCCGAGCCCGACAGCAACGGCGAGCGCCGCTCGGAGGACGGCGACCTGGAGC	151		
Db				
125	CCGACCCATGGGGTCCGACCGGACCAACCTGGGGGGGAGACAGCGCTGTGCCCTCCGA	184		
QY	152	CCGGCGACATCTCCCCGGGCAATCCCGGTCAATCAACGGCGGCTCTACTCCGTAAGTGTTCG	211	
Db	185	CCGGCGAGTCCCTCCATGTATCAACGGCCATCAAGATCATGGCCCTCTTACCTCATCGTGTGCG	244	
QY	212	TCGGGGGTGGGGGCACTCGCTGGTCAATTTGGTATCATTCGGATACAAAGATGA	271	
Db	245	TGGTGGGGGCTCTTGGGAACTTCCGTGTCAATGATGTAATGTCAAGATACACCAAGATGA	304	
QY	272	AGACGACCAACCAATTTACATATTTAACTGGCTTTGGAGATCCTTGTAGTTACTACA	331	
Db	305	AGACTGCCACCAACATCTTACATTTTCAACCTTGTCTGTGGAGATGCCCTTAGGCCACAGTA	364	
QY	332	CCATGCCCTTTCAAGATACGGTCTTACTGATGAATTCCTGGCCTTTTGGGGATGTGCTGT	391	
Db	365	CCCTGCCCTTCAAGATGTGAATTAACCTAAATGGGAAACATGGCCATTGGAACCATCTCTT	424	
QY	392	GCAAGATATGTATTTCCATTTGATTAATCAACATTTTACACGACATCTTCACTTGACCA	451	
Db	425	GCAAGATATGTATCTCCATAGATTAATTAACATGTTTACACGACATTTCAACCTCTGTGA	484	
QY	452	TGATGAGCGTGGACCGGCTACATTTGGCGGTGGACCCCGTGAAAGGCTTTGGACTTCCGA	511	
Db	485	CCATGAGTGTGATCGATACATTTGACGTCTGCCACCTCTGTCAAGGCTTTAGATTTCCGTA	544	
QY	512	CACCTTTGAAGGCAAAAGATCATTAATCTGCAATCTGGCTGTGTGTATCTGTGTGCA	571	
Db	545	CTCCCGGAAATGCCAAATTAATCAATGCTGCAACTGTGATCCTCTTCAAGCATTTGGTC	604	
QY	572	TCTCTGCATATGTCTTTGGAGGCAACAAAGTCAAGGAAAGAGTGCATGTCTTAAGTGTCT	631	
Db	605	TTCTGTAAATGTTATGGCTTCAACAAATAACAGGCAAGG-----TTCCATAGATTTGTA	658	
QY	632	CCTTGACGTTCCAGATGATGATCACTCTGTGGTGGGACCTCTCTTANTGAAGATCTGCTCT	691	
Db	659	CATTAACATTTCTTCATCCAACTGTGTACTGGGAAACCTTG--TGAAGATCTGTGTTT	715	
QY	692	TCATCTTTGCTCTTGATCCCTGTCTCATCATCATCATGTCTGTCTACACCTCATGATATCC	751	
Db	716	TCATCTTGCTTCAATTAATGCAAGTGCATCATTAACGTGTGTCTATGGAATCATGATATCT	775	
QY	752	TGCGTCTCAAGAGCGTCCGCTCTCTTTTGGCTCCCGAAGAAAGATGGCAACTTGGCTA	811	
Db	776	TGCGCTCTCAAGAGTCCGCAATGCTCTCTGTGCTCCAAAGAAAGAGACAGGAATCTTTCGAA	835	

; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 10
; LENGTH: 1149
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: nucleotide sequence of MOR-V2R chimera
US-09-993-844-10

Query Match 37.3%; Score 430.4; DB 9; Length 1149;
Best Local Similarity 68.1%; Pred. No. 4,5e-114;
Matches 631; Conservative 0; Mismatches 286; Indels 9; Gaps 2;

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OY 110 ACAGAACGGGACCGCGCTGGAGAGACGGCAGCTGGAGCCCGGACATCTCCCGG 169
DB 137 ACCGACCGGGCTTGAGCGGAAACGACGCTTGCCCTCAGACCGGACGCTTCATAG 196
OY 170 CCATCCGGGTCAATCAACGGCGTCTACTCCGTAGTGTTCGTGGGCTTGGTGGCA 229
DB 197 TCACAGGCATTACCATCAGAGGCCCTTACTCTATGCTGTGTAGTGGGCTTCCGAA 256
OY 230 ACTCGCTGTCAATGCTTCTGATCATCCGATACCAAAAGATGAAGACAGCAACCAAT 289
DB 257 ACTTCCTGGTCAATGATGATGTAGATACACCAAAATGAAGACTGCCACCAATCT 316
OY 290 ACATTTTAACCTGGCTTGGAGATGCTTAGTTACTACAAACCATGCCCTTTCAGATA 349
DB 317 ACATTTCAACCTTCTCTGCGAGAGCGCTTAGCGACCATGACCTGCTTCAGAGTG 376
OY 350 CGGTCTACTGTGATTCCTGGCCTTTTGGGATGTGCTGTGCAAGATAGTAATTTCCA 409
DB 377 TCAACTACCTGATGGAAACATGCGCTTCGGAACATCCTCTGCAAGATCGATCTCA 436
OY 410 TTGATTACTACAAATGTTTACACAGACATCTTCACTTGAACATGATGAGCGTCT 469
DB 437 TAGATTACTACAAATGTTTACACAGACATCTTCACTTGAACATGAGCGTCTCT 496
OY 470 ACATGGCGGTGGACCCCGTGAAGGCTTGGACTTCGCGACACCTTGAAGGAAAGA 529
DB 497 ACATTTGCTGTGCGACCCAGTCAAGCCCTGGATTTCCGTACCCCGGAAATGCCAAA 556
OY 530 TCATCAATATCTGCAATCTGCTGTGCTGTGCTCATCTGTGGCATCTCTGCAATAGCT 589
DB 557 TCGTCAAGGTCTGCAACCTGGAATCCTCTCTGCGCATGGTCTGCTGAATGTTCA 616
OY 590 GAGGACCAAACTCGGGAAGAGCTGATGTCATGAGTGTCTCTTGAAGTTCCAGATG 649
DB 617 CAACCAAAAATACAGGCA-----GGGATCCATGATGACCTCTCAAGTTTCCACC 670
OY 650 ATGACTACTCGTGGGAGCCTCTTCATGAGATGCGGTCTTCATCTTGGCTTCGGA 709
DB 671 CAACCTGGTACTGGGAGAACCTGCTC---AAATCTGTGTCTTTATCTTGGCTTCA 727
OY 710 TCCCTGTCTGATCATCATCTGCTGCTACACCTGATGATCTGTGCTCAAGAGCTGC 769
DB 728 TGGCATCTCATCATCACTGTGTGTTAOGGCTGATGATCTTACGACTCAAGAGCGTTC 787
OY 770 GCGTCTTTTGTGGCTCCCGAGAGAAAGATCGCAACCTGCTGATGATCAACGAGCTG 829
DB 788 GCATGCTATCGGGCTCCAAAGAAAGAGACAGAAATCTCGAGGATVCAACCGGATG 847
OY 830 TGGTGTGTGTGGAGTCTTGTGCTGTGCTGAGATCCCATTCACATATTCATCCGTGG 889
DB 848 TGGTGTGTGTGGCTTATTTATGCTGTGCTGAGACCCCATTCACATCTACATCATCA 907
OY 890 AGGCTTGGGAGACCTCCACACAGACAGCTGCTCTCCAGCTATTAATCTTGCATCG 949
DB 908 AAGGCTGATCATCGATTCAGAAACACATTTACAGACGTTTCCGAGACTTCGCAATG 967
OY 950 CCTTAGGCTATACCAAGATAGCTGATTCGATTTCTTACGCTTTTGTGATGAAACT 1009
DB 968 CTTTGGGTTACAGAAAGCTGCTGATTCAGATTCATTCGCTTCTGATGAAAACT 1027
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OY 1010 TCAAGCGGTGTTCCGGGACTTCTGC 1035
DB 1028 TCAGCGATGCTTCAGAGAGTTCTGC 1053
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RESULT 73
US-09-761-962-4

; Sequence 4, Application US/09761962
; Patent No. US20020077285A1

; GENERAL INFORMATION:

; APPLICANT: Memorial Sloan-Kettering Cancer Center

; TITLE OF INVENTION: Identification and Characterization of Multiple Splice

; TITLE OF INVENTION: Variants of Mu-

; FILE REFERENCE: 83002-2000.1

; CURRENT APPLICATION NUMBER: US/09/761,962

; PRIOR FILING DATE: 2001-01-17

; PRIOR APPLICATION NUMBER: 09/743,872

; NUMBER OF SEQ ID NOS: 46

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 4

; LENGTH: 1542

; TYPE: DNA

; ORGANISM: Mus musculus

US-09-761-962-4

Query Match 37.2%; Score 429.2; DB 9; Length 1542;
Best Local Similarity 65.6%; Pred. No. 1.2e-113;
Matches 661; Conservative 0; Mismatches 338; Indels 9; Gaps 2;

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OY 92 CCGGCTGGGCGGACCGGACGCAACGAGCGCGGCTGGAGAGCGGAGCTGAGC 151
DB 185 CCGACCATGCGTCTTACCGACGAGGCTTGGCGGAGCCAGACCTGCTCAG 244
OY 152 CCGGACATCTCCCGGACATCCCGGTATCATCAGCGGCTTACTCCGTAGTCTG 211
DB 245 CCGGACGCTTCCATGATGATCAGCCATCAACATCAAGGCTTATTTATCTGCTG 304
OY 212 TCGTGGCTTGGTGGGCACTCGTGTCTATGTTCTGATCTCGATACCAAAATGA 271
DB 305 TAGTGGGCTCTTTTGAAGTCTCTGCTGATGATGATGATGATGATGATGATG 364
OY 272 AGAAGAACCAATTTATTAATTTAACTGCTTGGAGAGCTTATGTTACTGAA 331
DB 365 AGATGCGACCAATCATCTACATTTTCAACCTGTGCGAGATGCTTACGACTGCA 424
OY 332 CCATGCCCTTTCAGAGTACGCTTACTTGTATGATTCCTGCGCTTTTGGGATGCTGT 391
DB 425 CGCTGCCCTTTCAGAGTATTAATCTGATGAGAGTGGAGTGGCCCTTGGAAACATCTCT 484
OY 392 GCANAGATGATTTTCCATGATTTACTTACAAATGTTTACAGATTTTCACTTGA 451
DB 485 GCANAGATGATTTTCCATGATTTACTTACAAATGTTTACAGATTTTCACTTGA 544
OY 452 TGAAGAGGAGGACCGGTATCATGCTGCTGCGACCCCGTGAAGGCTTGGACTTCCGA 511
DB 545 CCATGATGATGAGCGGCTTACATGCTGCTGCGACCCCGTGAAGGCTTGGACTTCCGA 604
OY 512 CACCTTGAAGGACCAAGATCATATATCTGATCTGCTGCTGCTCATCTTGTGGCA 571
DB 605 CCGGCGGAAATGCGAAATTTGTCAATGTCTGCAATCTGATCTCTCTTCCATTTGGT 664
OY 572 TCTTGCATATGCTCTTGAAGGACCAAGTCAAGGAAAGCTGATGATGATGATG 631
DB 665 TGCCTGTAATGTTTATATGCAACCAAAATACAGGCGGAGTCTC-----CATGATG 718
OY 632 CTTGAGTTCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 691
DB 719 CCTTCAAGTTCTTCACTCCCAATGATGATGATGATGATGATGATGATGATGATG 775
OY 692 TCATCTTGGCTTGTGATCTCTGCTCTCATCATCATCATCATCATCATCATCAT 751
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SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/823,114
 FILING DATE: 29-Mar-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/148,351
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: MURASHIGE, KATE H.
 REGISTRATION NUMBER: 29,959
 REFERENCE/DOCKET NUMBER: 22000-20526.22
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 887-1500
 TELEFAX: (202) 887-0763
 TELEX: 90-4030 MRSNFOERSWSH
 INFORMATION FOR SEQ ID NO: 15:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1981 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 15:
 US-09-823-114-15

Query Match 37.2%; Score 429.2; DB 9; Length 1981;
 Best Local Similarity 65.6%; Pred. No. 1.3e-113;
 Matches 661; Conservative 0; Mismatches 338; Indels 9; Gaps 2;

92 CCGGCTGGGCGGAGCCGACAGCAAGGCGGCGCTCGAGAGGACCGCAGCTGAGC 151
 374 CCGAGCCATGGGCGTCTTAACCCGAGGGCCTTGGGGAGACAGCCTGCGCCCTGAGA 433
 152 CCGGCAATCTCCCGGCGCATCCGGTCATCATACGCGGCTTACTCTCGTAGTCTCG 211
 434 CCGGAGCCCTTCCATGCTACAGCCATCACCATCATGCGCCCTTATCTATCGTGTG 493
 212 TCGGGGCTGGTGGGGAACCTCGCGTCATGTTGATCATCCGATACCAAGATGA 271
 494 TAGTGGGCTCTTGGAACTTCCTGGTCATGATGATGATTAAGATATACCAAAATGA 553
 272 AGACAGCAACCAACATTACATATTAACTGGCTTTGGCAGAGTCTTAGTACTACAA 331
 554 AGACGCAACCAACATCTACATTTTCAACCTTGTCTGGCAGATGCTTAGCAGCTACA 613
 332 CCATCCCTTTCAAGTACGCTTACTGATGAATTCCTGGCTTTGGGAGTGTCTGT 391
 614 CGTGCCTTTCAAGTGTAACTACGATGGGAACGTGGCCCTTTGAAACAATCTCT 673
 392 GCAAGATGTAATTCATGATTTAATTAACTAACAATGTTGACAGCACTTTTCACTGACA 451
 674 GCAAGATGTAATTCATGATTTAATTAACTAACAATGTTGACAGTATCTTCACTGACA 733
 452 TGATGAGCGTGGACCGTACATTTGCGGTGCGCACCCCGTGAAGGCTTTGACTCCGCA 511
 734 CCATGAGTGAACCGCTACATTTGCGGTGCGCACCCCGTGAAGGCTTTGACTCCGCA 793
 512 CACCTTGAAGGCAAAATCATCAATATCTGATCTGCTGTCTGTCATCTGTGGCA 571
 794 CCCCCGAAATGCCAAATTTGTCATGCTGCAATGTGATCCTCTTCTGCAATGTGTC 853
 572 TCTCTGCAATAGTCTTGGAGGACCAAGTCAGGGAAGACGTGATGCTATGAGTCT 631
 854 TGCCGTAATGTTCAATGCAACCAAAATACAGGCAAGGCTC-----CATAGATGCA 907
 632 CTTGCAAGTCCCAAGATGATGACTACTCTGCTGGGAGACCTCTTCATGAAGATCTGCT 691
 908 CCGTCAAGTCTCTCTATCCCATGCTGAGTACGAGAACTGCTC---AAAATCTGTCTCT 964
 692 TCATCTTGGCTTGTGATCCCTGTCTCATCATCATGCTGTCTGCTACACCTGATGATCC 751
 965 TCATCTTGGCTTGTGATCCCTGTCTCATCATCATGCTGTCTGCTGCTGATGATGATCT 1024

QY 752 TGGCTTCAGAGGCGTCCGCTCTTCTGAGCTCCCGAGAGAAAGATGCAACCTGCGTA 811
 DB 1025 TACAGCTCAGAGTGTCCGATGCTGTGCGGCTTCCAAAGAAAGACAGAACTTGGCCA 1084
 QY 812 GAATCACCAGACTGTGCTCGTGGTGGTGGGAGTCTTGTCTGTCTGAGCTCCATTC 871
 DB 1085 GGATCACCAGGATGTGCTGGTGGTGGTGGGAGTCTTGTCTGTCTGAGCTCCATTC 1144
 QY 872 ACATATTCATCCGTGGAGGCTTGGGAGACCTCCCAACAGACAGCTGCTCTCCCA 931
 DB 1145 ACATCTATGTCATATCAAAAGACATGATCAAGATTCAGAAACCACTTCCAGACTGTT 1204
 QY 932 GCTATTAATCTTGTGATGCGCTTGAAGCTATACCAACAGTACCTGAATCCATTTCTACG 991
 DB 1205 CTTGCACTTCTGATGATGCTTGGGTTACCAAAACAGCTGCTGAACCCAGTTCTTATG 1264
 QY 992 CTTTCTTGATGAAACTTCAAGCGGTGTTCCGGGACTTCTGCTTCCACTGAAGATGA 1051
 DB 1265 CGTTCGTGATGAAGAACTTCAAAAGATGTTTAAAGAGTTCTGATCCCACTTCTCCA 1324
 QY 1052 GGATGAGCGGCAAGCACTAGCAGATCCGAATTAAGTTCAAGTTC 1099
 DB 1325 CAATCGAACAGCAAACTCTGCTGAATCCGTCAAAACACTAGGGAAC 1372

RESULT 76
 US-10-290-748-15
 Sequence 15, Application US/10290748
 Publication No. US20030124672A1
 GENERAL INFORMATION:
 APPLICANT: EVANS, CHRISTOPHER J.
 KEITH, DUANE E.
 TITLE OF INVENTION: OPIOID RECEPTOR GENES
 NUMBER OF SEQUENCES: 25
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORRISON & FOERSTER
 STREET: 2000 PENNSYLVANIA AVENUE, NW, Suite 5500
 CITY: WASHINGTON
 STATE: DC
 COUNTRY: USA
 ZIP: 20006-1888
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/290,748
 FILING DATE: 07-No. US20030124672A1-2002
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/405,271A
 FILING DATE: 14-MAR-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: MURASHIGE, KATE H.
 REGISTRATION NUMBER: 29,959
 REFERENCE/DOCKET NUMBER: 22000-20526.22
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 887-1500
 TELEFAX: (202) 887-0763
 TELEX: 90-4030 MRSNFOERSWSH
 INFORMATION FOR SEQ ID NO: 15:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1981 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 15:
 US-10-290-748-15

Query Match 37.2%; Score 429.2; DB 15; Length 1981;
 Best Local Similarity 65.6%; Pred. No. 1.3e-113;
 Matches 661; Conservative 0; Mismatches 338; Indels 9; Gaps 2;

QY 92 CCGGCTGGGCGAGCCCGACAGCAACGGCAGGCGCGCTCGAGGACGCGCAGCTGGAGC 151
DB 374 CCGAGCCATCGCGCTCTTAACCCGAGCGGCTTGGCGGAGACAGCCTGTGCCCTCACA 433
QY 152 CCGGCGACATCTCCCGGCGCATCCGGTGCATCATCGCGGGTCTACTCCGAGTGTTCG 211
DB 434 CCGGAGCGCTTCCATGTCACAGCAGCATCACCATCATGGCCCTCTATTCTATCGGTGTG 493
QY 212 TCGTGGGCTTGGTGGGCACTCGCTGTCTATGTTGTGATCATCCGATACACAAAGATGA 271
DB 494 TAGTGGGCTCTTGGAAACTTCGTGTCTATGTGATGTGAAGATATACCAAAATGA 553
QY 272 AGACGCAACCAACATTTACATATTTAACTGGCTTTGGCAGATGTTTATGTTACTACA 331
DB 554 AGACGCGCACCAACATTTACATATTTTCACTGTCTGTGGCAATGCTTACAGCAGCTGCA 613
QY 332 CCATGCCCTTTGAGAGTACGCTCTACTTATGAAATTCCTGGCCTTTTGGGAGTGTCTGT 391
DB 614 CGCTGCCCTTTGAGAGTGTAACTACTATCTATGGAACGTCGCCCTTTGGAAACATCCTCT 673
QY 392 GCAAGATAGTAATTTTCATTTGATTACTACACATGTTTACAGCATCTTACCTTGAACCA 451
DB 674 GCAAGATCGTATCTCAATAGACTACTACACATGTTTACAGTATCTTCACTCCTGCA 733
QY 452 TGATGAGCGTGAACCGCTTACTTGGCGGTGCGCACCCCGTGAAGGCTTGGACTTCGCA 511
DB 734 CCATAGAGTGTAGACCGCTTACATTTGCGCTGTGCAACCCCGTCAAGGCGCTGGAATTCG 793
QY 512 CACCTTGAAAGCAAGATCATCAATATCTGCATCGTGTGCTGTCTGATCTGTTGGCA 571
DB 794 CCCCCGAAATGCCAAATTTGTCATGTGTGCAACTGATCCTCTCTTGTGCAATTTGGTC 853
QY 572 TCTCTGCAATAGTCTTGGAGGACCAAAAGTCAGGAGAACGTCGATGATGAGTGTCT 631
DB 854 TGCCCGTATGTTTACATGAGCAACCAAAATACAGGAGGAGTCTC-----CATAGATTTGA 907
QY 632 CTTTGAAGTCTCCCAATGATGATGATCTCTGTGGGACTCTTTCATGAAGATCTGCTCT 691
DB 908 CCTCAGCTTCTCTATCCACATGATGATGATGATGATGATGATGATGATGATGATGAT 964
QY 692 TCATCTTGGCTTGGATCGCTGTCTGATCATGATGATGATGATGATGATGATGATGATG 751
DB 965 TCATCTTGGCTTGGATCGCTGTCTGATCATGATGATGATGATGATGATGATGATGATG 1024
QY 752 TCGCTCTCAAGACGCTCGGCTCTTCTGCTCCGAGAGAAAGATCGCAACTGCGCTA 811
DB 1025 TACAGCTCAAGAGTGTGCGCATGCTGTGGGCTCCAAAGAAAGACAGGAACCTGCGCA 1084
QY 812 GGATCAACAGACTGCTGT 871
DB 1085 GGATCAACCGGAGT 1144
QY 872 ACATATTAATCTGAGGAGGCTCTGGGAGGACCTCCACAGCAGCTGTCTCTCA 931
DB 1145 ACATATTAATCTGAGGAGGCTCTGGGAGGACCTCCACAGCAGCTGTCTCTCA 1204
QY 932 GCTATTAATCTGAGGAGGCTCTGGGAGGACCTCCACAGCAGCTGTCTCTCA 991
DB 1205 CTTGAGGAGGCTCTGGGAGGACCTCCACAGCAGCTGTCTCTCTTATG 1264
QY 992 CTTTCTTGTGATGAAATCTTCAAGCGGCTTTCGGGAGCTTGTGCTTTCATGAAAGATGA 1051
DB 1265 CTTTCTTGTGATGAAATCTTCAAGCGGCTTTCGGGAGCTTGTGCTTTCATGAAAGATGA 1324
QY 1052 GGATGAGGAGGAGAGCACTAGCAGAGTCCGAAATTAAGTTTCAAGATC 1099
DB 1325 CAATGAGAGGAGAGCACTAGCAGAGTCCGAAATTAAGTTTCAAGATC 1372

RESULT 77
US-09-823-114-7
; Sequence 7, Application US/09823114

Patent No. US2002061544A1
GENERAL INFORMATION:
APPLICANT: EVANS, CHRISTOPHER J.
KEITH, DUANE E.
TITLE OF INVENTION: OPIOID RECEPTOR GENES
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FORBSTER
STREET: 2000 PENNSYLVANIA AVENUE, NW, Suite 5500
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/823,114
FILING DATE: 29-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/148,351
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: MORASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 22000-20526.22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030 MRSNFORBWSH
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1829 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 29..1144
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-823-114-7
Query Match 36.6%; Score 422.6; DB 9; Length 1829;
Best Local Similarity 67.1%; Pred. No. 1e-111;
Matches 634; Conservative 0; Mismatches 299; Indels 12; Gaps 2;
QY 93 CCGGCTGGGCGAGCCCGACAGCAACGGCAGGCGCGCTCGAGGACGCGCAGCTGGAGCC 152
DB 91 CCGCTTTCGACGCGCTTCCCGAGCGCGCGCGCAATGCTGTGGGAGTGGCGGAGCCCG 150
QY 153 CCGGCAATCTCCCGGCGCATCCGGTGCATCATCGGCGGTCTACTCGTATGTTGTGT 212
DB 151 TAGTGGGCTTGTGGGCACTGTCTGTATGTTTGGACATCGTCGGGTACACAAATTTGA 210
QY 213 CTTGGGCTTGTGGGCACTCGCTGTGATGTTCTGTATCATCCGATACACAAAGATGA 272
DB 211 AGTGGGCTTGTGGGCACTGTCTGTATGTTTGGACATCGTCGGGTACACAAATTTGA 270
QY 273 GACAGCAACCAATTTACATATTTAACTGGCTTTGGCAGATGCTTTATGTTACTACAAC 332
DB 271 GACCCGCAACCAATTTACATATTTAACTGGCTTTGGCAGATGCTTTATGTTACTACAAC 330
QY 333 CATGCCCTTTCAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 392
DB 331 GCTGCCCTTTCAGAGGCGCAAGTATGATGATGATGATGATGATGATGATGATGATGATG 390
QY 393 CAAGATAGTAATTTTCATTTGATTTACTACACATGTTTACACAGATCTTCACTTGACAT 452
DB 391 CAAGGCTGTGCTCTCATTTGACTACTACACATGTTTACACAGATCTTCACTTGACAT 450


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Db      862 CATCTTCGATCGCTGAGAGCTGTGGACATCAATGGCGCGACCACTTGCTGTGGC 921
Qy      930 CAGCTATTACTTCTGCATCGCTTAGGCTATACCAAGTAGCTGAATCCATTCTCTA 989
Db      922 CGCACTGCACCTGTGCATCTGCGCTGGGCTACCGCAACAGCAGACCTTCAACCCCGTCTCTA 981
Qy      990 CGCCTTCTGTATGAAACTTCAAGCGGCTGTTCCGGGACTCTCTG 1034
Db      982 CGCCTTCTGTAGAGAACTTCAAGCGCTCTTCCGCCAGCTCTG 1026

RESULT 79
US-09-214-904-3
; Sequence 3, Application US/09214904
; Patent No. US20010047519A1
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: TRANSGENIC ANIMAL IN WHICH THE EXPRESSION
; TITLE OF INVENTION: OF OPiate RECEPTORS IS MODIFIED
; NUMBER OF SEQUENCES: 6
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/214,904
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR97/01282
; FILING DATE:
; APPLICATION NUMBER: FR 96.08810
; FILING DATE: 15-JUL-1996
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 58..1173
; US-09-214-904-3

Query Match      36.6%; Score 422.6; DB 9; Length 2218;
Best Local Similarity 67.1%; Pred. No. 1.1e-111;
Matches 634; Conservative 0; Mismatches 299; Indels 12; Gaps 2;

Qy      93 CGGCTGGGCGGAGCCGACAGCAAGCGCGCGCTTGGAGAGCGCGCAGCTGAGGC 152
Db      120 CGCCTTCCCAAGCGCTTCCCAAGCGCGGCGCAATGCTGGGAGTCCCGGAGCCG 179
Qy      153 CGCGCAATCTTCCCGGCGCATCCGGTCAATCAACGGGGCTACTCCGTAGTGTGCT 212
Db      180 TAGTGCCTCTGCTCCCTGCGCTTAGCCATCGCCATCACCGGCTCTACTCGGCTGTGTGGC 239
Qy      213 CGTGGGCTTGTGGGCAACTCGCTGATCATGTTCTGTGATCATCCGATACACAAGATGAA 272
Db      240 AGTGGGGCTTCTGGGCAAGCTGCTGTCAATGTTTGGCATCTGCTCCGATACCAAAATTGAA 299
Qy      273 GACAGCAACCAATTTATCATATTTAACTGAGCTTTGGAGAGTCTTTAGTTACTACAAC 332
Db      300 GACCGCCACAACATCTCATCTTCATCTGCTTTGGCTGATGCGCTGGCCACAGCAGC 359
Qy      333 CATGCCCTTTCAGATAGCTACTTGAATGAAATCCGCTTTTGGGAGATGTCTGTG 392
Db      360 GCTGCTTTCAGAGCGCCAAAGTACTTGAATGAAACGTGGCCGTTTGGAGACTCTGTG 419
Qy      393 CAAGATAGTAAATTTCAATGATTACTACAAATGTTCCAGACATCTTCACTTGACCAT 452
Db      420 CAAGCTGTGCTCTCACTTGAATCAAAATGTTCACTAGATCTTCACTTCACTTCACT 479
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Qy      453 GATGAGCGTGAACCGCTACATTTGCGGTGAGCCAGCCCGGAAAGGCTTTGGAATTCGCGAC 512
Db      480 GATGAGCGTGAACCGCTACATTTGCTGTGCTGATCTGTGCAAGCCCTGGACTTCGAGC 539
Qy      513 ACCCTTGAAGGCAAGATCATCATATATCTGCATCTGCTGTGTGTGATCTTTGGCAT 572
Db      540 ACCAGCCAAAGGCAAGCTGATCAATATATGATCTGGGCTTGGCTTCAAGTGTGGGCT 599
Qy      573 CTGTCAATTAATCTTGAAGGCAACCAAGTCAAGGAAAGCTGATGTCAATGAATGCTC 632
Db      600 CCCCATCATGTGATGAGGAGTGAACCAACCCCGGATGTGTGATGATGATGATGATCA 659
Qy      633 CTGCAATTTCCAGATGATGATCTACTCCGAGGAGACCTTTATGAAGATCTGGGCTT 692
Db      660 GTTCCCAAGTCC-----CAGCTGTGATGGAACACTGTGACCAAGATCTGGGCTT 710
Qy      693 CATCTTTCCTTCTGTGATCCCTGTCTCATCATCATCTGCTGCTACACCTGATGATCTT 752
Db      711 CCTCTTTCCTTCTGTGATCCCTGTCTCATCATCATCTGCTGCTGCTGCTGCTGCTACT 770
Qy      753 GCGTCTCAAGAGCTGCGGCTCTCTTCTGCTCTCCGAGAAAGATCGCACTTGGCTAG 812
Db      771 GCGCTGCGCAGCGTGTGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 830
Qy      813 GATCAACGACTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 872
Db      831 CATCAGCGCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 890
Qy      873 CATATTCATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 929
Db      891 CATCTTTCCTTCTGTGATCCCTGTCTCATCATCATCTGCTGCTGCTGCTGCTGCT 950
Qy      930 CAGCTATTACTTCTGCATCGCTTAGGCTATACCAAGTAGCTGAATCCATTCTCTTA 989
Db      951 CGCACTGCACCTGTGATCTGCGCTGGGCTACGCCAAGCAGAGCTTCAACCCGCTTCTCTA 1010
Qy      990 CGCCTTCTGTATGAAACTTCAAGCGGCTGTTCCGGGACTCTCTG 1034
Db      1011 CGCCTTCTGTAGAGAACTTCAAGCGCTGCTTCCGCCAGCTCTG 1055

RESULT 80
US-10-112-599A-1
; Sequence 1, Application US/10112599A
; Publication No. US20030005476A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Keith D.
; TITLE OF INVENTION: DELTA OPIOID RECEPTOR DISRUPTIONS,
; TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATING THERETO
; FILE REFERENCE: R-678
; CURRENT APPLICATION NUMBER: US/10/112,599A
; CURRENT FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/280,513
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 1
; LENGTH: 2219
; TYPE: DNA
; ORGANISM: Mus musculus
; US-10-112-599A-1

Query Match      36.6%; Score 422.6; DB 15; Length 2219;
Best Local Similarity 67.1%; Pred. No. 1.1e-111;
Matches 634; Conservative 0; Mismatches 299; Indels 12; Gaps 2;

Qy      93 CGGCTGGGCGGAGCCGACAGCAAGCGCGCGCTTGGAGAGCGCGCAGCTGAGGC 152
Db      121 CGCCTTTCCAAGCGCTTCCCAAGCGCGGCGCCAAATGCTGCGGCTGCGCGGAGCCG 180
Qy      153 CGCGCAATCTTCCCGGCGCATCCGGTCAATCAACGGGGTCTACTCCGTAGTGTGCT 212
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Db 181 TAGTGCCTGTCCTCCGCTAGCCATGCGCATCACCGGCTCTACTGAGCTGTGTGCGC 240
Qy 213 CGTGGGCTTGGTGGGCACTGCTGTGATGTCGTGATCATCCGATACACAAATGAA 272
Db 241 AGTGGGGCTTCTGGGCAACGTGCTGTGATGTTTGGCATTCGTCGGTACACAAATGAA 300
Qy 273 GACAGCAACCAACATTTATATTTAACTTGAAGCTTTGGCAGATGTTAGTTACTACAAC 332
Db 301 GACCGCCACCAACATTTATATTTAACTTGAAGCTTTGGCAGATGTTAGTTACTACAAC 360
Qy 333 CATGCCCTTTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 392
Db 361 GCTGCCCTTTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
Qy 393 CAGATATATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 452
Db 421 CAGGCTGTGCTCTCATTTGATGATGATGATGATGATGATGATGATGATGATGATG 480
Qy 453 GATGAGCTGAGCCGCTACATGCGGTGCGACCCCGTGAAGGCTTTGAGCTTTGAGC 512
Db 481 GATGAGCTGAGCCGCTACATGCGGTGCGACCCCGTGAAGGCTTTGAGCTTTGAGC 540
Qy 513 ACCCTTGAAGGCAAGATCATATATATATATATATATATATATATATATATATAT 572
Db 541 ACCAGCCAAAGGCAAGATCATATATATATATATATATATATATATATATATATAT 600
Qy 573 CTCTGCAATATGCTCTTGGAGGACCAAGATCAGGGAAGACCTGATGTCATTTAGTCTC 632
Db 601 CCCCATCATGCTGATGAGGACCAAGATCAGGGAAGACCTGATGTCATTTAGTCTC 660
Qy 633 CTGAGATTTCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 692
Db 661 GTTCCCAAGTC-----CAGCTGTGATGAGGACCTGATGATGATGATGATGATG 711
Qy 693 CATCTTTCCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 752
Db 712 CCTCTTTCCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 771
Qy 753 GCGTCTCAAGAGCGCTGCTCTTCTGAGCTCCGAGAGAAAGTCCGACCTGAGCTG 812
Db 772 GCGCTGCGAGCGCTGCTCTTCTGAGCTCCGAGAGAAAGTCCGAGCTGAGCTG 831
Qy 813 GATCAGCAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 872
Db 832 CATCAGCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 891
Qy 873 CATATTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 929
Db 892 CATCTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 951
Qy 930 CAGCTATTAATTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 989
Db 952 CGCACTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1011
Qy 990 CGCCTTTCCTGATGAAAACTTCAAGCGGTGTTCCGGGACTTCTG 1034
Db 1012 CGCCTTTCCTGATGAAAACTTCAAGCGGTGTTCCGGGACTTCTG 1056

RESULT 81

US-10-435-655-1

; Sequence 1, Application US/10435655

; Publication No. US20040096940A1

; GENERAL INFORMATION:

; APPLICANT: KIEFER, BRIGITTE

; TITLE OF INVENTION: NOVEL POLYPEPTIDES HAVING OPIOID RECEPTOR ACTIVITY,

; FILE REFERENCE: EX92009-US

; CURRENT APPLICATION NUMBER: US/10/435,655

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 2219
; TYPE: DNA
; ORGANISM: Mus sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (59) .. (1174)
US-10-435-655-1
Query Match 36.6%; Score 422.6; DB 17; Length 2219;
Best Local Similarity 67.1%; Pred. No. 1.1e-111;
Matches 634; Conservative 0; Mismatches 299; Indels 12; Gaps 2;
Qy 93 CGGCTGGCCGAGCCGCAACAGCAACGCGAGCCGCTCGGAGGACCGGAGCTGAGCC 152
Db 121 CGCCTTTCGAGGCGCTTCCCAAGCGGGGCGCAAGTCGTCGGGGTTCGCGGAGCCG 180
Qy 153 CGCGCATCTCCCGGCGCATCCGGTTCATCATCGCGGCTTACTTCCGATGTTGT 212
Db 181 TAGTGCCTGTCCTCCGCTAGCCATGCGCATGCGCGCTCTACTCGGCTGTGTGCG 240
Qy 213 CGTGGGCTTGGTGGGCACTGCTGTGATGTCGTGATCATCCGATACACAAATGAA 272
Db 241 AGTGGGGCTTCTGGGCAACGTGCTGTGATGTTTGGCATTCGTCGGTACACAAATGAA 300
Qy 273 GACAGCAACCAACATTTATATTTAACTTGAAGCTTTGGCAGATGTTAGTTACTACAAC 332
Db 301 GACCGCCACCAACATTTATATTTAACTTGAAGCTTTGGCAGATGTTAGTTACTACAAC 360
Qy 333 CATGCCCTTTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 392
Db 361 GCTGCCCTTTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
Qy 393 CAGATATATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 452
Db 421 CAGGCTGTGCTCTCATTTGATGATGATGATGATGATGATGATGATGATGATGATG 480
Qy 453 GATGAGCTGAGCCGCTACATGCGGTGCGACCCCGTGAAGGCTTTGAGCTTTGAGC 512
Db 481 GATGAGCTGAGCCGCTACATGCGGTGCGACCCCGTGAAGGCTTTGAGCTTTGAGC 540
Qy 513 ACCCTTGAAGGCAAGATCATATATATATATATATATATATATATATATATATAT 572
Db 541 ACCAGCCAAAGGCAAGATCATATATATATATATATATATATATATATATATATAT 600
Qy 573 CTCTGCAATATGCTCTTGGAGGACCAAGATCAGGGAAGACCTGATGTCATTTAGTCTC 632
Db 601 CCCCATCATGCTGATGAGGACCAAGATCAGGGAAGACCTGATGTCATTTAGTCTC 660
Qy 633 CTGAGATTTCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 692
Db 661 GTTCCCAAGTC-----CAGCTGTGATGAGGACCTGATGATGATGATGATGATG 711
Qy 693 CATCTTTCCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 752
Db 712 CCTCTTTCCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 771
Qy 753 GCGTCTCAAGAGCGCTGCTCTTCTGAGCTCCGAGAGAAAGTCCGACCTGAGCTG 812
Db 772 GCGCTGCGAGCGCTGCTCTTCTGAGCTCCGAGAGAAAGTCCGAGCTGAGCTG 831
Qy 813 GATCAGCAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 872
Db 832 CATCAGCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 891
Qy 873 CATATTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 929
Db 892 CATCTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 951
Qy 930 CAGCTATTAATTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 989
Db 952 CGCACTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1011
Qy 990 CGCCTTTCCTGATGAAAACTTCAAGCGGTGTTCCGGGACTTCTG 1034

Db 1012 CGCCTTCCTGAGAGAACTCAAGGCTGCTCCGCGACGCTCTG 1056

RESULT 82
US-09-935-061-13

; Sequence 13, Application US/09935061
; Publication No. US20030129649A1
; GENERAL INFORMATION:
; APPLICANT: Kobilka, Brian M.
; APPLICANT: Ghanouni, Pejman
; APPLICANT: Lee, Tae Weon
; TITLE OF INVENTION: Conformational assays to detect binding
; FILE REFERENCE: STAN213
; CURRENT APPLICATION NUMBER: US/09/935,061
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 60/286,250
; PRIOR FILING DATE: 2001-04-24
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 13
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: ' Opioid receptor with TEV site in 2nd
; OTHER INFORMATION: intracellular loop
; NAME/KEY: CDS
; LOCATION: (1)...(1176)
US-09-935-061-13

Query Match 36.0%; Score 415.6; DB 10; Length 1176;
Best Local Similarity 65.1%; Pred. No. 9e-110;
Matches 648; Conservative 0; Mismatches 339; Indels 9; Gaps 2;

92 CCGGCTGGGCGGAGCCGACGACGAGCGCGCTCGGAGAGACCGCGACGTGAGC 151
Db 125 CCGAGCCATCGGCTCGAAGCCGACCGACGAGCTGGGCGGAGAGACGCGCTGCCAA 184
92 CCGGCTGGGCGGAGCCGACGACGAGCGCGCTCGGAGAGACCGCGACGTGAGC 151
125 CCGAGCCATCGGCTCGAAGCCGACCGACGAGCTGGGCGGAGAGACGCGCTGCCAA 184
152 CCGGCGACATCTCCCGGCGCATCCGCTCATCATCAGCGCGCTCTACTCCGAGTGTG 211
Db 185 CCGGAGTCCCTCCATGATCAGCGGCGCATCATGCGCTCTACTCCGAGTGTG 244
212 TCGTGCGCTGTGGGCGCACTCGCTGTCTGTGATCTCCGATACCAAGATGA 271
Db 245 TGGTGGGCTCTTCGAAACCTTCGTGTCATGTATGTGATGTACAGATACCAAGATGA 304
272 AGACGACCAACCACTTATCATATTTAACTGGCTTTGGCAGATGTTAGTACTACA 331
Db 305 AGACGACCAACCACTTATCATATTTAACTGGCTTTGGCAGATGTTAGTACTACA 364
332 CCATGCCCTTTGAGAGTACGCTCTACTGATGAATTTCCGCGCTTTGGGAGTGTGCT 391
Db 365 CCCTGCCCTTCAGAGTGTGATTTACCTTAATGGAAACATGGCATTTGAAACCATCTTT 424
392 GCAAGATGATATTTTCATGATTTAATAACATGTTCAACGATCTTTCACCTTGACCA 451
Db 425 GCAAGATGATGATTTTCATGATTTAATAACATGTTCAACGATCTTTCACCTTGACCA 484
452 TGATAGAGGTGACCGCTCATATTTGGCGGTGTGCAACCCGTGAAGGCTTTGACCTGCGCA 511
Db 485 CCATAGAGTGTGATGATATCATTTGACGCTGTCACCCCTGTCAAGGAAACCTTCACTTCC 544
512 CACCTTGAAGGCAAGATCATCAATATCTGCATCTGGCTGTGTCATCTGTTGCA 571
Db 545 AGGGGCGAAATGCCAAATATCATATGTGTGCACTGATCTCTTTCAGCATTGGTC 604
572 TCTCTGCAATAGTCTCTTGGAGGCGACCAAGTCAAGGAGACGTCGATGCTATGAGTGT 631
Db 605 TTCCTGATATGTTTATAGTACACAAATAATACAGGCAAG-----TTCATATGATTTGA 658

Qy 632 CTTTGACAGTTCACAGATGATGACTACTCCGTGGTGGAGACTCTTTCATGAGATCTGCGTCT 691
Db 659 CACTAACATTTCTCTATCCAACTGTGTAATGGGAAACCTGC---TGAAGATCTGTGTT 715
Qy 692 TCATCTTTGCTCTGTGATTCCTGTCTCATCATCATGTGTGTCTACACCTGATGATTC 751
Db 716 TCATCTTGGCTTCATTTATGACAGTCTATCATATCCGTGTGCTATGAGCATGATGATCT 775
Qy 752 TGGCTCTAAGAGCGCTCCGCGCTCTTCTGTGCTCCGAGAGAAAGATGCAACCTGGCGTA 811
Db 776 TGGCTCTAAGAGTGTCCGATGCTCTGTGCTCCAAAGAAAGAGAGAAATCTTCGAA 835
Qy 812 GGATCAGCAGATGCTGCTGGTGGTGGAGAGTCTTCTGCTGTGAGTCTCCATTC 871
Db 836 GGATCAGCAGATGCTGCTGGTGGTGGAGAGTCTTCTGCTGTGAGTCTCCATTC 895
Qy 872 ACATATTCATCTGTGGAGGCTCTGGGAGACCTCCACAGACAGCTGCTCTCTCA 931
Db 896 ACATTTAGTCAATCTTAAAGCTTGTGTTACATCCAGAACTACGTTCCAGACTGTTT 955
Qy 932 GCTATTTCTTGTGATGCTGCTGCTTAAAGCTTATACCAAGATAGCTGATTCCTTACG 991
Db 956 CTGGCACTTCTGCAATGCTCTTAAAGTTCACAAACAGCTGCTCAACCACTCTTAAAG 1015
Qy 992 CTTTCTGATGAAACTTCAAGCGGTGTTCCGGAATCTTCTTCCACTGAAGATGA 1051
Db 1016 CATTTCTGATGAAACTTCAAGCGGTGTTCCGGAATCTTCTTCCACTGAAGATGA 1075
Qy 1052 GGATGAGCGGCGAGACACTAGCAGATCCGAAATA 1087
Db 1076 ACATTTAGCACAACAACTCCACTGCAATTCGTGCA 1111

RESULT 83
US-10-692-071-13
; Sequence 13, Application US/10692071
; Publication No. US20040157268A1
; GENERAL INFORMATION:
; APPLICANT: Kobilka, Brian K.
; APPLICANT: Ghanouni, Pejman
; APPLICANT: Lee, Tae Weon
; TITLE OF INVENTION: Conformational assays to detect binding
; FILE REFERENCE: STAN-213CIP
; CURRENT APPLICATION NUMBER: US/10/692,071
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: PCT/US02/13250
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 09/935,061
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 60/286,250
; PRIOR FILING DATE: 2001-04-24
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 13
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: ' Opioid receptor with TEV site in 2nd
; OTHER INFORMATION: intracellular loop
; NAME/KEY: CDS
; LOCATION: (1)...(1176)
US-10-692-071-13

Query Match 36.0%; Score 415.6; DB 17; Length 1176;
Best Local Similarity 65.1%; Pred. No. 9e-110;
Matches 648; Conservative 0; Mismatches 339; Indels 9; Gaps 2;

Qy 92 CCGGCTGGGCGGAGCCGACGACGAGCGCGCTCGGAGAGACCGCGACGTGAGC 151
Db 125 CCGAGCCATCGGCTCGAAGCCGACCGACGAGCTGGGCGGAGAGACGCGCTGCCAA 184

QY 152 CCGGCAATCTCCCCGCGATCCGGTCATCATCAGCGGGCTTACTCCGAGTTCG 211
DB 185 CCGGAGTCCCTCCATGATCAAGGCGATCATCATGAGCCCTCTACTCCATCGTGGC 244
QY 212 TCGTGGGCTGGTGGGCAACTCGTGTGATGTTGATCATCCGATACCAAGATGA 271
DB 245 TGGTGGGGCTCTTGGAACTTCCGTGTCATGTATGTATTTGTACAGATACCAAGATGA 304
QY 272 AGACGCAACCAACATTTACATATTTAACTGGCTTTGGAGATGTTAGTTACTACA 331
DB 305 AGACTGCCAACCACTACATTTTCAACTTGTCTGGCAGATGCTTAGCCACCAATA 364
QY 332 CCATGCCCCCTTCAGAGTACGGTCTCTTGAATTTCCGGCTTTGGGGATGTCGT 391
DB 365 CCGTCCCTCTCCAGAGTGAATTAACCTATGGAACATGGCCATTTGGAACATCTTT 424
QY 392 GCAAGATGTAATTTCCATGATTAATACTCAACATGTTCAACGATCTTCACTTGACA 451
DB 425 GCAAGATGATGATCTCCATAGATTACTATTAACATGTTCAACGATATTTCAACCTCTGCA 484
QY 452 TGATGAGGTGAGCCGCTACATTTGCGTGGCCACCCCGTGAAGGCTTTGACCTTCGCA 511
DB 485 CCATGAGTGTGATGATATACATTTGCAAGTCCGACCCCTGTCAAGGAAACCTCTACTTCC 544
QY 512 CACCTTTGAAGGCAAGATCATCATATCTGATCTGGCTGTGTCGTATCTGTTGCA 571
DB 545 AGGGCGAAATGCCAAATTAATCAATGTCATGACCTGATCTCTTCAAGCAATTTGGTC 604
QY 572 TCTCTGCAATAGTCTCTTGGAGGCAACCAAGTCAAGGAAAGACGTGATCATTTAGTGT 631
DB 605 TTCCGTGATGTTTCAATAGTACAAATAACAGGCAAGG-----TTCCATAGATTGTA 658
QY 632 CTTTCAGTTCCTCAATGATGACTACTCTCGTGGGACTCTTCAATGAAGATCTGCT 691
DB 659 CACTAACATTTCTCTATCCACCTGTGTACTGGGAAACCTGC---TGAAGATCTGTGTT 715
QY 692 TCATCTTTGCTCTCGATACCTGTCCTCATCATATGTCGTCATACCCGATGATGCC 751
DB 716 TCATCTTGGCTTTCATATGATGATGCTCATATTAACGTGTGATGAGTGTGATGATCT 775
QY 752 TCGCTCTCAAGAGCTCCGAGCTCTTTCGCTCCGAGAGAAAGATGCAACTGCGTA 811
DB 776 TCGGCTCAAGAGTGTCCGAGCTCTCTGCTCCAAAGAAAGACAGGATCTTCGA 835
QY 812 GGATACCAAGACTGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 871
DB 836 GGATACCAAGAGT 895
QY 872 ACATATTCATCTCGT 931
DB 896 ACATATTCATCTCAATTAAGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 955
QY 932 GCTATTAATCTTCATGCTGCTTGAAGCTATACCAAGATGAGTGTGTGTGTGTGTGTGT 991
DB 956 CTGGGCACTTTCGATGT 1015
QY 992 CTTTCTTGATGAAACTTCAAGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1051
DB 1016 CATTTCTGATGAAACTTCAAGCGATGCTTCAAGAGATGTTCTGTATCCCACTCTTCA 1075
QY 1052 GGATGAGGCGGAGGCACTACAGAGTCCGAATA 1087
DB 1076 ACATTTAGCAACAAACTCCTCACTCGAATTCGTAGA 1111

RESULT 84
US-09-761-962-12
; Sequence 12, Application US/09761962
; Patent No. US20020077285A1
; GENERAL INFORMATION:
; APPLICANT: Memorial Sloan-Kettering Cancer Center
; TITLE OF INVENTION: Identification and Characterization of Multiple Splice

; TITLE OF INVENTION: Variants of Mu-
; TITLE OF INVENTION: Opioid Receptor (MOR-1) Gene
; FILE REFERENCE: 830002-2000.1
; CURRENT APPLICATION NUMBER: US/09/761,962
; PRIOR APPLICATION NUMBER: 2001-01-17
; PRIOR FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 1346
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-761-962-12

Query Match 35.6%; Score 411; DB 9; Length 1346;
Best Local Similarity 65.7%; Pred. No. 2,1e-108;
Matches 663; Conservative 0; Mismatches 335; Indels 11; Gaps 4;
QY 92 CCGGCTGGGCGGAGCCGACAGCAAGGCGCGGCTCGGAGGACGCGAGCTGAGC 151
DB 185 CCGACCATGCGGCTCTTAACCGCAGGGGCTTGGCGGAGCCACAGCTGTGCCCTACGA 244
QY 152 CCGGCAATCTCCCGGCGATCCCGGTATCATACGCGGCTTACTCCGTAAGTTCG 211
DB 245 CCGGAGCCCTTCATAGGTGACAGCATACCATCATGAGCCCTCTATTTCTATGTTGTG 304
QY 212 TCGTGGGCTGGTGGGCAACTCGTGTGATGTTGATGATCATCCGATACCAAGATGA 271
DB 305 TATGGGGCTTTTGGAACTTCTGTGATGATGATGATGATGATGATGATGATGATGATGAT 364
QY 332 AGACGCAACCAACATTTACATATTTAACTGGCTTTGGAGATGTTAGTTACTACA 331
DB 365 AGACTGCCAACCACTACATTTTCAACTTGTCTGTGAGATGCTTGTGCAAGATCTCT 424
QY 425 CCGTCCCTTTCAAGTGTTAATACTGATGAGGAAAGTGGCCCTTTGAAACATCTCT 484
QY 452 TCGTCTCAAGTACGCTTAACTGATGAATCTGCGCTTTTGGGAGTGTCTGT 391
DB 485 CCGTCCCTTTCAAGTGTTAATACTGATGAGGAAAGTGGCCCTTTGAAACATCTCT 484
QY 492 GCAAGATGTAATTTCCATGATTAATACTGATGATGATGATGATGATGATGATGATGAT 451
DB 512 TCGATGAGGTGAGCCGCTACATTTGCGGTGCCACCCCGTGAAGGCTTTGACTTCGCA 544
QY 545 CCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 604
QY 572 CACCTTTGAAGCAAGATCATCAATATCTGATGATGATGATGATGATGATGATGATGAT 571
DB 605 CCCCCGAAATGCCAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 664
QY 632 TCTCTGCAATAGTCTTGTGAGGCAACCAAGTCAAGGAAAGATGATGATGATGATGAT 631
DB 665 TCGCGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 718
QY 692 CTTTCAGTTCCTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 691
DB 719 CCGTCAAGTTCCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 775
QY 752 TCATCTTTGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 751
DB 776 TCATCTTGGCTTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 835
QY 812 TCGCTCAAGAGGCTCCGCTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 811
DB 836 TACGATCAAGAGTGTCCGATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 895
QY 872 GGATACCAAGACTGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 870
DB 896 GGATACCAAGAGT 954
QY 932 CACATATTCATCTGTGTGAGGCTTGTGGGAGCACTTCCACAGCAAGCTGTCTCTCC 930

Db	955	CACATCTATGTCATATATCAAAAGCACTGATTCACGATTTCCAGAAACCACTTTCCAGCTGTT	1014
Qy	931	AGCTATTACTTCTGCATCGCCTTAGGCTATACCAACAGTAGCCTGAATCCGATTTCTCTAC	990
Db	1015	TCCTGGCACTTCTGATGTTGCCTTGGGTTACACAAACACACTGCTGTAACCCAGTTCTTTAT	1074
Qy	991	GCCTTTCTTGATGAAACCTTCAAGCGGTGTTCCGGGACCTTCTGCTTCCACTGAAGATG	1056
Db	1075	GCGTTCTCGATGAAACCTTCAAAACGATGTTTATAGAGATTTCTGCATCCCAACTTCCCTC	1134
Qy	1051	AGGATGAGCGGCGACAGCACTAGCAGATCCGGAATACAGTTCCAGATC	1099
Db	1135	ACAATCGAACAGCAAACTTGCTCTCGATCCGTCAAAACACTGAGGAAC	1183

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RESULT 85
US-10-283-300-12
/ Sequence 12, Application US/10283300
/ Publication No. US20030103972A1
/ GENERAL INFORMATION:
/ APPLICANT: Memorial Sloan-Kettering Cancer Center
/ TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF MULTIPLE SPLICE VARIANTS
/ TITLE OF INVENTION: OF THE MU-OPIOID RECEPTOR GENE
/ FILE REFERENCE: 830002-2000.3
/ CURRENT APPLICATION NUMBER: US/10/283.300
/ CURRENT FILING DATE: 2002-10-29
/ PRIOR APPLICATION NUMBER: 09/761,962
/ PRIOR FILING DATE: 2001-01-17
/ PRIOR APPLICATION NUMBER: 09/743,872
/ PRIOR FILING DATE: 2001-01-16
/ PRIOR APPLICATION NUMBER: PCT/US99/15974
/ PRIOR FILING DATE: 1999-07-15
/ NUMBER OF SEQ ID NOS: 46
/ SOFTWARE: Patentin version 3.0
/ SEQ ID NO 12
/ LENGTH: 1346
/ TYPE: DNA
/ ORGANISM: Mus musculus
US-10-283-300-12

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Query Match	35.6%	Score 411;	DB 157;	Length 1346;
Basic Local Similarity	65.7%;	Pred. No. 2.1e-105;		
Matches 663;	Conservative	0;	Matches 138;	Indels 11; Gaps 4;
QY	CCGGCTGGGGCCGAGCCCGACAGCAACGGCAGCGCGGCTCGGAGGAGCCGCGAGCTGAGGC	151		
Db	185 CCGAACCATGGGGTCTTAACCGCAGCGGGGCTTGGGGGAGCCACAGCTGTGGCCCTCAGA	244		
QY	152 CCGGCGACATCTCCCCGGCCATCCCGGTATCATCAGCGGGTCTACTCCGGTGTTCG	211		
Db	245 CCGGAGGCGCTTCATGGTGTCAAGAGCATCACCATATGAGCCCTCATTTCTATCGTGTG	304		
QY	212 TCGTGGGCTTGGTGGGCAACTCGCTGTGCATGTTGATCATCCGATACCAAAAGATGA	271		
Db	305 TAGTGGGCTCTTTGGAACTTCCGTGTCATGTATGTATTTGAAGATATACAAAATGA	364		
QY	272 AGACAGCAACAACATTATTAATATTAACTGGCGTTTGGCAGAGTCTTTAGTTACTACA	331		
Db	365 AGACTGCCACAACATCTTACATTTTCAACTTGGCTGTGGCAGATCCCTTACGCCATACCA	424		
QY	332 CCATGGCCCTTTCAAGATACGGTCTTACTGTAGTAATTCCTGGCGTTTGGGAGTGGCGT	391		
Db	425 CGCTGCCCTTTCAAGGTGTTAATTAACCTGATGGGAAGTGGCCCTTTGGAAACATCTCT	484		
QY	392 GCAGATAGTAAATTTCAATTGATTACTACCAACATGTTCAACGACATCTTCACTTGACCA	451		
Db	485 GCAAGATCGTATCTCAATAGACTACTACAAACATGTTCAACGATATCTTCAACCTGTCA	544		
QY	452 TGTATAGGTGGACCGGTCATATGGCGGTGGCAACCCGTAAAGGCTTTGACCTTCGCA	511		
Db	545 CCATAGGTATGAACCGGTACATTTGGCGCTGTGCACACCGGTCAAGGCCCTTGATTTTCCTA	604		
QY	512 CACCCTTAAAGCAAAAGATCATCATATCTGCATCTGGCTGTGCTGCATCTGTTTGCA	571		

[illegible]

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RESULT 86
US-10-112-599A-3
; Sequence 3, Application US/10112599A
; Publication No. US20030005476a1
; GENERAL INFORMATION:
; APPLICANT: Allen, Ketch D.
; TITLE OF INVENTION: DELTA OPIOID RECEPTOR DISRUPTIONS,
; TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATING THERETO
; FILE REFERENCE: R-678
; CURRENT APPLICATION NUMBER: US/10/112,599A
; PRIORITY FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/280,513
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: fastseq for windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1773
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-112-599A-3

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Query Match	35.4%	Score 408.6;	DB 15;	Length 1773;
Best Local Similarity	64.7%;	Pred. No. 1.2e-107;		
Matches 644;	Conservative 0;	Indels 339;	Indels 12;	Gaps 2;
QY	44	CCTGCGCCCGGAGGCGCTGCTGCTGCCCCCAACAGCAGGCGCTTGTTTCCGGCTGGGCGG	103	
Db	247	CCTCGCGCGGCGCGAGCTGCAGGCCCGCCGCTTTGCGCAAGCCCTCGAGCCCTTACCTTA	306	
QY	104	AGCCCGAACAGCAAGGCGACGCGCGCGCTTGGAGGACGCGCACTGTGAGCGCGGCACATCT	163	
Db	307	GCGGCTTTCCTCCAGGCGTGGCGCCATAGTGTGGGAGCGCCAGGACCGGAGAGCGCTCTGT	366	

OY	164	CCCGGCGCATCCGGGATCATCAAGGAGGATCTACTCCGATGGTTGTCGTGAGGCGTTGG	223
Db	367	CCCTGGCCCTGGCAATGCCATACCGGCGCTTACTCGGCGGTGCGCGTGGGCGTGC	426
OY	224	TGGGCAACTCGGTGTCATGTTCTGTGATCATCCGATACCAAGATGAGACGACACCA	283
Db	427	TGGGCAACGTTGTTGCATGTTTCGGCATGTCGCGGTACCTAAGATGAGAGCGGCACCA	486
OY	284	ACATTTACATATTTAACCTGGCTTTGGCAGATGCTTTAGTTACTAACACATGCGCTTTC	343
Db	487	ACATTTACATCTTCAACCTGGCGTTTACCGATGCGGTGCGCACACACAGCTGCGCTTTC	546
OY	344	AGAGTAGCGTCTACTTGTGATGAATTCCTCGGCGTTTGGGATGAGTGCCTGCAGATAGTAA	403
Db	547	AGAGTGCCAAAGTACCTGATGAGAGAGTGCGCCCTTGGGAGAGCGTCTCTGAAGGCGTGC	606
OY	404	TTTCCATTTGATTACTACCAACATGTTTCAACGACATCTTCACTTGAACATGATGAGCGTGG	463
Db	607	TCTTCATGACACTACATACATATGTTTCAACGAGATCTTCAACGCTCACACATGATGAGTGTG	666
OY	464	ACCGTCACTTGCCTGGTGGCCACCCCGTGAAGGCTTTGAGACTTTCGGCACACCGCTTGAAG	523
Db	667	ACCGTCACTGCTGCTGTGCGACCGCTGTGAAGGCGCTTGAAGCTTTCGGACGCGCTGCCAAG	726
OY	524	CAAGATCATCAATATCTGCATCTGAGCTGTGCTGTCATCTGTGTGGCATCTGTCAATAG	583
Db	727	CCAAGCTATCAACATCTGATCTGGGTCCTGAGCGCTCAAGCGTGTGGCGTGCATCATGG	786
OY	584	TCCTTGAGAGGACCAAGTCAGGGAGAACGTGATGTCTATGAGTCTCCTTGAGATTCC	643
Db	787	TCATGCGTGTGACCGGTCGCCGAGACGGTGCAGTGTGTCATGCTCAAGTTCGCCAGCTC	846
OY	644	CAGATGATGACTACTCTGTGAGGACCTTTATGAGAACTGCGCTTCATCTTGTGCGCT	703
Db	847	C-----CAGCTGATACGTGGGACAGGTGACCAAGATCTGCGTTCCTTTCGCGCT	897
OY	704	TCGTGATCCCTGTCTCTCATCATCATGCTGTGCTTACACCTGTATGATCTGCGCTTCAGA	763
Db	898	TCGTGATGCCCATCTCTCATCAACCGTGTGCTATGCGCTTCAATGCTGCGCGCCTGCGCA	957
OY	764	GCGTCCGCGCTCCTTTCTGGCTCCCGAGAGAAAGATGCAACCTGGGTAGATACACAGAC	823
Db	958	GTTGCGCGCTGCTGTGCGGCTTCAAGAGAGAGAACCGACGCTGCGGCGCATACGCGCA	101
OY	824	TGTTCTGTGTGTGTGTGTCAGTCTTTCGTGTGCTGTGCACTCCATTCAATATTCATCC	883
Db	1018	TGTTGCTGTGTGTGTGTGTGGCGGCTTTCGTGTGTGTGTGTGGCGGCCCATTCACATCTTCGTCA	107
OY	884	TGTGTGAGGCGCTGTGGGAGCACTCC---CAAGACAAGTGTCTCTTCCAGCTATTAAT	940
Db	1078	TCGTGTGACGCTGTGTGACATTCGACCGGCGGACCGCTGTGTGTGTGTGCGCTGCAC	113
OY	941	TCTGCATGCGCTTAGGCTATACCAACAGTAGCGCTGAATCCATTCTTACGCGCTTTCCTTG	1000
Db	1138	TGTGCATGCGCGCTGTGGCTTACCGCAATAGAGAGCTTCAACCGCGTGTCTTACGCTTTCCTGG	119
OY	1001	ATGAAACTTCAAGCGGTGTTCCTCGGAGCTTCTGC	1035
Db	1198	ACGAGAACTTCAAGCGGTGTTCCTCGGAGCTTCTGC	1232

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; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 107
; LENGTH: 1773
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-225-567A-107

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Db 134 CCTCGCCCTGGCAATCCGCATCACCGGCTTACTCGGCGGTGCGCGGTGGGCTGC 193
Qy 224 TGGGAACCTCGGTGATGTTGATGATCGGATACCAAGATGAGACAGCAACA 283
Db 194 TGGGCAAGGTGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 253
Qy 284 ACATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 343
Db 254 ACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 313
Qy 344 AGAGTACGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 403
Db 314 AGAGTACGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 373
Qy 404 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 463
Db 374 TCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 433
Qy 464 ACCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 523
Db 434 ACCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 493
Qy 524 CAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 583
Db 494 CAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 553
Qy 584 TCGTGGAGGACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 643
Db 554 TCGTGGAGGACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 613
Qy 644 CAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 703
Db 614 C-----CAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 664
Qy 704 TCGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 763
Db 665 TCGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 724
Qy 764 GCGTCCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 823
Db 725 GCGTCCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 784
Qy 824 TCGTCCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 883
Db 785 TCGTCCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 844
Qy 884 TCGTCCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 940
Db 845 TCGTCCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 904
Qy 941 TCGTCCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1000
Db 905 TCGTCCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 964
Qy 1001 ATGAAATCTCAAGCGGTGTTCCGGGACTTCTGC 1035
Db 965 ACGAAGACTTCAAGCGGTGTTCCGGGACTTCTGC 999

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RESULT 90
US-09-935-061-15
; Sequence 15, Application US/09935061
; Publication No. US20030129649A1
; GENERAL INFORMATION:
; APPLICANT: Kobilka, Brian M.
; APPLICANT: Ghanouni, Pejman
; APPLICANT: Lee, Tae Weon
; TITLE OF INVENTION: Conformational assays to detect binding
; TITLE OF INVENTION: to G protein-coupled receptors
; FILE REFERENCE: STAN213
; CURRENT APPLICATION NUMBER: US/09/935,061
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 60/286,250

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; PRIOR FILING DATE: 2001-04-24
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 1197
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: ' Opioid receptor with TRV site in 3rd
; OTHER INFORMATION: Intracellular loop
; NAME/KEY: CDS
; LOCATION: (1) ... (1197)
US-09-935-061-15

Query Match 34.9%; Score 402.2; DB 10; Length 1197;
Best Local Similarity 64.8%; Pred. No. 7e-106;
Matches 659; Conservative 0; Mismatches 38; Indels 30; Gaps 3;

Qy 92 CCGGCTGGGCGGAGCCGACAGCAAGGACGCGGCTCGAGAGACGCGAGCTGAGC 151
Db 125 CCGAACCATGCGGTCCGAACCGCACCGACTGGGCGGAGAGACGCTGCTCCAA 184
Qy 152 CCGGCAATCTCCCGGCAATCCCGATCATCAAGCGGTCTACTCGGTAGTTGG 211
Db 185 CCGGCAATCTCCCGATCATCAAGCGGTCTACTCGGTAGTTGG 244
Qy 212 TCGTGGGCTGGTGGGCACTCGCTGATGATGATGATGATGATGATGATGATGAT 271
Db 245 TGGTGGGCTGGTGGGCACTCGCTGATGATGATGATGATGATGATGATGATGAT 304
Qy 272 AGACAGCAACCAATTTATGATTTAACTGGCTTGGGAGATGATGATGATGATGAT 331
Db 305 AGATGCGCACCAATCTGATTTTAACTGGCTTGGGAGATGATGATGATGATGAT 364
Qy 332 CCAATGCTTTCAGAGTACGCTGATGATGATGATGATGATGATGATGATGAT 391
Db 365 CCGTCCCTTTCAGAGTACGCTGATGATGATGATGATGATGATGATGATGAT 424
Qy 392 GCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 451
Db 425 GCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 484
Qy 452 TGATGAGGTGAGCCGCTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 511
Db 485 CCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 544
Qy 512 CACCTTGAAGCAAGATCATCAATGATGATGATGATGATGATGATGATGATGAT 571
Db 545 CTCGCCCAATGCAAAATTTCAATGATGATGATGATGATGATGATGATGATGAT 604
Qy 572 TCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 631
Db 605 TTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 658
Qy 632 CCTGCAAGTCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 691
Db 659 CACTAATTTCTCTATCCCACTGATGATGATGATGATGATGATGATGATGATGAT 715
Qy 752 TCGCTTCAAGAGGTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 797
Db 776 TGGCTTCAAGAGGTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 835
Qy 798 -----TCGCAACTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 850
Db 836 TCGAGGGAGGAATCTTGAAGATCACAGATGATGATGATGATGATGATGATGATGAT 895
Qy 851 TCGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 910

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Db	896	TCGTCTGTGAGACTCCCATTCACATTTAGTCATCTATTAAAGCTTGTTAGACATCCAG	955
Qy	911	ACAGCAGACGTGCTCTCTCCAGCTATTACTTTCGATCGCCTTAGGCTATTACCAACAGTA	970
Db	956	AAACTACGTTCCAGACGTGTTCTTGGCACTTCGTGACTTGCTGTAGGTTACAAACAGCT	1011
Qy	971	GCCTGAATCCCATTTCTCTACGCTTTCTTGATGAAACTTCAAGCGGTGTTTCCGGAGCT	1033
Db	1016	GCCTCAACCCCACTCCCTTATGATTTCTGATGAAAACTTCAACGATCTTCACAGAGCT	1077
Qy	1031	TCGTCTTCCACTGAAGATGAGAGTAGAGCGGCAGACACTAGCAGAGTCCGAATA	1087
Db	1076	TCGTGATCCCAACCTCTTCCACATTGAGCAACAAATCTCCACTGGAATTCGTGAG	1132

```

RESULT 91
US-10-692-071-15
? Sequence 15, Application US/10692071
? Publication No. US20040157268A1
? GENERAL INFORMATION:
? APPLICANT: Koblika, Brian K.
? APPLICANT: Ghannoui, Pejman
? APPLICANT: Lee, Tae Weon
? TITLE OF INVENTION: Conformational assays to detect binding
? TITLE OF INVENTION: to membrane spanning, signal-transducing proteins
? FILE REFERENCE: STAN-213CIP
? CURRENT APPLICATION NUMBER: US/10/692,071
? CURRENT FILING DATE: 2003-10-22
? PRIOR APPLICATION NUMBER: PCT/US02/13250
? PRIOR FILING DATE: 2002-04-24
? PRIOR APPLICATION NUMBER: 09/935,061
? PRIOR FILING DATE: 2001-08-21
? PRIOR APPLICATION NUMBER: 60/286,250
? PRIOR FILING DATE: 2001-04-24
? NUMBER OF SEQ ID NOS: 22
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 15
? LENGTH: 1197
? TYPE: DNA
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: ' Opioid receptor with TEV site in 3rd
? OTHER INFORMATION: intracellular loop
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (1) ... (1197)
? US-10-692-071-15

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Query Match	34.9%	Score 402.2	DB 17	Length 1197
Best Local Similarity	64.8%	Pred. No.76-106		
Matches	659	Conservative	0	MisMatches 328; Indels 30; Gaps 3
Qy	92	CCGGCTGGGGCCGAGGCCGACAGCAACGGCAGCGCCGCTCGAGAGACGGCAGCTGGAGC	151	
Db	125	CCGACCCATGCGGCTCCGAACGGCACCGACTGGGGGGAGAGACAGCTGTGCTCCCA	184	
Qy	152	CCGGCGACATCTCCCCGGCCATCCGGTCATCATCACGCGGGTCTACTCCGTAAGTTTCG	211	
Db	185	CCGGCAGTCCCTCCATGATCAAGCGGCATCAGCATATGGCCCTTACTCATCTCATCGTGTGG	244	
Qy	212	TCGTGGGCTTGTTGGGCACTCGCTGTCATGTTGTTGATCATCCGATACACAAAGATGA	271	
Db	245	TGTTGGGGCTCTTCGGAACCTTCCTGGTCATGTAATGTGATCGATCACCAAGATGA	304	
Qy	272	AGACGACCAACCAATTTACATATTAACTGGCTTTGGCAATGTTTAGTTACTACA	331	
Db	305	AGACTGCCAACCAACTTACATTTTCAACTTTCCTGGCAATGCTTAAGCACACAGTA	364	
Qy	332	CCATGCCCTTTAGAGTAGCGGTCTACTTGATGAATTTCCGTGGGCTTTTGGGAGATGTCGT	391	
Db	365	CCCTGCCCTTCCAGAGTGTGAATTAACCTAATGGGAACATGGCCATTTTGGAACACATCTTT	424	
Qy	392	GCAAGTAGTATTTTCCATGTGATTACTACACATGTTCCACGACTCTTCACCTTGACCA	451	

Db	425	GCAGATGATGATCTCCATAGATTAATTAACATGTTCCACGACATATTCACTTCTCGCA	484
OY	452	TGATAGCGGTGACCCGCTACATATGGCGTGTGACACCCTCGAAGCTTTGSACTTCCGCA	511
Db	485	CCATGAGTGTGATGATACATATGGACGTCTGCACTCTGTCAAGGCTTATGATTTCCGTA	544
OY	512	CACCTTGAAGGCAAAAGATCATCAATATCTGCATCTGGCTGCTGTCTCATCTGTGGCA	571
Db	545	CTCCCCGAAATGCCCCAAATTAATTCATATGCTGCAACGTGATCCCTCTTACGCACTTGGTC	604
OY	572	TCTCGCAATATGCTCTTGGAGGCAACAAGTCAGGGGAAACGTCGATGTCAATTGAGTGTCT	631
Db	605	TTCCGTATGTTCAATAGCTACACAACAAATATACAGGAA-----GGTTCATATGATTTGA	658
OY	632	CTTGGACATTTCCACAGATGATGACTACTCCGTGTGGAGCCTCTTTCATGAAGATCTGGCTCT	691
Db	659	CACATACATTTCTCTCATCCAAACCTGTGTACTGGGAAACCTGTCT---GAAGATCTGTGTTT	715
OY	692	TCATCTTTGCTTGTGTGATCCCTGTCTCTCATCATCATGTCTGTCTACACCTGTATGATCC	751
Db	716	TCATCTTGTGCTTCAATTATATGACAGTGTCTCATATTACCTGTGTCTATATGACATGATATCT	775
OY	752	TGGCTCTCAAGAGGCTCCGGGCTCCTTTGCGGCTCCCGAGAGAAGA-----797	
Db	776	TGGCTCTCAAGAGTGTCCGACATGCTCTCTGGCTCTCCAAAGAAAAGACGAAACCTTACT	835
OY	798	-----TCGCAACCTGTGTAGGATCACCAGACTGGTCTGTGTGTGTGTGGCAGTCTTG	850
Db	836	TCCAGGGGAGGAACTTTCGAAGGATCACAGAGATGGTGTGGTGGTGTGGCTGTGTCTCA	895
OY	851	TCGTCTGTGTGACTTCCCATATTCATATTCATCTCTGTGTGAAGCTCTGGGGAGCACTTCCC	910
Db	896	TCGTCTGTGTGACTTCCCATTCACATTTACGTATCATATTAACCTTTGTATCAATCCAG	955
OY	911	ACAGACAGCTGTCTCTCCAGCTATTACTTCTGTGATGCGCTTAAAGCTATACCAACAGTA	970
Db	956	AAACTAGCTTCCAGACTGTCTTCTTGGCACTTTCGATTTGCTTAGTTACACAAAGCT	101
OY	971	GCTGGAATCCCATTTCTACGCTTTCTTGATGATAAACTTCAAGCGGTGTTTCCGGGACT	1033
Db	1016	GCTTCAACCGAGTCTTTATGATTTCTTGATGATAAACTTCAAGCGGTGTTTCCGGGACT	107
OY	1031	TCTGCTTTTCCACTGAAGATGAGAGTGAAGCGGCAAGACATGACAGATGCCCAATA	1087
Db	1076	TCTGTATCCCAACTCTTCCCAACTTGAAGCAAAACCTCCACTGCAATTTGTGCAGA	1132

```

RESULT 92
US-10-435-655-3
; Sequence 3, Application US/10435655
; Publication No. US20040096940A1
; GENERAL INFORMATION:
; APPLICANT: KIEFER, BRIGITTE
; TITLE OF INVENTION: NOVEL POLYPEPTIDES HAVING OPIOID RECEPTOR ACTIVITY,
; TITLE OF INVENTION: NUCLEIC ACIDS CODING THEREFOR AND USES THEREOF
; FILE REFERENCE: EX92009-US
; CURRENT APPLICATION NUMBER: US/10/435,655
; CURRENT FILING DATE: 2003-05-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; LENGTH: 998
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(996)
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (922)
; OTHER INFORMATION: a, t, c, g, other or unknown
; FEATURE:

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NAME/KEY: modified_base
LOCATION: (927)
OTHER INFORMATION: a, t, c, g, other or unknown
FEATURE:
NAME/KEY: modified_base
LOCATION: (931)..(932)
OTHER INFORMATION: a, t, c, g, other or unknown
US-10-435-655-3

Query Match 34.6%; Score 399; DB 17; Length 998;
Best Local Similarity 67.8%; Pred. No. 5.4e-105;
Matches 593; Conservative 0; Mismatches 270; Indels 12; Gaps 2;

163 TCCCGGCGATCCCGGATCATCATACGCGGCTCTACTCCGATGCTGCTGGGGCTG 222
13 TCCCGGCGGCTGGCAATGCGCATACCGGCTCTACTCGCCGTGTGGCGGCTGGCTG 72
223 GTGGGCAATCGCGTGTGATGTTCCGTGATCATCCGATACCAAAAGATGAGACCAACC 282
73 CTGGGCAACGTGCTGTATGTTCGTGGCATGCTCGGATACCTAAGATGAGACCAACC 132
283 AACATTACATTTTAACTGCTTTGGCAATGCTTTAGTTACTTAAACCAATGCTCTTT 342
133 AAGATCTACATCTTCAACCTGGCTTAGCGGATGCGTGGCCACGACGACGCTGCTTC 192
343 CAGAGTACGCTCTATTGATGATGATTCGCGCTTTTGGGAGATGCTGACATGATTA 402
193 CAGAGTACGCTCTATTGATGATGATTCGCGCTTTTGGGAGATGCTGACATGATTA 252
403 ATTTCATTGATTTATACACATGTTTCAACGACATCTTCACTTGACCATGATGACGTG 462
253 CTCTCATCTGATCTATACATATGTTTCAACGACATCTTCACTTGACCATGATGATG 312
463 GACCGCTACATTCGCGTGTGCAACCCGCTGAAAGCTTTGAGTTCGCAACCTTTGAG 522
313 GACCGCTACATTCGCGTGTGCAACCCGCTGAAAGCTTTGAGTTCGCAACCTTTGAG 372
523 GCAAGATCATCATATCTGATCTGCGCTGCTGCTGATCTGTTGGGATCTGTCATTA 582
373 GCAAGATCATCATATCTGATCTGCGCTGCTGCTGATCTGTTGGGATCTGTCATTA 432
583 GTCTTGGAGGACCAAAAGTACGAGGAGACGTGATGATGATGATGCTCTTGGAGTTC 642
433 GTCTTGGAGGACCAAAAGTACGAGGAGACGTGATGATGATGATGCTCTTGGAGTTC 492
643 CCAGATGATGATCTCTGCTGCTGCTCTTCAATGAAAGTCTGCTTCACTTTGCTG 702
493 CC-----CAGCTGTGACTGGGACACGCTGACCAAGATCTGCTGCTCTTCCGCC 543
703 TTCTGATCCGCTGCTGATCATCATCTGCTGCTGCTGATCCTGATGATCTGCTGCTG 762
544 TTCTGATCCGCTGCTGATCATCATCTGCTGCTGCTGATCCTGATGATCTGCTGCTG 603
763 AGCGTCCGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 822
604 AGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 663
823 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 882
664 ATGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 723
883 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 939
724 ATCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 783
940 TTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 999
784 CTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 843
1000 GATGAAATCTTCAACGCTGCTTTCGCGGACCTTTCTG 1034
844 GACGAGACTTCAAGCGCTGCTTCCGCGAGCTCTG 878

RESULT 93

US-09-905-186A-9

Sequence 9, Application US/09905186A
Publication No. US2003008289A1
GENERAL INFORMATION:
APPLICANT: laForce, Karl Steven
TITLE OF INVENTION: Alleles of the Human Orphanin
TITLE OF INVENTION: FQ/No. US2003008289A1Orphanin Receptor Gene, Diagnostic Methods
FILE REFERENCE: 600-1-284N
CURRENT APPLICATION NUMBER: US/09/905.186A
PRIOR FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/218,205
PRIOR FILING DATE: 2000-07-14
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9
LENGTH: 1829
TYPE: DNA
ORGANISM: homo sapiens
US-09-905-186A-9

Query Match 34.2%; Score 395; DB 10; Length 1829;
Best Local Similarity 65.2%; Pred. No. 1.1e-103;
Matches 616; Conservative 0; Mismatches 320; Indels 9; Gaps 2;

153 GCGGCAATCTCCCGGCGATCCCGGCTCATCATCAGCGGCTCTACTCCGATGCTTCGT 212
162 GCGCTTCTGCGCCCTCGGGCTCAAGTCAACCATGCTGGGGCTTACTCGGCGGTGTGT 221
213 CTGGGCTTGGTGGGCACTCGCTGCTCATGTTGTGATCATCCGATACCAAAAGTAA 272
222 CGAGGGCTCTCTGGGAACTGCTCTGATGATGATGATGATGATGATGATGATGATG 281
273 GACAGCAACCAATTTATCATATTTAACTGCTGCTTGGGAGATCTTTAGTTACTTAAAC 332
282 GACAGCAACCAATTTATCATATTTAACTGCTGCTTGGGAGATCTTTAGTTACTTAAAC 341
333 CATGCCCTTGAAGTACGCTCTACTGATGATGATGATGATGATGATGATGATGATG 392
342 GCTGCCCTTCAAGGACAGGACATCTCTGCGCTTCTGCGCTTGGGATGCGCTGTG 401
393 CAAGTATGATTTTCAATGATTTTCAATGATTTTCAATGATTTTCAATGATTTTCAATG 452
402 CAAGTATGATTTTCAATGATTTTCAATGATTTTCAATGATTTTCAATGATTTTCAATG 461
453 GATGAGCGTGAACGCTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 512
462 CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 521
513 ACCCTTGAAGCAAAAGTATCATATTTCTGATCTGCTGCTGCTGCTGCTGCTGCTG 572
522 GTCCAGCAAAACCGAGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 581
573 CTCTGCAATGATCTTGGAGGACCAAAAGTCAAGGAAAGTCAAGTCAATGATGATGCTC 632
582 TCCCGTTCATCATGAGGCTGCGACAGTCT-----GAGATTAAGAGATGAGTGTCT 635
633 CTTCAGATTTCCCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 692
636 GGTGAGATCTCTTACCCCTCAGATTAC---TGGGGCCCGGTGTTTGGCATCTGATCTT 692
693 CATCTTGGCTTCTGATATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 752
693 CCTCTTCTCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 752
753 GCTGCTCAAGAGCTCGGGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 812
753 GCGGCTCGGTGATTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 812
813 GATCACCAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 872

CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 PENNSYLVANIA AVENUE, NW, Suite 5500
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/290,748
FILING DATE: 07-Mar-2002
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/405,271A
FILING DATE: 14-Mar-1995
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 22000-20526.22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 1805 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 10..1119
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-290-748-18

Query Match 34.1%; Score 393.4; DB 15; Length 1805;
Best Local Similarity 65.1%; Pred. No. 3.1e-103;
Matches 615; Conservative 0; Mismatches 321; Indels 9; Gaps 2;

QY 153 CGCGCAATCTCCCGGCGATCCCGGTGATCATCAGCGGGGTCTACTCCGTAAGTTCGT 212
DB 138 CGCTTCTGCGCCCTCGGGCTCAAGGTACATCTGGGGCTCTACCTGGCCGTGTGT 197
QY 213 CGTGGCTTGTGGCACTCGCTGTCATGTTCTGTATCATCCGATACACAAAGATGA 272
DB 198 CGAGGGCTCTCGGGGAAGTGGCTTGTATGATGATCTGCTGAGGACACCAAAATGAA 257
QY 273 GACGCAACCAACATTTACATTTTAACTGGCTTGGCAATGTTTAACTTAACTAAC 332
DB 258 GACAGCCACCAATATTTACATCTTTAACTGGCCCTGCGACACTCTGCTGCTGAC 317
QY 333 CATGCCCTTTCAGAGTACGCTTACTTATGATGAATTCCTGGCCTTTTGGGAATGTGCTGT 392
DB 318 GCTGCCCTTTCAGAGGACGAGATCTCTGAGCTTCTGGCCGTTTGGAAATGCGCTGTG 377
QY 393 CAAGATGTAATTTTCATGATTTACTACAAAGTTCACAGCATCTTACCTTGACCAT 452
DB 378 CAAGACATGATTCGATTTACTACTACAACTGTTACAGCACTTACACCTTAATGAC 437
QY 453 GATAGCGTGAACCGCTACATTCGCGTGTGCAACCCCGTGAAGGTTTGGACTTCCGAC 512
DB 438 CATAGTGTGATGCTGTATGTAGCCATCTGCACCCCATCCGTGCTCGACGCTCCGAC 497
QY 513 ACCCTGAAGCAAGATCATCATATATCTGCATCTGGCTGCTGTGCTGATCTGTTGGCAT 572
DB 498 GTCCAGCAAGCCCAAGGCTGTCAATGTGCGCATCTGGGCCCTTGTGTTCGGTGT 557
QY 573 CTCTGCAATAGTCTTGGAGGCAACCAAGTCAAGGAAAGCTGATGTCTTGAAGTGTCT 632

DB 558 TCCCGTTCATCATGAGGCTCGGACAGGTC-----GAGATGAAGATCGATGCTCT 611
QY 633 CTTCGATTTCCCAATGATGACTACTCTGTGTGGACCTCTTCAATGAAGATCTGTCTT 692
DB 612 GGTGAGATCTCCCTACCCCTCAGATTAAC---TGGGGCCCGGTGTTTGGCATCTGCATCTT 668
QY 693 CATCTTGGCTTCGNGATCCCTGTCATCATCATGCTGTGTACACCTGATGATCTCT 752
DB 669 CTCTTCTCTTCAATGCTCCCGTGTCTGTATCTGTCTGTCTACAGCTTCAATGATCCG 728
QY 753 GCGTCTCAAGACGCTCGGCTCTCTTCTGCTCCGAGAGAAGATGCAACTGCGTAG 812
DB 729 GCGGCTCGGTGAAGTCCGCTGTCTCTGCGGCTCCGAGAGAAGACCGGAACCTGCGCG 788
QY 813 GATACCAAGATGCTCTGT 872
DB 789 CATCACTCGGT 848
QY 873 CATATTCATCTGT 932
DB 849 GGTCTTGT 908
QY 933 CTATTAATCTTGTATGCTGT 992
DB 909 TCTGCGCTTGTGACAGGCTGT 968
QY 993 CTCTTGTATGTAATTAATTTCAAGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1052
DB 969 CTCTCTGATGTAAGATTTCAAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1028
QY 1053 GATGAGGCGGAGAGCACTAGACAGATCCGAAATACATTCAGGA 1097
DB 1029 CCGGAGCTGTGAGT 1073

RESULT 96
US-09-905-186A-10
Sequence 10, Application US/09905186A
Publication No. US2003008289A1
GENERAL INFORMATION:
APPLICANT: Kretek, Mary Jeanne
INVENTOR: LaForge, Karl Steven
TITLE OF INVENTION: Alleles of the Human Orphanin
TITLE OF INVENTION: Alleles, and Methods of Treatment Based Thereon
FILE REFERENCE: 600-1-284N
CURRENT FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/218,205
PRIOR FILING DATE: 2000-07-14
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PasteSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 1829
TYPE: DNA
ORGANISM: homo sapiens
US-09-905-186A-10

Query Match 34.1%; Score 393.4; DB 10; Length 1829;
Best Local Similarity 65.1%; Pred. No. 3.1e-103;
Matches 615; Conservative 0; Mismatches 321; Indels 9; Gaps 2;

QY 153 CGCGCAATCTCCCGGCGATCCCGGTGATCATCAGCGGGGTCTACTCCGTAAGTTCGT 212
DB 162 CGCTTCTGCGCCCTCGGGCTCAAGGTACCATGTGGGCTCTACTGCGCTGTGTGT 221
QY 213 CGTGGCTTGTGGCACTCGCTGTCATGTTCTGTATCATCCGATACCAAAAGATGA 272
DB 222 CGAGGGCTCTCGGGGAAGTGTCTGTGATGATGATCTGACGACACCAAAATGAA 281
QY 273 GACGCAACCAACATTTACATTTTAACTGGCTTGGCAATGCTTTTAACTTAACTAAC 332
DB 282 GACAGCCACCAATATTTACATTTTAACTGGCCCTGCGGACACTCTGCTGTGAC 341

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OY      333 CATGCCCTTTGAGAGTAGCGTCTACTTGATGTAAATTCCNAGCCTTTGGGGATGTGTGTG   392
Db      342 GCTGCCCTTCACAGGGCACAGACATCTCTCGGGCTTTCTGACCCTTTGGGAATGCGCTGTG   401
OY      393 CAGAATAGTAATTTCCATTTGATTTACTAACAACATGTTCAACAGCATCTTGACCTTGACCAT   452
Db      402 CAAGACAGCATTTGCCTATTGACTACTACAAACATGTTTACACAGCATCTTGACCTTAATGCG   461
OY      453 GATGAGCGTGAACCGCTACATTGCGGTGTGCCAACCCCGTGAAGACTTTGAACTTCCGANC   512
Db      462 CATGAGTGTGATTCGCTATGTAGTACCCTATCTGCACACCCCATCCGNGCCCTCGACGTCCGAC   521
OY      513 ACCCTTGAAGGCAAAAGATCATCATTTCTGCAATCTGGCTGTGTGTCTCATCTGTTGGCAT   572
Db      522 GTCCAGCAAAGCCACAGGCTGTCAATGTGGCCATCTGGGGCCCTGGCCCTCTGTGTGTCCGTGT   581
OY      573 CTCTGCATAATGCTCTTTGAGAGCACCAAAATGCAAGGGAAGAGTGTGATGTATTGAGTGTG   632
Db      582 TCCCGTGTGCATCATGTGGGCTCGGACAGGTTC-----GAGAATGAAGAATGTAGAGTCT   635
OY      633 CTTCGAGTTCCCAAGATGATGACTACTCTCTGTGGGAGCTCTTCATGAAGATCTGCGCTTT   692
Db      636 GGATGAGATCCCTTACCCCCTCAGGAATTAC---TGGGGCCCGGTGTGTTGCCATCTGCATCTT   692
OY      693 CATCTTGGCTTCGTGATTCCTGTCTCTCATCATCATTCGTCTGTCTACACCTGTATGATCTT   752
Db      693 CCTCTTCTCTTCATGTGTCTCCGATGCTGTGTGTCTGTGTCTGTCTGTACAGCTTCATGATGTGG   752
OY      753 GCGTCTCAAGACGTCCTCGGCTCTCTTCTGTGGCTCTCCGAGAAAGATCGCAACCTGCGTAG   812
Db      753 GCGGCTCGGTGAAGTCCGCTGCTCTCTCGGGCTCTCCGAGAAAGAACCGGAACCTGCGGAG   812
OY      813 GATCACCAAGACTGTCTGTGTGTGTGTGGCACTCTTGTGTGTGTGTGTGATCTCCATTCA   872
Db      813 CATCACTCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT   872
OY      873 CATATTCAATCCGTGGTGAAGGCTCTGGGGAGCAACCTCCACACAGCATGCTCTCTCCAG   932
Db      873 GGTCTTTCGTGTGGCCCAAGGGCTGTGGGCTTACGCTGACAGAGAGACTGTCCGTGGCCAT   932
OY      933 CTATTACTTCTGCATCGCTTAGGCTATATCAACAAGTAGCTGAATCCCATTTCTATCGC   992
Db      933 TCTGGGCTTTCTGCACGGGCTGTGGGCTACGTCAACAGCTGTCTCAACCCCATCTCTACGC   992
OY      993 CTTTCTTGATGAATTCACAGCGGTGTTTTCCGGGACTTCTGTCTTCCAATAAGATGAG   1052
Db      993 CTCTCTGATGAACTTCAAGGCTGTCTCCGCAAGTCTCTGTGTGATCTGTCCCTGCG   1052
OY      1053 GATGAGCGGCGACAGACATGACAGAGTCCGAATACAGTTCCAG   1097
Db      1053 CCGGATGTGACAGGTGTCTGACCGCGGTGCGACAGCATTTGCCAAGA   1097

RESULT 97
US-09-186A--11
; Sequence 11, Application US/09905186A
; Publication No. US20030008289A1
; GENERAL INFORMATION:
; APPLICANT: Kreek, Mary Jeanne
; APPLICANT: LaForge, Karl Steven
; TITLE OF INVENTION: Alleles of the Human Orphanin
; TITLE OF INVENTION: Pol/No. US20030008289A1cReptIn Receptor Gene, Diagnostic Methods
; TITLE OF INVENTION: Alleles, and Methods of Treatment Based Thereon
; FILE REFERENCE: 600-1-284N
; CURRENT APPLICATION NUMBER: US/09/905,186A
; CURRENT FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/218,205
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 1829
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; TYPE: DNA
; ORGANISM: homo sapiens
US-09-905-186A-11

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Query Match	34.1%	Score 393.4;	DB 10;	Length 1829;
Best Local Similarity	65.1%	Pred. No. 3.1e-103;		
Matches 615; Conservative	0;	Mismatches 321;	Indels 9;	Gaps 2

Oy	153	CGGCCAATCTTCCCGGCGATTCGCCGGTATATCAAGCGGCTACTCCGTAGTGTCT	212
Db	162	CGCCTCTCTGCCCCCTCGGGCTCAAGGTCACCATGTGGGGCTTACTCTGGCGGTGT	221
Oy	213	CGTGGCGTTGGTGGGCACTCGCTGTGCATGTTCTGTATCATCCGATACACAAGATGA	272
Db	222	CGAGGGGCTCTGGGGAACTGCTTGTATGATGATCTCATCTCAGGACACCAAAATGAA	281
Oy	273	GACGACCAACCACTTTCATATTTTAACTGTGGCTTTGGCAGATGCTTTAGTTACTAAC	332
Db	282	GACAGCCACCAATTTTAACTTTAACTGTGGCCCTGGCCGACACTCTGTGTCTCTGAC	341
Oy	333	CATGCCCTTTAGAGTAAAGGTCATCTGTAATGAATTCCTGGGCTTTTGGGGATGTGTG	392
Db	342	GCTCCCTTCCAGGACAGGACATCTCTGGGCTTTGGGCCGTTTGGGAATGGCTGTG	401
Oy	393	CAAGATAGTATTTCCATTGATTACTACACATGTTTCCACAGCATCTTACCTTGACAT	452
Db	402	CAABACAGTACTTTGGCATGACTACTACAACTGTATCAGACACTTTCACCTTAATG	461
Oy	453	GATGAGCGTGAACCGTACATTCGCCGTGTGCCAACCCTGTAAGGCTTTGAACTTCCGAC	512
Db	462	CATAGGTGTGATGCTATGTAGGCATCTGCAACCCCACTCGTGCCCTGACGTCCGAC	521
Oy	513	ACCTTGAAGGCAAAATCATCAATATGTGATCTGGTGTGCTGTGATCTGTGGCAT	572
Db	522	GTCACGACAAACCCAGGCTGTCAATGTGGCAATCTGGGCCCTTGCGCTTGTGTGGGT	581
Oy	573	CTCTGCAATAGTCCCTTGAGGACACCAAGTCAGGGAAACGTGCATGTATGATGAGTGC	632
Db	582	TCCGCTTGCCATCATGGGCTCGGACAGTCT-----GAGATGAAGAATGAAATGCT	635
Oy	633	CTTGCAGTTCGAGATGATGACTACTCTGTGTGGACCTCTTCATGAAGAATCTGCTCTT	692
Db	636	GGTGAAGATCCCTACCCCTCAGAGATTAC---TGGGGCCGGGTGTTCGCATCTGCATCTT	692
Oy	693	CATCTTGGCTCTCGTATTCCTGTCTCTATCATGTCTGTGCTACACCTGTATGATCTCT	752
Db	693	CTCTCTTCTCTTCACTGTCGCCCGTCTGTCTATCTGTCTGTCTACACCTCATATATCG	752
Oy	753	GGCTCTCAAGAGCGTCCGGCTCTTTTGGCTCCCGAAGAAAGATTCGACCTGCGTAT	812
Db	753	GGGCTCCGTTGGAGTCCGCTGTCTCTCGGGCTCCGAAAGAAAGACCGGAACCTTCGGG	812
Oy	813	GATCACCAGACTGTGTCCTGTGTGTGTGTGTGGCAGTCTTCTGTCTGTCTGAGACTCCATTCA	872
Db	813	CATCACTCCGCTGT	872
Oy	873	CATATTATCTGTGTGAAGGCTCTGGGGAGCACTCCACACGACAGCTGCTCTTCCAG	932
Db	873	GGTCTTGT	932
Oy	933	CTATTATCTTGCATGCGCTTAAGGCTTATACCAACAGTAGTCCGTAATCCCATCTTACGC	992
Db	933	TCTGCGCTTCTGCAAGGCTCTGGCTACGTACAGACAGCTCTCAACCCCATCTTTAGCC	992
Oy	993	CTTTCTTATGAAAACTTCAAGCGGTGTTCCTGGGACTTCTGCTTTCACATGAAGATAG	1053
Db	993	CTTCTCGATGAAACTTTCAAGGCTGTGTTCCGAAAGTTCTGTGTGATCTGCGCTCG	1053
Oy	1053	GATGAGCGGACAGCACTAGCAGAGTCCGAATATCACTTACGA 1097	
Db	1053	CCGGGACGTGACGGTGTCTGACCCCGTGGCAGATTTGCCAAGA 1097	

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RESULT 98
US-10-305-720-1391
; Sequence 1391, Application US/10305720
; Publication No. US20040010136A1
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression
; FILE REFERENCE: PA-0002-1 CON
; CURRENT APPLICATION NUMBER: US/10/305,720
; PRIOR FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 09/016,434
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 1490
; SOFTWARE: PERL Program
; SEQ ID NO: 1391
; LENGTH: 1973
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: GenBank ID No. US20040010136A1 g471316
US-10-305-720-1391

Query Match      34.1%; Score 393.4; DB 16; Length 1973;
Best Local Similarity 65.1%; Pred. No. 3.2e-103;
Matches 615; Conservative 0; Mismatches 321; Indels 9; Gaps 2;

QY 153 CGCGACATCTCCCGGCCATCCGGTCAATCAACGCGGCTCTACTCTCGTAGTTCGT 212
DB 306 CGCCTTCTCGCCCTCGGGCTCAAGTCAACCTCGGGGCTCTACCTCGCGCTGTGT 365
QY 213 CGTGGCTTGTGGGCACTCGCTGTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 272
DB 366 CGAGAGGCTCCCGGGAACCTGCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 425
QY 273 GACGACACCAATTTATATATTAATTAACCTGTGTGTGTGTGTGTGTGTGTGTGT 332
DB 426 GACGACACCAATTTATATATTAATTTAATCTGTGTGTGTGTGTGTGTGTGTGTGT 485
QY 333 CATGCCCTTTCAGAGTACGCTTACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 392
DB 486 GCTGCTCTTCCAGGGGACGAGATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 545
QY 393 CAAGATGATATTTTCATGATTTACTCAACAATTTTCAACGACATTTTCACTTGACAT 452
DB 546 CAAGACAGTATTCATGATTTACTCAACAATTTTCAACGACATTTTCACTTGACAT 605
QY 453 GATGACGCTGACCGCTTACTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 512
DB 606 CATGATGTGTATCGCTATGTATGACATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 665
QY 513 ACCCTTGAAGGCAAGATCATCATATTCGATCTGTGTGTGTGTGTGTGTGTGTGTGT 572
DB 666 GTTCCAGCAAGCCGAGCTGTCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 725
QY 573 CTCTGCAATATGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 632
DB 726 TCCCGTTGGCATCATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 779
QY 633 CTTCGAGTTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 692
DB 780 GGTGAGATTCCTTACCCCTCAGATTAAC---TGGGGCCGGGTGTGTGTGTGTGTGTGT 836
QY 693 CATCTTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 752
DB 837 CCTCTTCTCTTCAATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 896
QY 753 GGTCTCAAGAGGTCCGGCTCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 812
DB 897 GGGGCTCCGTGAGTCCGGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 956
QY 813 GATCACAAGACTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 872
```

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DB 957 CATCACTGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTCA 1016
QY 873 CATATTCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 932
DB 1017 GGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1076
QY 933 CTATTATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 992
DB 1077 TCTGGCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1136
QY 993 CTTCCTGTATGATAAATCTTCAAGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1052
DB 1137 CTTCCTGTATGATAAATCTTCAAGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1196
QY 1053 GATGAGCGGCAAGACACTAGTACAGATCCGAATATACAGTTAGGA 1097
DB 1197 CGGAGACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1241

RESULT 99
US-10-641-643-1417
; Sequence 1417, Application US/10641643
; Publication No. US20040077003A1
; GENERAL INFORMATION:
; APPLICANT: Cocke, Benjamin G.
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/641,643
; FILING DATE: 14-Aug-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1417:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1973 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g471316
; SEQUENCE DESCRIPTION: SEQ ID NO: 1417 :
US-10-641-643-1417

Query Match      34.1%; Score 393.4; DB 17; Length 1973;
Best Local Similarity 65.1%; Pred. No. 3.2e-103;
Matches 615; Conservative 0; Mismatches 321; Indels 9; Gaps 2;

QY 153 CGCGACATCTCCCGGCCATCCGGTCAATCAACGCGGCTCTACTCTCGTAGTTCGT 212
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Db 306 CGCCTTCGCGCCCTCGGGCTCAAGGTCAACATCGGGGCTCTACCTGCGCGTGTGT 365
Qy 213 CGTGGGCTTGGTGGGCACTCGCTGTGATGTTCTGGATCATCCGATACAAAGATGA 272
Db 366 CGAGGGCTCCCTGGGGAACTGCTGTGTCTGTACGTCACTCCACGACACCAAAATGA 425
Qy 273 GACAGCAACCAATTTACTATATTAACCTGGCTTGGAGATGCTTTAGTTACTACAA 332
Db 426 GACAGCCACCAATTTACTATATTTACTTAACTTGGCCCTGGCCGACACTCTGGTCTGTAC 485
Qy 333 CATGCCCTTTCAGAGTACGGTCTACTGTATGTATGTAATTCCTGGCCCTTTGGGGATGTCTGTG 392
Db 486 GGTGCGCTTTCAGAGGAGCGGACATCTCTCGGGCTTCTGGCCGTTTGGGAAATGCGCTGTG 545
Qy 393 CAAGATAGTAAATTTCTATTGATTACTACAAATGTTTACCAAGATCTTCACTTGAACAT 452
Db 546 CAAGACAGTCAATGGCTACTACTACAAATGTTTACCAAGATCTTCACTTGAACATGTC 605
Qy 453 GATGACGCTGACCGCTACATTCGCTGTGACACCCCGGAAAGGCTTGGACTTTCGAC 512
Db 606 CATGAGTGTGATCCGTATGTAGCAATCGCAACCCCATCCGTGCGCTTCGACGTCCGAC 665
Qy 513 ACCCTTGAAGGCAAGATCATCAATATCTGATCTGGCTGTGCTGTGATCTGTTGGCAT 572
Db 666 GTCCAGCAAAAGCCAGGCGTGTCAATGTGGCCATCTGGGCCCTGGCTCTGTTGTGCGTGT 725
Qy 573 CTCTCAATAGTCTCTTGGAGGCAACCAAGTCAAGGAAAGATGTCATTTAGTGTCTC 632
Db 726 TCCCGCTTGCATCATGGGCTCGGACAGGTCTC-----GAGGATGAAGATGAGTGTCT 779
Qy 633 CTGAGATCCCAATGATGATCTACTCTCGTGGGACCTCTTCATGAAGATGTGGTCTT 692
Db 780 GGTGAGATCCCTTACCCCTCAGGATTTAC--TGGGGCGCGTGTGTTGCCATCTGATCTT 836
Qy 693 CATCTTGGCTTCTGTATCCCTGTCTCATCTCATCTGCTCTTCAACCCCTGATGATCT 752
Db 837 CCTCTTCTCTTCAATCTGCTCCGCTGTCTCATCTGTCTGTCTCAAGCTCATGATCTCG 896
Qy 753 GCGTCTCAAGAGCGTCCGGCTCTCTTCTGCTCCGAGAAAGATCGCAACTCTGCTG 812
Db 897 GCGGCTCGGTGAGTCCGCTGCTCTCGGGCTCCGAGAGAGACCGGAACTCTCGGG 956
Qy 813 GATCACAGACTGTGCTCTGT 872
Db 957 CATCACTGGGCTGT 1016
Qy 873 CATATTCACTCTGT 932
Db 1017 GGTCTTCTGT 1076
Qy 933 CTATTACTTCTGTGATCGCTTGTAGGCTATACCAAGATGACCTGAATCCCATTTCTTACGC 992
Db 1077 TCTGGCTTCTGTGACGGCCCTGGGCTAGGTCAACAGCTGCTCAACCCCATCTTACGC 1136
Qy 993 CTTTCTTGTATGAAAATTCAAGCGGTGTTTCCGGGACTTCTGCTTTCACATAAATGAG 1052
Db 1137 CTTCTGTGATGAACTTCAAGGCTGTCTTCCGCAAGTTCGTGTGATCTGCGCTGTG 1196
Qy 1053 GATGAGCGGAGAGACACTGAGAGATCCGAATACAGTTACAGA 1097
Db 1197 CCGGACGTGACGTGTCTGACCGGCTGTGGCAGCATTGCMAAGA 1241

RESULT 100
US-10-087-345A--22

; Sequence 22. Application US/10087345A

; Publication No. US20030045696A1

; GENERAL INFORMATION:

; APPLICANT: Ouyang, Chung

; TITLE OF INVENTION: ORPHANIN FQ RECEPTOR NUCLEIC ACIDS

; FILE REFERENCE: UM-06962

; CURRENT APPLICATION NUMBER: US/10/087,345A

; CURRENT FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 2534
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-087-345A--22
Query Match 34.1%; Score 393.4; DB 15; Length 2534;
Best Local Similarity 65.1%; Pred. No. 3.6e-103;
Matches 615; Conservative 0; Mismatches 321; Indels 9; Gaps 2;
Qy 153 CGCGCAATCTCCCGGCAATCCGGTATATATCAAGCGGCTTCTCGTGTGTGTGT 212
Db 246 CGCCTTCTGCGCCCTCGGGCTCAAGGTCAACATCGGGGCTCTACCTGGCGTGTGT 305
Qy 213 CGTGGGCTTGGTGGGCACTCGCTGTGATGTTCTGGATCATCCGATACAAAGATGA 272
Db 306 CGAGGGCTCCCTGGGGAACTGCTGTGTCTGTACGTCACTCCACGACACCAAAATGA 365
Qy 273 GACAGCAACCAATTTACTATATTAACCTGGCTTGGAGATGCTTTAGTTACTACAA 332
Db 366 GACAGCCACCAATTTACTATATTTACTTAACTTGGCCCTGGCCGACACTCTGGTCTGTAC 425
Qy 333 CATGCCCTTTCAGAGTACGGTCTACTGTATGTATGTAATTCCTGGCCCTTTGGGGATGTCTGTG 392
Db 486 GGTGCGCTTTCAGAGGAGCGGACATCTCTCGGGCTTCTGGCCGTTTGGGAAATGCGCTGTG 485
Qy 453 GATGACGCTGACCGCTACATTCGCTGTGACACCCCGGAAAGGCTTGGACTTTCGAC 512
Db 606 CATGAGTGTGATCCGTATGTAGCAATCGCAACCCCATCCGTGCGCTTCGACGTCCGAC 665
Qy 513 ACCCTTGAAGGCAAGATCATCAATATCTGATCTGGCTGTGCTGTGATCTGTTGGCAT 572
Db 666 GTCCAGCAAAAGCCAGGCGTGTCAATGTGGCCATCTGGGCCCTGTTGTGCGTGT 725
Qy 573 CTCTCAATAGTCTCTTGGAGGCAACCAAGTCAAGGAAAGATGTCATTTAGTGTCTC 632
Db 726 TCCCGTGTCCATCATGGGCTCGGACAGGTCTC-----GAGGATGAAGATGAGTGTCT 779
Qy 633 CATCTTGGCTTCTGTATCCCTGTCTCATCTCATCTGCTCTTCAACCCCTGATGATCT 752
Db 837 CCTCTTCTCTTCAATCTGCTCCGCTGTCTCATCTGTCTGTCTCAAGCTCATGATCTCG 896
Qy 753 GCGTCTCAAGAGCGTCCGGCTCTCTTCTGCTCCGAGAAAGATCGCAACTCTGCTG 812
Db 897 GCGGCTCGGTGAGTCCGCTGCTCTCGGGCTCCGAGAGAGACCGGAACTCTCGGG 956
Qy 813 GATCACAGACTGTGCTCTGT 872
Db 957 CATCACTGGGCTGT 1016
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Qy 933 CTATTACTTCTGTGATCGCTTGTAGGCTATACCAAGATGACCTGAATCCCATTTCTTACGC 992
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Qy 993 CTTTCTTGTATGAAAATTCAAGCGGTGTTTCCGGGACTTCTGCTTTCACATAAATGAG 1052
Db 1077 CTTCTGTGATGAACTTCAAGGCTGTCTTCCGCAAGTTCGTGTGATCTGCGCTGTG 1136

Qy 1053 GATGAGCGGCAAGCACTAGCAGAGTCCGAAATACAGTTCAAGA 1097
Db 1137 CCGGAGCGTGCAGGTGTGTGACCGCGGTGGCGCAGCATTTGCCAAGA 1181

Search completed: August 31, 2004, 14:23:26
Job time : 626 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 30, 2004, 16:58:44 ; Search time 3490 Seconds
(without alignments)
9874.200 Million cell updates/sec

Title: US-09-904-584-1

Perfect score: 1154

Sequence: 1 atgagctcccccagatcagat.....ccagatgactagctcgtgga 1154

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database :

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2: em_eatbm:*
3: em_eatbn:*
4: em_eatbu:*
5: em_eatbv:*
6: em_eatpl:*
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9: gb_eatcl:*
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26: em_eatbm:*
27: em_eatbm:*
28: gb_eatcl:*
29: gb_eatcl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	805.2	69.8	895	14	CB565888 AGENCOURT
2	470.6	40.8	837	14	CF593603 AGENCOURT
3	468	40.6	480	13	BX092912 BX092912
4	430.8	37.3	2405	11	AK038389 Mus muscu

5	420	36.4	4022	11	AK043873
6	367.8	31.9	2919	11	AK038620
7	367.8	31.9	2959	11	AK079529
8	352	30.5	879	29	AY10745
9	335.6	29.1	2940	11	AK044178
10	327.4	28.4	2974	11	AK043275
11	327	28.3	3101	11	AK031926
12	325.8	28.2	879	29	AY10747
13	311.4	27.0	1053	29	CNS04C2T
14	277.6	24.1	788	13	BX874804
15	271.4	23.5	883	13	BE676176
16	268.6	23.3	917	13	BU219878
17	239.8	20.8	657	10	BB588668
18	231.2	20.0	682	29	AY10746
19	229.6	19.9	1176	29	AY100827
20	227.4	19.7	389	10	BE649947
21	226.6	19.6	1176	29	AY100829
22	226.6	19.6	2014	11	AK046464
23	224.6	19.5	980	12	BM543468
24	223	19.3	632	10	BB641725
25	221.4	19.2	1006	29	AY100676
26	217.6	18.9	784	13	BQ179053
27	214.8	18.6	1006	29	AY100674
28	214	18.5	429	12	BM342951
29	213.8	18.5	2432	11	AK051189
30	213	18.5	836	29	CNS02261
31	213	18.5	866	14	CD246184
32	211	18.3	531	29	CE517843
33	208.6	18.1	877	29	CNS02SC2
34	208.2	18.0	842	29	CNS02SKU
35	207.8	18.0	697	13	BU139251
36	207.8	18.0	757	13	BU614716
37	203.4	17.6	785	12	BT754749
38	202.8	17.3	810	12	BM943972
39	199.2	17.3	649	13	BU219037
40	195.6	16.9	816	13	BQ179148
41	194	16.8	787	29	BX286633
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43	190.6	16.5	954	29	AY10421
44	189.8	16.4	546	28	A226406
45	182.2	15.8	2848	11	AK039151
46	181.8	15.8	318	29	CG536117
47	181.2	15.7	776	14	CF550026
48	180.4	15.6	1176	29	AY100828
49	179.2	15.5	735	13	BU366266
50	178.8	15.5	987	29	AY101571
51	178.4	15.5	2724	11	BC033145
52	178.4	15.5	433	10	AM489031
53	178.4	15.5	741	13	BU613017
54	177.8	15.4	720	12	BT753905
55	176	15.3	828	13	BX843850
56	171.6	14.9	1307	11	CNSL11BD
57	170.2	14.7	654	10	AM373832
58	170.2	14.7	990	29	AY101573
59	169	14.6	1095	29	AY100986
60	168.4	14.6	627	12	BT919235
61	168.2	14.6	183	14	R81583
62	166.4	14.4	710	29	AY10423
63	165	14.3	945	29	AY10423
64	164	14.2	1257	29	AY100332
65	162.2	14.1	1052	13	BX280512
66	162	14.0	798	14	CD559493
67	161.4	14.0	1089	29	AY100988
68	160	13.9	714	10	BB631900
69	159.4	13.8	550	10	BF193020
70	159.4	13.8	987	29	AY101572
71	159.2	13.8	768	13	BU318522
72	158.8	13.7	795	14	CD559491
73	158.4	13.7	910	29	AY10422
74	156.2	13.5	1287	29	AY100334
75	156	13.5	701	14	CF147827
76	155.4	13.5	688	13	BU057593
77	153.4	13.3	916	13	BX433241

78	153.2	13.3	702	28	A2966515	A2966515	2M0237H04	151	106.6	9.2	1761	11	AK041106	AK041106	Mus muscu	BM911763	AGENCYCOURT
79	153	13.3	741	12	BI224313	BI224313	602940621	152	106.2	9.2	952	12	BM911763	BM911763	Mus muscu	BQ053936	AGENCYCOURT
80	152.8	13.2	663	10	BB656301	BB656301		153	106.6	9.2	1167	12	BQ053936	BQ053936	Mus muscu	BX846165	AGENCYCOURT
C 81	152.2	13.2	927	29	CNS04RP2	ALJ04175	Tetraodon	154	104.6	9.1	621	13	BX846165	BX846165	Mus muscu	BM471950	AGENCYCOURT
C 82	151.6	13.1	881	29	CNS03JCN	AL246704	Tetraodon	155	104	9.0	697	12	BG471950	BG471950	Mus muscu	BQ2512853	AGENCYCOURT
C 83	151	13.1	662	14	CBS57233	CBS57233	AGNNUC:U	156	103.8	9.0	789	12	BG205056	BG205056	Mus muscu	RST24475	AGENCYCOURT
C 84	150.2	13.0	792	14	CDS59492	CDS59492	AGENCYCOURT	157	103.4	9.0	2284	11	AK089875	AK089875	Mus muscu	AK089875	Mus muscu
C 85	150	13.0	1114	13	BX390825	BX390825	BX390825	158	103.4	9.0	2396	11	AK089895	AK089895	Mus muscu	AK089895	Mus muscu
86	148.8	12.9	663	10	BB632308	BB632308		159	102.6	8.9	602	10	BB642114	BB642114	Mus muscu	BB642114	Mus muscu
87	148.8	12.9	789	13	BU028175	BU028175		160	102.6	8.9	884	12	BG182330	BG182330	Mus muscu	RST1196	AGENCYCOURT
88	147.2	12.8	898	29	AY400987	AY400987	Pan trogl	161	101.6	8.8	826	29	AY399910	AY399910	Mus muscu	AY399910	Mus muscu
89	147	12.7	835	13	BU708032	BU708032	UI-M-FRO-	162	101.4	8.8	1086	29	AY399293	AY399293	Mus muscu	AY399293	Mus muscu
90	143.4	12.4	153	14	RJ1984	RJ1984	YH622C10. r1	163	101.4	8.8	2118	11	AK031109	AK031109	Mus muscu	AK031109	Mus muscu
91	142	12.3	785	12	BI757249	BI757249	603030754	164	101.4	8.8	2292	11	AK036597	AK036597	Mus muscu	AK036597	Mus muscu
92	141	12.2	714	12	BM951523	BM951523	UI-M-BGO-	165	101.4	8.8	2432	11	AK036690	AK036690	Mus muscu	AK036690	Mus muscu
93	141	12.2	1383	12	BM546464	BM546464	AGENCYCOURT	166	100.4	8.7	899	10	BF581225	BF581225	Mus muscu	BF581225	602100435
94	140.2	12.1	937	29	CNS03GSG	AL243385	Tetraodon	167	100.4	8.7	890	29	AY399909	AY399909	Mus muscu	AY399909	Mus muscu
95	139.8	12.1	791	14	CDS59647	CDS59647	AGENCYCOURT	168	100.2	8.7	618	13	BU340701	BU340701	Mus muscu	BU340701	603520741
96	139.4	12.1	642	10	BE252309	BE252309	601114162	C 169	100.2	8.7	794	29	CNS01WCI	ALJ52677	Tetraodon	ALJ52677	ALJ52677
97	139.4	12.1	793	13	BU137021	BU137021		170	100	8.7	1027	9	ALJ52677	ALJ52677	Mus muscu	AY400424	Mus muscu
98	139.2	12.1	791	14	CP147826	CP147826	AGENCYCOURT	171	98.8	8.6	1062	29	AY400424	AY400424	Mus muscu	AY400424	Mus muscu
99	138.6	12.0	791	14	CDS59646	CDS59646	AGENCYCOURT	172	98.6	8.5	1046	29	AY407666	AY407666	Mus muscu	BE938149	Mus muscu
100	138.2	12.0	792	14	CDS59648	CDS59648	AGENCYCOURT	C 173	98.4	8.5	549	10	BE938149	BE938149	Mus muscu	AK076275	Mus muscu
101	138.2	12.0	821	13	BX880870	BX880870		174	98.2	8.5	2708	11	AK076275	AK076275	Mus muscu	CE505010	tigr-g88-
C 102	134.8	11.7	730	13	EX319389	EX319389	BM919389	175	97.2	8.4	620	29	CE505010	CE505010	Mus muscu	ALJ452673	ALJ452673
C 103	133.4	11.6	563	28	AZ557931	AZ557931	1M0099P13	176	97	8.4	770	9	ALJ452673	ALJ452673	Mus muscu	BU464426	603368069
C 104	132	11.4	904	12	BG329444	BG329444	602429002	177	97	8.4	928	11	AK049671	AK049671	Mus muscu	BU464426	603368069
C 105	131.2	11.4	581	13	BY265591	BY265591		178	97	8.4	4435	13	AK049671	AK049671	Mus muscu	BI906283	603063222
C 106	131	11.4	427	9	AM047705	AM047705	UI-M-BH1-	179	96.6	8.4	876	12	CA988251	CA988251	Mus muscu	CA988251	AGENCYCOURT
C 107	131	11.4	995	29	CNS04RQE	ALJ04223	Tetraodon	180	96.2	8.3	830	14	CA988251	CA988251	Mus muscu	BU296746	603733882
108	130.4	11.3	640	10	BB656973	BB656973		181	95.2	8.2	775	13	BU296746	BU296746	Mus muscu	BG404113	602420022
109	128.2	11.1	463	13	BU406028	BU406028	604140427	182	94.8	8.2	1045	12	BG404113	BG404113	Mus muscu	AG066310	Pan trogl
C 110	128.2	11.1	637	14	CBS76776	CBS76776	AMGNNUC:C	183	94.4	8.2	685	29	AG066310	AG066310	Pan trogl	CG539937	OST131408
111	128.2	11.1	755	12	BI772443	BI772443		184	94	8.1	164	29	CG539937	CG539937	Homo sapi	AY417249	Homo sapi
112	128	11.1	1257	29	AY400333	AY400333	Pan trogl	185	94	8.1	1143	29	AY417249	AY417249	Homo sapi	AY400438	Pan trogl
113	127.8	11.1	530	10	BF073470	BF073470	220178 MA	186	93.8	8.1	1089	29	AY400438	AY400438	Mus muscu	CF584648	AGENCYCOURT
114	127.8	11.1	1053	28	CC187882	CC187882	CH261--808	187	93.4	8.1	964	14	CF584648	CF584648	AGENCYCOURT	CE544428	NMSPO024
115	127.4	11.0	931	9	ALJ56712	ALJ56712		188	93.2	8.1	624	14	CF584428	CF584428	Mus muscu	BQ876264	AGENCYCOURT
116	126	10.9	1080	29	AY407960	AY407960	Mus muscu	189	92.8	8.0	859	13	BQ876264	BQ876264	Mus muscu	AY400439	Mus muscu
117	125.8	10.9	738	10	AM919332	AM919332	EST350636	190	92.8	8.0	1089	29	AY400439	AY400439	Mus muscu	AK031100	Mus muscu
118	125.2	10.8	730	14	CP147825	CP147825	AGENCYCOURT	191	92.8	8.0	2581	11	AK031100	AK031100	Mus muscu	AY417370	Pan trogl
119	124.6	10.7	468	13	BX281894	BX281894		192	92.6	8.0	984	29	AY417370	AY417370	Pan trogl	AY400437	Homo sapi
120	123.8	10.7	687	14	CF766885	CF766885	CES001048	193	92.6	8.0	1089	29	AY400437	AY400437	Homo sapi	AY417369	Homo sapi
121	121.2	10.5	1008	13	BX419487	BX419487		194	92.6	8.0	1119	29	AY417369	AY417369	Homo sapi	ALJ543359	ALJ543359
C 122	120.6	10.4	844	29	AY400830	AY400830	Homo sapi	195	92.6	8.0	1201	9	ALJ543359	ALJ543359	Mus muscu	AY407664	Homo sapi
C 123	120.4	10.4	844	29	CNS03CIX	ALJ237966	Tetraodon	196	92	8.0	1052	29	AY407664	AY407664	Homo sapi	AK039628	Mus muscu
124	120.2	10.4	772	12	BI819436	BI819436	603034220	197	91.8	8.0	3075	11	AK039628	AK039628	Mus muscu	BB629533	BB629533
125	119.4	10.3	1918	11	AK053776	AK053776	Mus muscu	198	91	7.9	666	13	BU205570	BU205570	Mus muscu	BU205570	604153723
126	119	10.3	870	13	BX340358	BX340358		199	91	7.9	666	13	BU205570	BU205570	Mus muscu	ALJ541044	ALJ541044
127	119	10.3	1043	13	BX37412	BX37412		200	91	7.9	706	14	CP994665	CP994665	AGENCYCOURT	BI908127	603067423
128	119	10.3	1074	12	BM917063	BM917063		201	90.8	7.9	780	12	BI908127	BI908127	Mus muscu	BY746585	BY746585
129	119	10.3	1086	29	AY399291	AY399291	Homo sapi	202	90.8	7.9	957	13	AK050615	AK050615	Mus muscu	AK050615	Mus muscu
130	118.4	10.3	614	14	CA377546	CA377546		203	90.8	7.9	3005	11	AK019478	AK019478	Mus muscu	AI959485	f410903. y
131	117.8	10.2	928	13	BX409846	BX409846		204	90.4	7.8	733	9	AI959485	AI959485	Mus muscu	BI954985	f410903. y
132	117.6	10.2	656	9	ALJ19185	ALJ19185		205	90.4	7.8	1780	11	BC057175	BC057175	Mus muscu	BC047931	Mus muscu
133	117.4	10.2	685	13	BY724027	BY724027		206	90.4	7.8	1849	11	BC047931	BC047931	Mus muscu	AK032901	Mus muscu
134	115.6	10.0	851	14	CK127495	CK127495	AGENCYCOURT	207	90.2	7.8	827	14	CF996947	CF996947	AGENCYCOURT	CA472324	AGENCYCOURT
135	115.4	10.0	348	13	BY231569	BY231569		208	90.4	7.8	648	14	CF996947	CF996947	AGENCYCOURT	CA472324	AGENCYCOURT
136	115.4	10.0	369	13	BY232542	BY232542		209	90.4	7.8	752	14	BI761664	BI761664	603046395	BI761664	603046395
C 137	115.4	10.0	539	9	ALJ18186	ALJ18186		210	90.2	7.8	827	14	BI761664	BI761664	603046395	BI761664	603046395
138	113.2	9.8	600	14	CA528907	CA528907	8091-57 M	211	90.2	7.8	752	14	BI761664	BI761664	603046395	BI761664	603046395
139	113	9.8	1497	13	BQ212191	BQ212191	AGENCYCOURT	212	90.2	7.8	827	14	BI761664	BI761664	603046395	BI761664	603046395
140	112.6	9.8	649	14	CA772710	CA772710	1083H03. Y	213	90.2	7.8	1083	29	AY398808	AY398808	Mus muscu	CA342706	672651 NC
141	112	9.7	812	14	CD759201	CD759201	AGENCYCOURT	214	89.6	7.8	808	14	CA342706	CA342706	Mus muscu	CA454255	AGENCYCOURT
C 142	111.6	9.7	901	29	CNS01SKS	ALJ65326	Tetraodon	215	89.6	7.8	876	14	CA454255	CA454255	AGENCYCOURT	AY407665	Pan trogl
143	111.4	9.6	1116	29	AY400832	AY400832	Mus muscu	216	89.6	7.8	655	29	CG582748	CG582748	Mus muscu	CG582748	OST224233
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370	82.6	7.2	765	14	CF270677	AGENCOURT	443	78.8	6.8	1224	29	AY420419	AY420419	Mus muscu
371	82.6	7.2	794	29	AY399911	Mus muscu	444	78.8	6.8	4676	11	AK038558	AK038558	Mus muscu
372	82.6	7.12	1201	9	AL556152	AL556152	445	78.2	6.8	600	12	B1987229	B1987229	3193-25 M
373	82.4	7.1	550	14	CB354574	CB354574	446	78.2	6.8	646	10	BB615654	BB615654	BB615654
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375	82.4	7.1	1114	12	BM605549	AGENCOURT	448	78.2	6.8	662	10	BB644135	BB644135	BB644135
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378	82.2	7.1	1201	13	BK421511	BK421511	451	78.2	6.8	665	13	EX398107	EX398107	EX398107
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381	82	7.1	558	14	CB287516	CB287516	454	78.2	6.8	965	13	BQ944555	BQ944555	AGENCOURT
382	82	7.1	561	10	BF591285	BF591285	455	78.2	6.8	1029	29	AY399294	AY399294	AY399294
383	81.8	7.1	623	12	BO038875	BO038875	456	78.2	6.8	1029	29	AY399294	AY399294	AY399294
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386	81.6	7.1	750	13	BU335137	BU335137	459	78	6.8	709	13	BU611590	BU611590	BU611590
387	81.6	7.1	623	14	CD468358	CD468358	460	78	6.8	932	29	CNS02SIR	AL707383	AL707383
388	81.6	7.1	710	14	CD18005	CD18005	461	78	6.8	1848	11	AK011967	AK011967	AK011967
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390	81.6	7.1	807	14	CB939828	CB939828	463	77.8	6.7	640	14	CD740138	CD740138	CD740138
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392	81.6	7.1	1119	12	BM543622	BM543622	465	77.8	6.7	710	13	BU613761	BU613761	BU613761
393	81.6	7.1	1143	29	AY417250	AY417250	466	77.8	6.7	3338	11	AK085990	AK085990	AK085990
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395	81.4	7.1	500	12	BG395247	BG395247	468	77.6	6.7	600	29	CE428488	CE428488	CE428488
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412	80.6	7.0	523	9	AL836006	AL836006	485	77	6.7	512	13	BX873014	BX873014	BX873014
413	80.6	7.0	753	14	CD492892	CD492892	486	77	6.7	512	13	BX880500	BX880500	BX880500
414	80.6	7.0	805	14	CD246171	CD246171	487	77	6.7	667	13	BY749844	BY749844	BY749844
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416	80.4	7.0	768	9	AJ444418	AJ444418	489	77	6.7	1201	9	AL547734	AL547734	AL547734
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421	80.2	6.9	666	10	AM966793	AM966793	494	76.6	6.6	1146	29	AY400451	AY400451	AY400451
422	80.2	6.9	770	14	CF595894	AGENCOURT	495	76.6	6.6	3335	11	AK049892	AK049892	AK049892
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424	80.2	6.9	1188	29	AY416699	AY416699	497	76.4	6.6	504	14	CAS78796	CAS78796	CAS78796
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ALIGNMENTS

RESULT 1
LOCUS CB565888
DEFINITION AGENCOURT 12691503 NIH MGC 146 Homo sapiens cDNA clone
IMAGE:6519213 5', mRNA_sequence.
ACCESSION CB565888
VERSION CB565888.1 GI:29485418
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 895)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Guthrie cDNA Resource Center
cDNA Library Preparation: Guthrie cDNA Resource Center
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: IRBP001 row: f column: 09
High quality sequence stop: 763.
Location/Qualifiers

FEATURES
source

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multiple; ORF's were PCR-amplified (from IMAGE clones or
from commercially available cDNA libraries) and cloned by
the Guthrie cDNA Resource Center (www.guthrie.org/cDNA)
into pCDNA3.1. For specific information on cloning sites
(which vary by clone), please refer to the Guthrie
website, using the Guthrie ID given in the file
ftp://image.llnl.gov/image.rearrayed_plates/IRBP.presv.dat
a. Note: this is a NIH_MGC library."
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ORIGIN

Query Match 69.8%; Score 805.2; DB 14; Length 895;
Best Local Similarity 97.1%; Pred. No. 2.6e-145;
Matches 841; Conservative 0; Mismatches 23; Indels 2; Gaps 2;

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RESULT 2
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DEFINITION
AGENCOURT_15623822 NIH_MGC_147 Homo sapiens cDNA clone
IMAGE:30531690 5', mRNA sequence.
CF593603
CF593603.1 GI:36347316
EST.

SOURCE
ORGANISM
Homo sapiens (human)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 837)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10K07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Stefan Haneson
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: NDAM622 row: n column: 19
High quality sequence stop: 592.
Location/Qualifiers

FEATURES
source

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Db	810	TACGACTCAAGAGTGTCCGCATGCTGTGGGGCTCCAAAAGAAAGGACGAAACCTGTGGCA	869
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Qy	872	ACATTTATTCCTGGTGGAGGCTCTGGGGAGGACCTCCGACGACAGCTGTCTCTCCA	931
Db	930	ACATTTATGTATCATCAAGACACTGATCAGATTCGAGAAACCATTTCCAGACTGTT	989
Qy	932	GCTATTACTTTCGATCGCTTAGGCTATACCAAGAGTAGGCTGATCCATTTCTCTACG	991
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RESULT 5	
LOCUS	AK043873
DEFINITION	AK043873 4022 bp mRNA linear HTC 19-SEP-2003
ACCESSION	AK043873
VERSION	AK043873.1 GI:26335979
KEYWORDS	Mus musculus 10 days neonate cortex cDNA, RIKEN full-length enriched library, clone:A830044L10 product:DELTA-TYPE OPTOID
SOURCE	RECEIVED, full insert sequence.
ORGANISM	AK043873
	HTC; CAP trapper.
	Mus musculus (house mouse)
	Mus musculus
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REFERENCE	1
AUTHORS	Carninci, P. and Hayashizaki, Y.
TITLE	High-efficiency full-length cDNA cloning
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)
MEDLINE	99279253
PUBMED	10349636
REFERENCE	2
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE	20499374
PUBMED	11042159
REFERENCE	3
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Kitsuwa, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazada, M., Nishine, T., Harada, A., Yamamoto, K., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kasaiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE	20530913
PUBMED	11076861
REFERENCE	4
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE	Functional annotation of a full-length mouse cDNA collection
JOURNAL	Nature 409, 685-690 (2001)
REFERENCE	5

AUTHORS THE FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

AUTHORS 6 (bases 1 to 4022)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiroaka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Nunazaki, R., Ohno, M., Ohseco, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akaiwa, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

TITLE Direct Submission

JOURNAL Submitted (16-JUN-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration and Chemical Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suenho-cho, Tsurumi-ku, Yokohama Kanagawa 230-0045, Japan E-mail: genome-resgsc.riken.go.jp, URL: http://genome-gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

REFERENCE Please visit our web site for further details. URL: http://genome-gsc.riken.go.jp/ URL: http://fantom.gsc.riken.go.jp/. Location/Qualifiers

FEATURES

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 Db 225 TAGTCCCTGCTCCCTCGCCCTTACCGCATCCGCATCAGCGGCTCTACTCCGCTGTGGCC 284
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ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE
 AUTHORS
 Carninci, P. and Hayashizaki, Y.
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 High-efficiency full-length cDNA cloning
 JOURNAL
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 THE RIKEN Genome Exploration Research Group Phase II Team and the
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 Functional annotation of a full-length mouse cDNA collection
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 Nature 409, 685-690 (2001)
 REFERENCE
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 JOURNAL
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 REFERENCE
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 Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
 Hayashida, K., Hayatsu, N., Hiramoto, K., Iizawa, T., Hirozane, T.,
 Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
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 Koye, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
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 Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takeku-Akahira, S.,
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 TITLE
 Direct Submission
 JOURNAL
 Submitted (16-JUN-2001) Yoshihide Hayashizaki, The Institute of
 Physical and Chemical Research (RIKEN), Laboratory for Genome
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
 RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
 Kanagawa 230-0045, Japan (E-mail: genome-res@gscc.riken.go.jp,
 URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,
 Fax: 81-45-503-9216)
 COMMENT
 cDNA library was prepared and sequenced in Mouse Genome
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 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Please visit our web site for further details.
 URL: http://genome.gsc.riken.go.jp/
 URL: http://fantom.gsc.riken.go.jp/
 URL: http://location.gsc.riken.go.jp/
 FEATURES
 source
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DEFINITION	Mus musculus adult male hypothalamus cDNA, RIKEN full-length enriched library, clone:A230027D20 product:NOTICEPTIN RECEPTOR (ORPHANIN FQ RECEPTOR), full insert sequence.		
ACCESSION	AK079529		
VERSION	AK079529.1	GI:263348047	
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SOURCE	Mus musculus (house mouse)		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
REFERENCE			
AUTHORS	1 Carninci, P. and Hayashizaki, Y		
TITLE	High-efficiency full-length cDNA cloning		
JOURNAL	Mech. Enzymol. 303, 19-44 (1999)		
MEDLINE	99279253		
PUBMED	10349636		
REFERENCE	2		
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AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, T., Nishi, K., Kitenuna, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishibe, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Yoneda, Y., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunawa, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.		
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multipipillary sequencer		
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MEDLINE	20530913		
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AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.		
TITLE	Functional annotation of a full-length mouse cDNA collection		
JOURNAL	Nature 409, 685-690 (2001)		
REFERENCE	5		

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 2959)

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TITLE Direct Submission

JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suenho-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

PLEASE VISIT OUR WEB SITE FOR FURTHER DETAILS.

URL: http://genome.gsc.riken.go.jp/

URL: http://fantom.gsc.riken.go.jp/

URL: http://lancm.gsc.riken.go.jp/

Location/Qualifiers

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db_xref="MGI:2402954"

db_xref="taxon:10090"

clone="A230027020"

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ORIGIN

Query Match 31.9%; Score 367.8; DB 11; Length 2959;

Best Local Similarity 63.4%; Pred. No. 1.6e-60;

Matches 599; Conservative 0; Mismatches 337; Indels 9; Gaps 2;

QY 154 GGGACATCTCCCGGCATCCCGGCATCATCAAGCGGCTGACTCCGTAGTTCGTC 213

DB 341 GCTTTCGCGCCCTTGAGCTCAAGGTCAACATCGGCGGCTCTACTGTGTCATC 400

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DB 401 GGGGGGCTCTGGGGAACTGCTGCTCATGATGATGATCTTCAAGCAACCAAGATGAAG 460

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DB 521 CTGCGCTTTCAGAGGACAGACATCTTCTGGGCTTCTGGCATTTGGGATGACCTGTGC 580

QY 394 AAGATAGTATTTTCATGATGATTTACAAACATGTTTACAGAGATCTTACCTTGAACATG 453

DB 581 AAGACGGTCAATTTGATGATGATTTACAAACATGTTTACAGAGATCTTCACTTGAACATG 640

QY 454 ATGACCGTGAACCGCTACATTTGCGCTGTGCGCAACCCGTAAGGCTTTGGAATTCGCGACA 513

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DB 701 TCCAGTAAAGCCAGGCGCTTAAATGATGATGATGATGATGATGATGATGATGATGATG 760

QY 574 TCTGCAATATGCTTTGAGGAGCAACCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGG 633

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QY 754 GCTCTCAAGAGCGTCCGCTCTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 813

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DB 992 ATCACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1051

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DB 1052 GTCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1111

QY 934 TATTACTTGTGATGCTGCTTGAAGCTTAAACCAACAGATGATGATGATGATGATGATGATG 993

DB 1112 CTGCGCTTCTGCAAGCGCTGCGCTGATGATGATGATGATGATGATGATGATGATGATG 1171

QY 994 TTTCTTGAATGAAATTTCAAGCGGCTTCCGGGACTTCTGCTTCCACTGAAGATGAGG 1053

DB 1172 TTTCTTGAATGAAATTTCAAGCGGCTTCAAGCGGCTTCAAGCGGCTTCAAGCGGCTTCA 1231

QY 1054 ATGAGCGGCGAGAGCATGAG 1098

DB 1232 CGGAGAGATGAGAGGTTTCTGATGATGATGATGATGATGATGATGATGATGATGATG 1276

RESULT 8

AY410745

LOCUS Homo sapiens ORP1 gene, VIRUAL TRANSCRIPT, partial sequence, 879 bp DNA 1linear GSS 16-DEC-2003

DEFINITION

ACCESSION AY410745

VERSION AY410745.1 GI:39766713

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 879)
 Clark, A.G., Gianowski, S., Nielson, R., Thomas, P., Kejarimal, A.,
 Todd, M.A., Tanenbaum, D.M., Civeello, D.R., Lu, F., Murphy, B.,
 Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
 Adams, M.D. and Cargill, M.
 Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios
 Science 302 (5652), 1960-1963 (2003)

JOURNAL PUBMED 14671302
 2 (bases 1 to 879)
 Clark, A.G., Gianowski, S., Nielson, R., Thomas, P., Kejarimal, A.,
 Todd, M.A., Tanenbaum, D.M., Civeello, D.R., Lu, F., Murphy, B.,
 Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
 Adams, M.D. and Cargill, M.
 Direct Submision
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA

TITLE JOURNAL
 This sequence was made by sequencing genomic exons and ordering
 them based on alignment

FEATURES
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 Db 593 GGAACCTGCGGCGCATCTACTCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 652
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 Db 653 CTGCGGTGGCATTCCTGT 712
 Qy 980 CCATCTCTACGCTTCTGT 1039
 Db 713 CCATCTCTACGCTTCTGT 772
 Qy 1040 CACTGAAGATGAGATGAGGCGGACAGACATAGAGTCCGAATTCAGTTCAAGA 1097
 Db 773 CATCTGCTGCGGCGCATCTACTCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 830

RESULT 9
 AK044178
 LOCUS DEFINITION
 AK044178 2940 bp mRNA linear HTC 19-SEP-2003
 Mus musculus 10 days neonate cortex cDNA, RIKEN full-length
 enriched library, clone:A830097K10 product:INOCICEPTIN RECEPTOR
 (ORPHANIN FQ RECEPTOR), full insert sequence.

ACCESSION AK044178
 VERSION AK044178.1 GI:26090219
 KEYWORDS HTC; CAP trapper.
 SOURCE Mus musculus (house mouse)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1
 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning
 Meth. Enzymol. 303, 19-44 (1999)
 99279253
 10349636

REFERENCE 2
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Komu, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes
 Genome Res. 10 (10), 1617-1630 (2000)
 20499374
 11042159

JOURNAL MEDLINE
 PUBMED 11076861

REFERENCE 3
 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
 Komu, H., Akiyama, U., Nishi, K., Kitanaka, T., Tashiro, H., Itoh, M.,
 Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
 Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kaishiwagi, K.,
 Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matsubiki, M.,
 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsumura, S., Kawai, J.,
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A. and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer
 Genome Res. 10 (11), 1757-1771 (2000)
 20530913
 11076861

JOURNAL MEDLINE
 PUBMED 11076861

REFERENCE 4
 The RIKEN Genome Exploration Research Group Phase II Team and the
 FANTOM Consortium.
 Functional annotation of a full-length mouse cDNA collection
 Nature 409, 685-690 (2001)

TITLE JOURNAL
 REFERENCE 5
 The FANTOM Consortium and the RIKEN Genome Exploration Research
 Group Phase I & II Team.
 Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)

JOURNAL MEDLINE
 PUBMED 12401400

REFERENCE 6
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,

Fukuda, S., Furuno, M., Hanezaki, T., Hara, A., Hasehira, W.,
 Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
 Hori, F., Imocani, K., Ishii, Y., Itoh, M., Kawaga, I., Kasukawa, T.,
 Katoh, H., Katoh, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
 Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
 Nakamura, M., Nishi, K., Nomura, K., Nunazaki, R., Ohno, M., Ohsato, N.,
 Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
 Sano, H., Saeki, D., Shibata, K., Shingawa, A., Shiraki, T.,
 Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takeki-Akchira, S.,
 Takeda, Y., Tanaka, T., Tomaru, A., Toyota, T., Yasunishi, A.,
 Muramatsu, M. and Hayashizaki, Y.
 Direct Submission
 Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
 Physical and Chemical Research (RIKEN), Laboratory for Genome
 Exploration and Research Group, RIKEN Genomic Sciences Center (GSC),
 RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama
 Kanagawa 230-0045, Japan (E-mail: genome-tesgscg.riken.go.jp,
 URL: http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
 Fax:81-45-503-9216)
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Please visit our web site for further details.
 URL: http://genome.gsc.riken.go.jp/
 URL: http://genom.gsc.riken.go.jp/.

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DB	363	GGGGGGCTCTGGGGAACTGCTCTGTCATCTGGAGGGGACATGAGGGAACTGAGACG 422
QY	255	CCGATATCAAAAGATGAAGACAGCAACCAACTTTACATATTTAACTGTGGCTTGGCAGA 314
DB	423	CAGGACACCAAGATGAAGAGACTGTCAACAACTTTACATATTTAACTGTGGCACTGGCTGA 482
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AK043275	LOCUS				
DEFINITION	Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:A730079J19 product:MOTICPPTIN RECEPTOR (ORPHANIN FQ RECEPTOR), full insert sequence.				
ACCESSION	AK043275				
VERSION	AK043275.1	GI:26089596			
KEYWORDS	HTC; CAP trapper.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE					
AUTHORS	Carninci, P. and Hayashizaki, Y.				
TITLE	High-efficiency full-length cDNA cloning				
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)				
MEDLINE	99279253				
PUBMED	10349636				
REFERENCE					
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, H., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.				
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to				

RESULT 10	
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LOCUS	AK043275
DEFINITION	2974 bp mRNA linear HTC 19-SEP-2003
ACCESSION	AK043275
VERSION	AK043275.1 GI:26089596
KEYWORDS	HTC; CAP trapper.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1
AUTHORS	Carninci, P. and Hayashizaki, Y.
TITLE	High-efficiency full-length cDNA cloning
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)
MEDLINE	99279253
PUBMED	10349636
REFERENCE	2
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okaaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)

JOURNAL
MEDLINE
PUBMED
11042159

REFERENCE
AUTHORS
3
Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
Konno,H., Akiyama,J., Nishi,K., Kitsuana,T., Tashiro,H., Itoh,M.,
Sunf,N., Ishii,Y., Nakamura,S., Hazama,M., Nishino,T., Harada,A.,
Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
Fujiwaki,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watanishi,M.,
Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J.,
Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)

JOURNAL
MEDLINE
PUBMED
20530913

REFERENCE
AUTHORS
4
The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)

JOURNAL
MEDLINE
PUBMED
11076861

REFERENCE
AUTHORS
5
The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

JOURNAL
MEDLINE
PUBMED
11042159

REFERENCE
AUTHORS
6
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
Hayashida,K., Hayatsu,N., Hiramoto,K., Hirooka,T., Hirozane,T.,
Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
Kato,H., Kawaji,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
Nakamura,M., Nishi,K., Nomura,K., Nunazaki,R., Ohno,M., Ohsato,N.,
Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
Sano,H., Sasaki,D., Shibata,K., Shingawa,A., Shiraki,T.,
Sugabe,Y., Tagami,M., Tagawa,A., Takahashi,P., Takaki-Akita,S.,
Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
Muramatsu,M. and Hayashizaki,Y.
Direct Submission

JOURNAL
MEDLINE
PUBMED
11042159

REFERENCE
AUTHORS
7
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsukuba, Ibaraki,
Kanagawa 230-0045, Japan (E-mail: genome-res@sc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.go.jp/
URL: http://fantom.gsc.riken.go.jp/
Location/Qualifiers

JOURNAL
MEDLINE
PUBMED
11042159

REFERENCE
AUTHORS
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ORIGIN
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1281 CAGGAT 1287
RESULT 11

AK031926 3101 bp mRNA linear HTC 18-SEP-2003
 LOCUS Mus musculus adult male medulla oblongata cDNA, RIKEN full-length
 DEFINITION enriched library, clone:6330500C19 product:NOCICEPTIN RECEPTOR
 (ORPHANIN FQ RECEPTOR), full insert sequence.
 ACCESSION AK031926
 VERSION AK031926.1 GI:26082601
 KEYWORDS HTC; CAP trapper.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1
 AUTHORS Carninci, P. and Hayashizaki, Y.
 TITLE High-efficiency full-length cDNA cloning
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)
 MEDLINE 99279253
 PUBMED 10349636
 REFERENCE 2
 AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
 JOURNAL prepare full-length cDNA libraries for rapid discovery of new genes
 MEDLINE 20499374
 PUBMED 11042159
 REFERENCE 3
 AUTHORS Shibata, K., Itoh, M., Atzawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
 Konno, H., Akiyama, J., Nishi, K., Katsunari, T., Tashiro, H., Itoh, M.,
 Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
 Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
 Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matsubara, M.,
 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 TITLE RIKEN integrated sequence analysis (RISA) system--384-format
 JOURNAL sequencing pipeline with 384 multicapillary sequencer
 MEDLINE 20530913
 PUBMED 11076861
 REFERENCE 4
 AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the
 JOURNAL PANTOM Consortium.
 MEDLINE Functional annotation of a full-length mouse cDNA collection
 PUBMED Nature 409, 685-690 (2001)
 REFERENCE 5
 AUTHORS The PANTOM Consortium and the RIKEN Genome Exploration Research
 JOURNAL Group Phase I & II Team.
 MEDLINE Analysis of the mouse transcriptome based on functional annotation
 PUBMED of 60,770 full-length cDNAs
 REFERENCE 6
 AUTHORS Nature 420, 563-573 (2002)
 JOURNAL (bases 1 to 3101)
 MEDLINE Adachi, J., Atzawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
 Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, M.,
 Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
 Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
 Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
 Koyata, K., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
 Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
 Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
 Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
 Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takekura, A.,
 Tanaka, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
 Muramatsu, M. and Hayashizaki, Y.
 TITLE Direct Submission
 JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
 Physical and Chemical Research (RIKEN), Laboratory for Genome
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
 RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
 Kanagawa 230-0045, Japan (E-mail: genome-research.riken.go.jp,
 URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,
 Fax: 81-45-503-9216)
 COMMENT cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Please visit our web site for further details.
 URL: http://genome.gsc.riken.go.jp/
 URL: http://fantom.gsc.riken.go.jp/.
 Location/Qualifiers
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 /organism="Mus musculus"
 /mol_type="mRNA"
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 /db_xref="MG1:2395305"
 /db_xref="taxon:10090"
 /clone="6330500C19"
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 /tissue_type="medulla oblongata"
 /clone_lib="RIKEN full-length enriched mouse cDNA library"
 /dev_stage="adult"
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 /note="NOCICEPTIN RECEPTOR (ORPHANIN FQ RECEPTOR)
 (SWISSPROT P35377, evidence: FASTA, 97.1%ID, 100%length,
 match=1135)
 putative"
 3078..3083
 polyA_signal
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 3101
 polyA_site
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 ORIGIN
 Query Match 28.3%; Score 327; DB 11; Length 3101;
 Beef Local Similarity 63.4%; Pred. No. 1.3e-52;
 Matches 536; Conservative 0; Mismatches 300; Indels 9; Gaps 2;
 254 TCCGATACCAAGATGAAGACAGACGACCAACATTTACATATTAACTGCTGGCAG 313
 580 TCAGGCACACCAAGATGAAGACTGCTACCAATTTACATATTATCTGGCAGCTGG 639
 314 ATGCTTTAGTTACTCAACCATGCTCTTTCAGAGTACGCTCTACTTGAATTCCTGGC 373
 640 ATACCTGCTCTTCTGTCGACATGCTCCCTTCAGGGACAGACATCTTCTGGCTCTGGC 699
 374 CTTTGGGGAGTGTGTGCAAGATGATGATATTCATGATTAATCAACATGTTCCACCA 433
 700 CATTTGGGAATGCACTGTGCAAGACGCTCATTTGATGACTACTCAACATGTTTACCA 759
 434 GCATCTGACCTTGCACATGATGAGCGTGAACCGCTACATGCTCGTGGCCACCCCGTGA 493
 760 GCATCTGACCTTGCACATGATGAGCGTGAACCGTGAACCGTGAACCGTGAACCGTGA 819
 494 AGGCTTGGACTTCCGACACACCTTTGAAGGCAAGATCATCAATCTGCACTGGCTGC 553
 820 GTGCCCTGATGTTGCGACATCAGTAAGCCAGCCGTTAATGTGGCATATGGGCC 879
 880 TGGCTTGGT 933
 554 TGT 933
 880 TGGCTTGGT 933
 614 TCGATGTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 673
 934 ATGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 990
 674 TCATGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 733
 991 TATTTGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1050
 734 GCTACACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 793
 1051 GCTACACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1110
 794 AAGATGCAACCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 853
 1111 AGGATGCAACCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1170

MEDLINE 20296633
 PUBMED 10835645
 REFERENCE 2
 AUTHORS Roest Crolius, H., Jallion, O., Dastiba, C., Ozouf-Costez, C., Fizime, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saulin, M., Bernot, A. and Weissenbach, J.
 TITLE Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
 JOURNAL Genome Res. 10 (7), 939-949 (2000)
 MEDLINE 20359837
 PUBMED 10899143
 REFERENCE 3 (bases 1 to 1053)
 AUTHORS Genoscope.
 TITLE Direct Submission
 JOURNAL Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91106 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
 COMMENT - Web : www.genoscope.cns.fr
 This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/tetraodon.
 FEATURES
 source
 1..1053
 /organism="Tetraodon nigroviridis"
 /mol_type="genomic DNA"
 /db_xref="taxon:99883"
 /clone="098806"
 /clone_11b="G"
 /note="Genoscope sequence ID : COB098DA03Sp1-end : PUC-Or1"
 ORIGIN
 Query Match 27.0%; Score 311.4; DB 29; Length 1053;
 Beat Local Similarity 65.4%; Pred. No. 8.7e-50;
 Matches 588; Conservative 8; Mismatches 229; Indels 74; Gaps 7;
 Db 257 GATACCAAGAATGAAGACAGACCAATATTATTAACCTGGCTTGCGAGATG 316
 961 GGTACACCAAGATGAAGACCGCACCAATCTACACTCTTCACTGGCTTGCGAGCG 922
 317 CTTTATTACTACCAACATGCGCTTTCAGAGTACGGTCTACTTGAATGATTCCTGCGCTT 376
 921 CTATGACCAAGACAGACCGCTCCCTTCAGAGGCGCAAGTACTGATGAAACAGTGTGTGT 862
 377 TTGGGAGTGTCTGTGCAAGATGATTAATTCATTGATTACTACCAATGTTACCAAGA 436
 861 TCGGGAGGTCTGTGCAAACTGTATCGCATTTGATCAACAATGTTTACCAAGA 802
 437 TCTTACCTTGA -CGATGATGAGCGTGA -CGCTAATGTCGGTGTGCAACCGGT -GA 493
 801 TCTTACCTTACCTCCATGATGAGCGTGCACCGCTTACGTTGCTTGTGCAACCGGTGCC 742
 494 AGGCTTTGGACTTCCGACACCGCTTGAAGGCAAGATCATCATATCTGCATCTGGTGC 553
 741 GGGGCTGAGCTTCCGACACCGCGCAAGGCCAATATCATCAAGTGTTCATCTGATGCC 682
 554 TGTCTGATCTGTGGCATCTCTGCAATATGTCCTTGAAGGCAACAAGTCAGGGAAGCG 613
 681 TCTCTCAGACCGTCCGAGAGTCCCGTGAATGATGATGGACGACGAAGAGACGATTAAG 622
 614 TCGA-----
 617
 621 GTGAGTACGAGATCGCGGTGCTCGAGCTCGCAGCAAGATCTGAACTTGTGGTTCTTAC 562
 618 -----TGTGATGAGTGTCTCTTGTGACAGTCCGAGATGATGATCTCTGTGGAGC 669
 561 CCGCAGGGAACATGCGGTGATGCTCAGGTTCCCAAAACGGAAGAACTGG---GAG 505
 670 CTCTTCATGAAGATCTGGCTCTTCACTTTTGGCTTGTGATGCCGTGCTCATCATC 729
 504 ACGACCATGAAGATCTGGCTGTTCATCTTCCCTTGTGGTTCCTGCTCGTCAATCAC 445
 730 GTCTGCTACACCTGATATGATCTGTGGTCTCAAGAGCGTCCGGCTCTTGTGGCTCCGA 789

Db 444 ATCTCTACGGGCTATATAT -CTGGGCTCAAGAGCGTCCGGCTGCTCCGGCTCAAA 386
 790 GAGAAAGATCGCAACCTGTGATGATCAACAGACTGTCTGTGTGTGTCAGTCTTC 849
 385 GAGAAAGACAGAAACCTCGCGGAGATCAACCCCATGTCTGTGTGTGTCGCGCTTC 326
 850 GTCTGCTGTGAGCTCCCATTCATATTCATCCGTGTGAGAGCGTCTGGGAGCACTTC 909
 325 ATGTGTGTGATCTCCATTCATCAATTCATCATGTCAGAGACGATGTCTCCATCGAC 266
 910 CAC---AGACAGCTGTCTCTCCAGTATTACTTGTGATGCGCTTGAAGTATCAAC 966
 265 CACAAGAACCTGTGTGTGTGTGTGTCAGCTGTGATGTCGCTGGGCTCATGAAAC 206
 967 AGTACCTGAATCCCATTTCTTCAAGCTTTTGTATGAAGTTCAAGCGTGTTCGG 1026
 205 AGCAGCTGAACCGGCTCTTCAAGCTTCTCGACGAGAACTTCAAAAGGTGCTTCAAG 146
 1027 GACTTGTCTTTCCTCACTGAAGATGAGATGAGCGCGCAGACACTAGCAGATCCGAA 1085
 145 GACTTGTCTGTGCTCCCGCGCTCCGCTCCGCTCGAGAGAAACAGCTTCTCCAGACAGARA 87

RESULT 14
 EX874804
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 EST.
 Oncorhynchus mykiss (rainbow trout)
 Oncorhynchus mykiss
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 1 (bases 1 to 783)
 GOvoroun, M., Guiguen, Y. and Le Gac, F.
 Construction and primary characterization of normalized cDNA libraries in rainbow trout, *Oncorhynchus mykiss*
 Unpublished (2003)
 JOURNAL
 COMMENT
 INRA - SCRIBE
 Campus de Beaulieu, RENNES cedex, 35042, France
 Tel: 02.23.48.50.09
 Fax: 02.23.48.50.20
 Email: Yann.Guiguen@beaulieu.rennes.inra.fr
 Sequence cleaned of vector, adaptor and repetitions. Contact us at sigenasupport@jouy.inra.fr to obtain the chromatogram of this sequence.
 Plate: 0002 row: 0 column: 24
 Seq primer: M13R.
 FEATURES
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 /dev_stage="from embryos to adults"
 /lab_host="DH10B"
 /clone_11b="AGENAE Rainbow trout multi-tissues-normalized (tcbk)"
 /note="Vector: pT73D-pac; Rainbow trout multi-tissues-normalized + 2 subtractions; Clone distribution : AGENAE Resource Centre, Francois PIMI, Francois Piumi@jouy.inra.fr, INRA, CERA Radiobiologie et Etude du genome (URB), Domaine de Vilvert, 78352, Jouy-en-Josas cedex, FRANCE, +33 (0) 1.34.65.28.02, +33 (0) 1.34.65.22.73"

ORIGIN

Query Match 24.1%; Score 277.6; DB 13; Length 783;
 Best Local Similarity 78.8%; Pred. No. 2.7e-43;
 Matches 331; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

QY 180 CATCATCAGCGGGCTACTCCGTAGTGTTCGTGCGGGCTGTGGGCACTCGCTGCT 239
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 DB 361 CATATACAGCTGTACTCCGTGTGTTTGTGTGGCTGTGGCACTGCTGCT 420

QY 240 CATGTCGTGATCATCCGATACAAAGATGAAGACAGACACATTTACATTTAA 299
 |||||
 DB 421 CATGATGTTATCATAGGATATCAAAAGATGAAGAGCGGCACCAATTTACATTTCAA 480

QY 300 CCGGCTTTGGCAGATGCTTTAGTTACTCAACCATGACCTTTTCAGAGTAGCGTACTT 359
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 DB 481 CTTGGCTTCGCGCAGCGCTGCTGACACAGAGATGCTTTTCAGAGACTGACTACT 540

QY 360 GATGAATTCCTGCGCTTTTGGGAGATGCTGTGCAAGATGATTAATTTCATGATTA 419
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 DB 541 GTTGAACCTGTCGCGCTTTTGGCGAGGTGTGTAAAGTTCATATCATGACTACTA 600

QY 420 CAACATGTTACACAGATCTTACCTTGAACATGATGAGCGTGACCGCTTACATTCGCT 479
 |||||
 DB 601 CAACATGTTACACAGATCTTACCTTGAACATGATGAGCGTGATGATGATGATGAT 660

QY 480 GTGCCACCCCGGTGAAGGCTTTGAGTTCGCGACACCTTGAAGGCAAGATCATCATAT 539
 |||||
 DB 661 GTGCCACCCCGGTGAAGGCTTTGAGTTCGCGACACCTTGAAGGCAAGATCATCATAT 720

QY 540 CTGCATCTGGCTGCTGTGCTCATCTGTTGGCATCTCTGCAATGATCTTTGAAGGCA 599
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 DB 721 GTGATCTGTGATGCTGTGCTGTGCGGACCGGAGATACAGACATTTACTGCGGGGAC 780

RESULT 15
 BF676176 888 bp mRNA linear EST 21-DEC-2000
 LOCUS 602084171P1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248400 5',
 DEFINITION mRNA sequence.
 ACCESSION BF676176
 VERSION BF676176.1 GI:11950071
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 888)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-rcmail.nih.gov
 Tissue Procurement: CLONTECH Laboratories, Inc.
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNLI)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILNLI at:
 http://image.llnl.gov
 Place: LDCM1066 row: n column: 17
 High quality sequence start: 6
 High quality sequence stop: 380.
 Location/Qualifiers
 1..888
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 /db_xref="taxon:9606"
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 /clone_lib="NIH_MGC_83"
 /note="Organ: prostate; Vector: pDNR-LIB (Clontech);
 Site_1: Still (ggcgcctggc); Site_2: Still
 (ggcctatggc); 5' and 3' adaptors were used in cloning
 as follows: 5' adaptor sequence: 5'-CACGGCATATGCGC-3'

ORIGIN

Query Match 23.5%; Score 271.4; DB 10; Length 888;
 Best Local Similarity 83.3%; Pred. No. 4.4e-42;
 Matches 419; Conservative 0; Mismatches 66; Indels 18; Gaps 9;

and 3' adaptor sequence:
 5'-ATTCTAGAGCCGAGGCGCGGCGACATG-dt(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.4
 kb (range 0.5-4.0 kb). 14/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA)."

QY 666 GACCTCTTCATGAAGATCGCTTCATCTTGGCTGCTGATTCCTGCTCCATCAT 725
 |||||
 DB 1 GACCTCTTCATGAAGATCGCTTCATCTTGGCTGCTGATTCCTGCTCCATCAT 59

QY 726 C-ATGCTGTACACCTGATGATTCCTGCTCAAGAGGCTCGGCTCTTCTGACT 784
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 DB 60 CTATGCTGTCTACACCTGATGATTCCTGCTCAAGAGGCTCGGCTCTTCTGACT 119

QY 785 CCGAGAGAAAGATGCAACCTGCTGATGATCACAGACTGCTGCTGCTGCTGCTG 844
 |||||
 DB 120 CCGAGAGAAAGATGCAACCTGCTGATGATCACAGACTGCTGCTGCTGCTGCTG 178

QY 845 TCTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 904
 |||||
 DB 179 TCTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 237

QY 905 CCTGCCACAGACAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 961
 |||||
 DB 238 CTCCACAGACAGACAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 297

QY 962 CCAACAGTAGCTGATTCATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
 |||||
 DB 298 CCAACAGTAGCTGATTCATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 357

QY 1021 TTCGGGAGCTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1078
 |||||
 DB 358 TCCGGAGCTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 417

QY 1079 ----TCCGAATATGATGATGATGATGATGATGATGATGATGATGATGAT 1130
 |||||
 DB 418 GAGCTCCGAATATGATGATGATGATGATGATGATGATGATGATGATGAT 477

QY 1131 TAAACCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1153
 |||||
 DB 478 AAACCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 500

RESULT 16
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 LOCUS 603749479F1 CSECHN04 Gallus gallus cDNA clone CHEST659n20 5', mRNA
 DEFINITION sequence.
 ACCESSION BU219878
 VERSION BU219878.1 GI:25405026
 KEYWORDS EST.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.
 1 (bases 1 to 917)
 Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
 Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
 A Comprehensive Collection of Chicken CDNs
 Curr. Biol. 12 (22), 1965-1969 (2002)
 22335534
 MEDLINE
 12445392
 PUBMED
 COMMENT Contact: Simon Hubbard
 Department of Biomolecular Sciences
 University of Manchester Institute of Science and Technology

(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers

FEATURES

source

1. 917
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="White Leghorn, Hixex"
/db_xref="taxon:9031"
/clone="ChEST659n20"
/tissue_type="whole embryo"
/dev_stage="20-21"
/lab_host="DH10B"
/clone_lib="CSEQCHN04"
/note="Organ: whole embryo; Vector: pBluescript II KS(+);
Site 1: EcoRI; Site 2: NotI; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunt-ended, ligated to NotI adapters, digested with
EcoRI, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."

ORIGIN

Query Match 23.3%; Score 268.6; DB 13; Length 917;
Best Local Similarity 65.7%; Pred. No. 1,6e-41;
Matches 441; Conservative 0; Mismatches 219; Indels 11; Gaps 3;

QY 372 GCCTTTGGGAGTGCCTGCAAGTATGTAATTTCCATTGATTAACAATGTTGAC 431
DB 1 GCCATTGGTCAATCTCTTGTAAAGTTGTATTCACATAGACTACTAACAATGTTGAC 60
QY 432 CAGCATCTTTCACCTTGACCATGATGAGCGCTGACCGCTACATTCGCGTGCACCCCGT 491
DB 61 CAGTATCTTTTACACTGTGACCATGATGATGATGCTAGTACCGCTTGGCACCCAGT 120
QY 492 GAAGCCTTTGACTTCGCAACCCCTTGAAGCAAAAGATCATATATTCGATCTGCT 551
DB 121 CAAGGCCCTTGAATTCGATCCGACCCCAAGAAATGTCATATGTCGCAACTGAT 180
QY 552 GCTGTCGATCTGTTGGATCTGTCGATATCTTGGAGGACCAAGTACAGGAAGA 611
DB 181 TCTTCTCTTGCATATGCTCTCCAGTTATGTTATGGCACTACTAAATPACAGGCAAG 240
QY 612 CGTCGATGTCATGATGCTCTCTTGGAGTCCCAAGATGATGACTACTCTCGTGGAGACT 671
DB 241 CTCTATGATCTGCACACCTACATCTCCACCCCTGT-----TGTACTGGGAAAA 291
QY 672 CTTCATGAAGATCTGGGCTTCTTATCTTTCCTGATCTCTGTCCTCATCATCTCT 731
DB 292 CCTACTGAAATATCTGTGTCTATCTTTCCTTCAATCATGCAAGTCTGATCATTA 351
QY 732 CTGCTACACCCGATGATCTGCTGTCAGAGCGCGCGCTCTTTCGCTGCCGAGA 791
DB 352 GTGCTATGGGCTGATGATTTTACGGCTTAAAGAGTGCACCATGTTATCTGCGCTTAA 411
QY 792 GAAAGATCGCAACTGCGTGAATACCAAGACTGCTGCTGCTGCTGCTGCTGCTGCT 851
DB 412 GAAGGACAGGAACCTGCGAAGATACCAAGATGTTCTTGTATGATGCTGCTGCTTAT 471
QY 852 CGTCTGCTGATCTCCATTCACATATTAATCTGCTGCTGCTGCTGCTGCTGCTGCT 911
DB 472 CATCTGCTGATCTCCATTCACATATTAATTAATTAAGCTGCTGCTGCTGCTGCTGCT 531
QY 912 CAGCAC-AGCTGCTCTCTCAGCTATTAATTTCTGATGCTGCTTAAAGCTATA-CGAAAGT 969

DB 532 AACTACTTTCAGACATGCTCTCCCTGGCACTTTTGTATGCTTTAGTATATAAATAAC 591
QY 970 AGCTGAATCCCATTTCTTACCCCTTTTGTATGAGAAACTTACAGCGGTCTTCCGGAC 1029
DB 592 TGCCTCAATCCAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 651
QY 1030 TTCTGCTTCC 1040
DB 652 TTCTGATCTCC 662

RESULT 17
LOCUS BB588668
DEFINITION BB588668 RIKEN full-length enriched, adult male hypothalamus Mus
ACCESSION BB588668
VERSION BB588668.2 GI:16449788
KEYWORDS EST
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Arai, K., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J.,
Kono, H., Kondo, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K.,
Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K.,
Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T.,
Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,
Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Arai, K., et al. 2001)
Unpublished (2001)

TITLE
JOURNAL
COMMENT On Nov 30, 2000 this sequence version replaced gi:11485212.
Contact: Yoshinori Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suenho-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gs.c.riken.go.jp
URL: http://genome.gsc.riken.go.jp/

Carinci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
Wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T.,
Matsunaga, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, K., Kira, A.
and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Kono, H., Fukumishi, Y., Shibata, K., Itoh, M., Carinci, P.,
Sugahara, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo, S., Shingawa, A., Saito, T., Kiyosawa, H., Yamanka, I.,
Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
Hayashizaki, Y.

Computational Analysis of Full-length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp/) for
further details.
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse cDNAs.

Db 412 CTTGCGTGTGTCGAAGGGCTGGGGGTTGAGCCGGGAGAGAGATGCGGTGGCAATTCT 471
Qy 936 TTACTTTCGATCGCTTGGGCTATACCAAGTACCTGATCCATTCTCTACGCCCTT 995
Db 472 GCGCTTCGACAGGGCCCTGGCTACGTCACAGCTCCCTCAACCCCATCTCTACGCCCTT 531
Qy 996 TCTTATGAAAACTTCAAGGGGTGTTCCGGGAGCTTCTGCTTCCACTGAAGTGAAGAT 1055
Db 532 CTTGATGAGAACTTCAAGGCCCTCTTCGCAAGTTCGTCTGTGCTTGTGCCCTGGCCG 591
Qy 1056 GGAGCGGAGAGACACTAGCAGAGTCCGAATACATTCACTCAGA 1097
Db 592 GGACGTCGAGGTGTGTGACCGGGGTGGCAGCATTTGCCAAGGA 633

RESULT 19
AY400827 1176 bp DNA linear GSS 15-DEC-2003
LOCUS Homo sapiens SSTR1 gene, VIRTUAL TRANSCRIPT, partial sequence.
DEFINITION genomic survey sequence.
ACCESSION AY400827
VERSION AY400827.1 GI:39756816
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1176)
AUTHORS Clark,A.G., Ghanowski,S., Nielson,R., Thomas,P., Kejaritwal,A.,
Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
Periera,S., Wang,G., Zheng,X.H., White,T.J., Slinky,J.J.,
Adams,M.D. and Cargill,M.
Interfering nonneutral evolution from human-chimp-mouse orthologous
gene trios
TITLE
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1176)
AUTHORS Clark,A.G., Ghanowski,S., Nielson,R., Thomas,P., Kejaritwal,A.,
Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
Periera,S., Wang,G., Zheng,X.H., White,T.J., Slinky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
TITLE Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source location/Qualifiers
1..1176
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
gene <1..>1176
/gene="SSTR1"
/locus_tag="HCM0687"

ORIGIN
Query Match 19.9%; Score 229.6; DB 29; Length 1176;
Best Local Similarity 55.1%; Pred. No. 6e-34;
Matches 523; Conservative 0; Mismatches 409; Indels 10; Gaps 3;

Qy 75 CAGCAGCCGCTGTTCCCGGCTGGGCGGAGCCCAAGCAAGGAGCGCGGCTCGGA 134
Db 72 CGGCGGAGCAAGGGGCCCGGCGGCGCTCGGAGCGCATGAGAGAGCCAGGCGGAAA 131
Qy 135 GAGACGCGAGCTGAGAGCCCGGCGCACTCTCCCGGCGCATCCGGTCAATCAGCGCGGT 194
Db 132 TGCCTCCCAAGACGGACCTTGAAGAGAGGCGGACGCGCATCTCTTTTCA 191
Qy 195 CTACTCCGTAAGTTCGTGCTGCTGGGCTTGGTGGCAACTGCTGTCATGTTGATCAT 254
Db 192 CTACTCCGTAAGTTCGTGCTGCTGGGCTTGGTGGCAACTGATGTCATCTAGTATCT 251

Qy 255 CCGATACAAAGATGAAGACAGCAACCAATTACATATTTAAGCTGGCTTGGCAGA 314
Db 252 GCGCTATGCGCAAGATGAAGACAGGCGGACCAACATCTAATCTTAACTGGCACTTGTGA 311
Qy 315 TGCCTTAAGTACTAACAACCATGCGCTTTGAGAGTACGGTCTACTTGATGAATTCCTGGCC 374
Db 312 TGAGCTGTCATGCTCAGCGGTGCCCTTCTAATGACCTTCAGGTTGTGGCCACATGGCC 371
Qy 375 TTTTGGGAGATGCTGTGTGAAGATAGTAATTTTCATTAATTAATACAAATGTTACCG 434
Db 372 CTTGCGTGGCTGCTCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 431
Qy 435 CATCTTCACTTGAACCATATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 494
Db 432 CATCTAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 491
Qy 495 GGCCTTGAAGCTTCCGACACCCCTTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 554
Db 492 GCGGCGCGCTACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 551
Qy 555 GTCCTCATCTGTGGCATCTGCAATAGTCTTGGAGGACCAAGTCAAGGAGAGAGCT 614
Db 552 ATGCTGTGCTGTGATCTGCGCATGCGCATGCGTGTCTCTGCGCGGCGGCGGCGGCGG 611
Qy 615 CGATGTCATTAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 674
Db 612 CACGG---TGGCTTGAACATGCTCTATGCGCAAGGCGGCTCAACGCTGCTGCTGCTGCT 668
Qy 675 CATGAAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 734
Db 669 GCT---GTTGTACACATTTCTATGAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 725
Qy 735 CTACACCTGATGATCTGCGCTCAAGAGCTCGGCTCTCTTCTGCTGCTGCTGCTGCTGCT 794
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Qy 795 AGATGCAACCTGCGGAGGATGACCAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 854
Db 786 CAGGCGCTGCGGAGGCGGAGATCATCTTAATGATGATGATGATGATGATGATGATGATGAT 845
Qy 855 CTGCTGAGATCTCCATTCATATATTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 914
Db 846 CTGCTGAGATCTCTTCTACGTGTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 905
Qy 915 CACAGCTGCTCTCTCAAGTATTAATCTTGCATTCGCTTGAAGCTATACCAAGATGCTCT 974
Db 906 CACGCTGAGTCT-----AGCTGCGTCTATCTCTGCGCTATGCGCAAGCTGCTGCG 953
Qy 975 GAATCCCATTTCTAGCGCTTCTTGAAGAACTTCAAGGGGTGCTCC 1024
Db 954 CAACCCCATCTCTATGCTTCTCTGACAGCACTTCAAGCGCTCTTTC 1003

RESULT 20
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LOCUS UI-M-BH3-ssd-d-09-0-UI-r1 NIH_BMAP_M_S4 Mus musculus cDNA clone
DEFINITION UI-M-BH3-ssd-d-09-0-UI 5', mRNA sequence.
ACCESSION BE649947
VERSION BE649947.1 GI:9975771
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 389)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
PUBMED 8889548
COMMENT Contact: Chin, H


```

Db      315 GCTGTCATGCTCAGAGTCCCTTTCTGTGTCACCTTCACAGCGCTTGGCCACCTGGCCCTT 374
Qy      378 TGGGAGATGCTGTGTCAGAGATAGTAATTTCCATTGATTAACACATGTTACACAGCAT 437
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Db      435 CTACTGCTGACTGTGCTTGTAGTGGACCGCTATGTGGTGTGTGTGTCACCCCATTCAGAGC 494
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Db      495 AGCGGGCTACCGTCCGCCACATGTGGCCAAAGTAGAAGACCTGGGGTGTGGGTCTGTGTC 554
Qy      558 GTCATCTGTGGCATCTCTGCATAATAGTCTTGGAGGCGCAAGAGTCAGGAAAGAGCTGCA 617
Db      555 ATTACTGGTATTCTTGGCCCATGCTGTGTCTTCTCAGCCACCGCAGCCAGATGGCAC 614
Qy      618 TGTCAATGAGTCTCTTGGCAGTTCGCCAGATGATGATCTCTGGTGGGACCTCTTCAT 677
Db      615 GG---TAGCTTGCACATGCTCATGCGCCGAGCCCGCCAGCGCTG3TGTGGGCTTGT 671
Qy      678 GAAGATCTGCGCTTTCATCTTGGCTTGGTCCGTGATCCCTGCTCATCATCATGCTGCTGCTA 737
Db      672 ---CTTATACACATTTTCATGAGGCTTCTGCTGCTGCTGCTGCGGGCCATTTGCTGTGTTA 728
Qy      738 CACCTGATGATCTGCGCTGCTCAAGAGCGTCCGGCTCTTCTGCTGCTCCGAGAGAGAGA 797
Db      729 TGTGCTCATCATTTGCCAAGATGCGCATGCTGAGCGCTCAAGGCTGGGTGACAGAGGCA 788
Qy      798 TGGCAACCTGCGTGAAGATCCAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 857
Db      799 GGGCTCAGAGCCCAAGATCATCTATATGATGATGATGATGATGATGATGATGATGATG 848
Qy      858 CTGAGCTCCCATTCACATATTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 917
Db      849 CTGAGTGCCTTCTCTAGTGTGATAGCTGTCAACGTTTCCGCGAGCAAGAGAGAGCCGAC 908
Qy      918 AGCTGCTCTCTCAGCTATTAATCTTCTGATGCTGCTTGAAGCTTATACCAACAGTAGCCTGA 977
Db      909 CGTGAAGC-----AGTGTCTGTCAATCTCGGCTATGCAACAGCTGTGCCAA 956
Qy      978 TCCCATTTCTTACGCTTCTTCTGATGAGAACTTCAAGCGGTGTTCCGGGACTTC 1032
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RESULT 22
AK046464      2014 bp      mRNA      linear      HTC 20-SBP-2003
LOCUS      AK046464
DEFINITION      Mus musculus adult male corpora quadrigemina cDNA, RIKEN
full-length enriched library, clone:B230396D21 product:SNOMATOSTATIN
RECEPTOR TYPE 1, full insert sequence.
ACCESSION      AK046464
VERSION      AK046464.1 GI:26338112
KEYWORDS      HTC; Cap trapper.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
REFERENCE      Carninci, P. and Hayashizaki, Y.
TITLE      High-efficiency full-length cDNA cloning
JOURNAL      Meth. Enzymol. 303, 19-44 (1999)
MEDLINE      99279253
PUBMED      10349636
REFERENCE      Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
AUTHORS      Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE      Normalization and subraction of cap-trapper-selected cDNAs to
JOURNAL      prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)

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MEDLINE      20499374
PUBMED      11042159
REFERENCE      3
AUTHORS      Shibata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P.,
Kono, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matsura, S., Kawai, J.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE      RIKEN integrated sequence analysis (RISA) system--384-format
JOURNAL      sequencing pipeline with 384 multicapillary sequencer
MEDLINE      Genome Res. 10 (11), 1757-1771 (2000)
PUBMED      20530913
REFERENCE      4
AUTHORS      The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
TITLE      Functional annotation of a full-length mouse cDNA collection
JOURNAL      Nature 409, 685-690 (2001)
REFERENCE      5
AUTHORS      The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
TITLE      Analysis of the mouse transcriptome based on functional annotation
JOURNAL      of 60,770 full-length cDNAs
PUBMED      Nature 420, 563-573 (2002)
REFERENCE      6
AUTHORS      (bases 1 to 2014)
ADACHI, J., AIZAWA, K., AKIMURA, T., ARAKAWA, T., BONO, H., CARNINCI, P.,
FUKUDA, S., FURUKO, M., HANAGAKI, T., HARA, A., HASEHIZUME, M.,
HAYASHIDA, K., HAYATSU, N., HIROMOTO, K., HIRAKA, T., HIROZANE, T.,
HORI, F., IMOTANI, K., ISHII, Y., ITOH, M., KAGAWA, I., KASUKAWA, T.,
KATCHI, H., KAWAI, J., KOJIMA, Y., KONDO, S., KONO, H., KONDA, M.,
KOYA, S., KURIHARA, C., MATSUYAMA, T., MIYAZAKI, A., MURATA, M.,
NAKAMURA, M., NISHI, K., NOMURA, K., NUMAZAKI, R., OHNO, M., OHSAO, N.,
OKAZAKI, Y., SAITO, R., SAITOH, H., SAKAI, C., SAKAI, K., SAKAZONO, N.,
SANO, H., SASAKI, D., SHIBATA, K., SHINGAWA, A., SHIRAKI, T.,
SOGABE, Y., TAGAMI, M., TAGAWA, A., TAKAHASHI, F., TAKEKURA, K.,
TAKEDA, Y., TANAKA, T., TOMARU, A., TOYA, T., YASUNISHI, A.,
MURAMATSU, M. and HAYASHIZAKI, Y.
TITLE      Direct Submision
JOURNAL      Submitted (16-JUN-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-reseq@riken.go.jp,
URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
COMMENT      cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/
URL:http://fantom.qualifiers
1. 2014
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="PANTOM,DB:B230396D21"
/db_xref="WGI:2411874"
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/dev_stage="adult"
426. 1601
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CDS

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ORIGIN

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Query Match      19.6%; Score 226.6; DB 11; Length 2014;
Best Local Similarity 54.8%; Pred. No. 2.8e-33;
Matches 523; Conservative 0; Mismatches 414; Indels 18; Gaps 3;

QY 78 CAGCCGCTGGTTCCTCCGCTGGGCGAGCCGACAGCAAGCGAGCGGCTCGAAGA 137
DB 500 CTGACAGCAGGGGTCCGGGGTCCGGGCTGGCGACGGCAGGAAGAGCCCTGGAGAAAGCG 559
QY 138 CGCGAGCTGAGCCCGCGCACATCTCCCGGCATCCCGTCATCATCAGCGGCTCTA 197
DB 560 TTCCAGAGATGGAGACTTAAGCAGAGGACAGGATAGCCCATCTCATCTCTTTATCTTA 619
QY 198 CTCCTAGTGTTCGTGCTGGGCTTGGTGGCACTCGCTGTCTATGTTCTGTATCATCG 257
DB 620 CTCCTGGATGCTTGGTGGGCTGTGGGGAACCTTAATGTCATCTATGATCTCTGG 679
QY 258 ATACCAAGATGAAGACAGCAACCACTTTACATATTTAACTGGCTTTGGCAGATGC 317
DB 680 CTACCCCAAGATGAAGACCGCTACCAACATCTAACTTAACTGGCTATTTGCTGATGA 739
QY 318 TTTAGTCTACCAACCATGCTCTTCAAGATGAGCTCTAGTATGAATCTTGGCTTT 377
DB 740 GGTGCTCATGCTCAGAGGTCCTTCTGTGTCCTTCCAGCTGTGGCCGACATGAGCTT 799
QY 378 TGGGATGTGCTGTGCAAGATAGTATTTCAATTGATTACTTAAACATGTTTACAGCAT 437
DB 800 CGGCGCGCTACTTTCGCGCTGGTGTCTCAGCTGATGGGTCACATGTTTACAGCAT 859
QY 438 CTTCACCTTGACATGATGAGGTGAGCCGCTACATTTGGCTGGCCACCCCGTAAAGC 497
DB 860 CTACGTCTGATGCTGTGTTAGTGTGACCGCTATGTGTGTGTGCAACCCGATAAAGC 919
QY 498 TTTGACTTCCGACACCTTGAAGCAAAAGATCAATATCTGATCTGGCTCTGTC 557
DB 920 AGCGGCTACCGTCCGCCCATCTGTGGCAAAAGTAACTGTGAGCTGTGTGCTGTG 979
QY 558 GTCACTGTGTGCACTCTGCAATAGTCTTGGAGGACCAAAAGTCAAGGAAAGAGCTGA 617
DB 980 ATTACTGGTTATCTTGGCCATGCTGTGTCTTCTCAGCAGCCGACCAAGCATGGCAC 1039
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QY 678 GAAAGATGCGCTCTCATCTTTGCTGTGATCTCCCTGCTCATCATCATGCTGTGCTA 737
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QY 798 TCGCACTGCTGAGATCAACAGCTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 857
DB 1214 GCGCTCAAGAGCGCAAGATCACTTAATGATGATGATGATGATGATGATGATGATG 1273
QY 858 CTGAGCTCCCATTTACATATTTGATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 917
DB 1274 CTGAGTGTCTTTCTACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1333
QY 918 AGTGTCTCTTCAAGCTATTAATCTTGTGATGCTTGAAGCTTAAGCTAATACCAAGATGCTGA 977
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DB 1334 CGTGAGCC-----AGTGTCTGTATCATCTGGGCTATGCAACACATGTGCCAA 1381
QY 978 TCCATTTCTTACGCTTTCTTGAAGAACTTCAAGCGGCTTTCCGGGACTTC 1032
DB 1382 CCCCATCTCTTACGCGCTTCTGTGTGGACAACTCAAGCGCTCTTTCAGCGCATC 1436
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RESULT 23

BM543468

LOCUS

DEFINITION

AGENCOURT 6492534 NIH_MGC_124 Homo sapiens cdna clone IMAGE:5726549

ACCESSION

BM543468

VERSION

BM543468.1

KEYWORDS

EST.

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE

1 (bases 1 to 980)

TITLE

NIH-MGC http://mgc.nci.nih.gov/.

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cga@bbs-rcmail.nih.gov

Tissue Procurement: Invitrogen

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LIML at:

http://image.llnl.gov

Plate: LIML2719 row: d column: 06

High quality sequence stop: 711.

FEATURES

source

1..980

Location/Qualifiers

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5726549"

/tissue_type="hippocampus"

/lab_host="DH10B"

/clone_id="NIH_MGC_124"

/note="Organ: brain; Vector: pCMV-Sport6; Site 1: EcoRV

/destroyed: Site 2: NotI; RNA source male hippocampus,

age 27. Library is oligo-dT primed and directionally

cloned (EcoRV site is destroyed upon cloning). Average

insert size 1.4 kb, insert size range 0.9-4 kb. Library is

normalized and enriched for full-length clones and was

constructed by C. Gruber (Invitrogen). Research Genetics

tracking code 012."

ORIGIN

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Query Match      19.5%; Score 224.6; DB 12; Length 980;
Best Local Similarity 64.8%; Pred. No. 5.2e-33;
Matches 383; Conservative 0; Mismatches 199; Indels 9; Gaps 3;

QY 153 CGCGCAATCTCCCCCGGCATCCCGGTCAATACAGCGGCTCACTCCGATGTTGCT 212
DB 295 CGCCTTCTGCGCTCCGCGGCTCAAGGTCAACCATGTGGGCTCTAATCGCGCGTGTGT 354
QY 213 CGTGGGCTTGGTGGCAACTGCTGTGATGTTGCTGATCATCCGATACCAAGATGAA 272
DB 355 CGAGGGGCTCTGGGGAATGCTCTTGTCAATGATGATCTTCAAGGACACCAAAATGAA 414
QY 273 GACAGCAACCAACATTTAATTTAACTGGCTTTGGCAGATGCTTTAGTTACTAACAC 332
DB 415 GACAGCAACCAATTTAATTTAATTTAACTGGCCCTGGCCGACACTGTGCTGTGAC 474
QY 333 CATGCCCTTTCAGAGTACGCTTACTTGATGAATTTCTGGCTTTTGGGATGTGCTGTG 392
DB 475 GCTGCCCTTTCAGAGGCAAGCATCTTCTGGGCTTCTGGCGCTTGGGAAATGGCTGTG 534
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QY 393 CAAGATAGTAATTTCATTGATTACTACACATGTTTACACAGATCTTGACCTTGACCAT 452
DB 555 CAAGACAGTCATGCTGACCTGATCTACACAACTGTCACACACACCTTACCTTAACCTGAC 594
QY 453 GATGAGCGTGAACCGCTACATTCGCGTGGCCACCCCGTGAAGCGCTTGGATCTGCGCAC 512
DB 595 CATGAGTGTGATTCGCTATGTAAGCATCTGCCACCCCATCCGTCCTCGAGTCCGCAC 654
QY 513 ACCCTTGAAGGCAAGATCATCATATCTGATCTGGCTGCTGCTGCTCATCTGTTGGCAT 572
DB 655 GTCCAGCAAGAGCCAGCGCTGTCAATGTGGCCATCTGGGCGCTGCGCTGTGTGCGTGT 714
QY 573 CTCTGCATATAGTCTCTTGAAGGSCACCAAGATCAGGAAAGCGTCATGTCTAGTGTCTC 632
DB 715 TCCCTTCCTGCATCATGAGGCTCGGACAGGTC-----GAGGATGAAGAGATGAGTGCCT 768
QY 633 CTTCGAGTTCCTCAGATGATGATCTACTCTGCTGGAGACCTTTCATGAAGATCTGCGTCT 692
DB 769 GGTGAGATCTCCCTACCCCTCAGAGATTAACG--GGGCGCGGCTGTGTCATCTGACATCTT 826
QY 693 CATCTTTGCGTTCGT-GATCCCTGTCTCATCATCATCTGCTGACACCC 742
DB 827 CCTCTTCTCCTCATCTGTCCTCCCGGCTGCTGTCATCTGTCTGACAGCC 877

RESULT 24
BB641725 632 bp mRNA linear EST 31-AUG-2001
LOCUS BB641725 RIKEN full-length enriched, 10 days neonate cortex Mus
DEFINITION musculus cDNA clone A830044L10 5', mRNA sequence.
ACCESSION BB641725
VERSION BB641725.1 GI:15401708
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 632)
AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T.,
Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J.,
Komno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K.,
Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K.,
Sano,H., Sasaki,D., Shibata,K., Shingawa,A., Shiraki,T.,
Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-ree@gsc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Komno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
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prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Matsuhiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
and Hayashizaki,Y.
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sequencing pipeline with 384 multipillar sequencer. Genome Res.
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Komno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P.,
Sugahara,Y. and Hayashizaki,Y.
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```

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Yamanaka,I., Kiyosawa,H., Kondo,S., Saito,T., Shingawa,A.,
Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K.,
Arakawa,T., Ishii,Y. and Hayashizaki,Y.
Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct.
Func. Genomics 2 pre, 172-186 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
e mouse tissues.
FEATURES
source
location/Qualifiers
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cortex"
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prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTT 3']. cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 20.0 and subtraction to Rot = 459.0. Second
strand cDNA was prepared with the primer adapter of
sequence [5' GAGAGAGATTCCTGACATTAATTAATCCCGCCCCCCC
3']. cDNA was cleaved with XhoI and BamHI. Vector: a
modified pBluescript KS(+) after bulk excision from Lambda
Phi I."
ORIGIN
Query Match 19.3%; Score 223; DB 10; Length 632;
Best Local Similarity 69.4%; Pred. NO. 8.8e-33;
Matches 301; Conservative 0; Mismatches 133; Indels 0; Gaps 0;
QY 93 CGCGTGGCGCGAGCCGACAGCAAGGCGCGCGCTCGAGAGCGCGAGCTGAGGC 152
DB 162 CGCGCTTCCAGCGCGCTTCCCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 221
QY 153 CGCGACATCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 212
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DB 342 GACCGCCACCAACATCTACATCTTCATCTGCTTGGCTGATGCGCGCGCGCGCGCGCG 401
QY 333 CATGCGCTTTCAGAGTACGCTCTACTGATGAATCTCGGCGCTTTTGGGAGATGCTGG 392
DB 402 GCTGCGCTTTCAGAGCGCGCAAGTACTATGAGAAAGTGGCGCGCTTGGCGAGCTCTGG 461
QY 393 CAAGATAGTAATTTCATTGATTACTACACATGTTTACACAGATCTTGACCTTGACCAT 452
DB 462 CAAGCTGNGCTCTTCATCTGATCTACTACACATGTTTACCTGACATCTTACCTCACCAT 521
QY 453 GATGAGCGTGAACCGCTACATTCGCGTGGCCACCCCGTGAAGCGCTTGGATCTGCGCAC 512
DB 522 GATGAGCGTGAACCGCTACATTCGCGTGGCCACCCCGTGAAGCGCTTGGATCTGCGCAC 581
QY 513 ACCCTTGAAGGCAAGATCATCATATCTGATCTGGCTGCTGCTGCTCATCTGTTGGCAT

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[illegible]

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OY		588	TGAGAGCACAAAGTCAGGGAAGACGTGCATGTCAATTAGTGCCTTCAGTTGCCAGA	647
Df		534	GATATACCGCGCCTCCGAGACAACAGTGSGGCGAAGACAGCTGACATCAACTGCGC	593
OY		648	TGATACTACTCTCTGTGGGACCTTTCATGAAAGATCTGCGCTTCATCTTTGCCCTTGT	707
Df		594	AGCGCAATCCGGGCGGTGTACACAGTTTTCAATTCTACGCTTCATCTGGGGTTCT	653
OY		708	GATCCCTGTTCATCATCATCTGTGTGTACACCTGATGATGATCCGTGCGCTCAAGAGCT	767
Df		654	GGTACCCCTTACCATCATTTTGTCTCTGTACTCTGTTTCATCATCATCAAGTAAGCTTC	713
OY		768	CCGGCTCCTTCTGTGGCTCCGAGAAAAGATGCACAACCTGCGTAGATACACAGACTGT	827
Df		714	TGAAATCCGAGTGGGATATATCCAGAGAAAAAGTCAAGAAAAAGTGACCCCGATGT	773
OY		828	CCTGTGTGTGTGCGAGTCTTCTGTCTGTCTGTGACCTCCCATTCATCATATTGATCTGT	887
Df		774	GTCCATCTGATGTGGCTGTCTTCATCTTCTGTGCTGCGCTCCCTTTCATCTTCAAGTCTC	833
OY		888	GGAGGCTCTGGGAGACACTCCACAGACAGACGTGCTCTCTCCAGCTATTACTCTGCAT	947
Df		834	TTCCGTCTGTGTGGCATCACTGCCACCACCCGCTGAAAGCAATTTGATCTTGTGT	893
OY		948	CGCCTTAGGCTATATCCAACAGTAGCCTGATATCCCATCTCTACGCTTTCTTGATAAA	1007
Df		894	GATCCTCACTATGCGAACACAGCTGCGCAACCCCATCTGTACGCTTCTGTCTGACAA	953
OY		1008	CTTCAAGCGGTGTTTCGCGGACTTCTGTCTTTCACCTGAAGATGAG	1052
Df		954	CTTCAAGAGAGCTTCCAGAAATGTTCTTGTGCTGTGTCAGGTGAG	998

RESULT 26
LOCUS B0179053

DEFINITION UI-M-EV0-bwc-j-18-0-UI.r1 NIH BMAP_EVO Mus musculus cDNA clone

ACCESSION B0179053

VERSION B0179053

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 784)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: gcgaps@remail.nih.gov
Tissue Procurement: Dr. James Lin, University of Iowa
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LDLN at:
<http://image.llnl.gov>
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)

Seq primer: pYX-5.
Location/Qualifiers
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FEATURES
source

/lab host="DH10B (T1 phage resistant)"
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 Site 2: Not I; The library was constructed according to
 Bonaldi, Lennon and Soares, Genome Research, 6:791-806,
 1996. Denatured mRNA was size fractionated on a 1% agarose
 gel. First strand cDNA synthesis was primed with an
 oligo-dT primer containing a Not I site. Double stranded
 cDNA was size selected according to mRNA size fraction,
 ligated with EcoR I adaptor, digested with Not I, and then
 cloned directionally into pY-Aac vector. The library tag
 sequence located between the Not I site and the polyA
 tail, is GTGCGTGA. This library was created for the
 University of Iowa Mouse Brain Molecular Anatomy Project
 (BMAP). Gene Discovery in the Developing Mouse Nervous
 System, supported by National Institutes of Mental Health
 (NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN

Query Match 18.9%; Score 217.6; DB 13; Length 784;
 Best Local Similarity 60.6%; Pred. No. 1.1e-31;
 Matches 396; Conservative 0; Mismatches 249; Indels 9; Gaps 2;

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 232 TGCATCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 291
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 745 ATGATCTGCGTCTCAAGAGCGTCCGCTCTTCTGCTGCCGAGAGAGAGAGAGAGAG 804
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RESULT 27
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 DEFINITION Homo sapiens STR2 gene, VIRUTAL TRANSCRIPT, partial sequence,
 genomic survey sequence.

ACCESSION AY400674 GI:39756663
 VERSION GSS.
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 1006)
 Authors Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
 Todd,M.A., Tanendaa,D.M., Civallo,D.R., Lu,F., Murphy,B.,
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
 Adams,M.D. and Cargill,M.
 Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios
 JOURNAL Science 302 (5652), 1960-1963 (2003)
 PUBMED 14671302
 REFERENCE 2 (bases 1 to 1006)
 Authors Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
 Todd,M.A., Tanendaa,D.M., Civallo,D.R., Lu,F., Murphy,B.,
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
 Adams,M.D. and Cargill,M.
 Direct Submission
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 This sequence was made by sequencing genomic exons and ordering
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ORIGIN

Query Match 18.6%; Score 214.8; DB 29; Length 1006;
 Best Local Similarity 54.0%; Pred. No. 4.1e-31;
 Matches 485; Conservative 0; Mismatches 407; Indels 6; Gaps 2;

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 215 TGGGCTGTGGGCACTCGCTGTGATGTTGTGATCATCCGATACAAAGATGAGA 274
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 167 TTTGGTGTGTGGCAACACTGTTCATTATGATCTCTCGCTATGCAAGATGAGA 226
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 275 CAGCAACCACTTATCATATTATTAAGTGTGGAGATGCTTATGATTAACCA 334
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QY TCTTTGGCCTTCGTGATCCCTGTCCTTATCATCATCGTCTGTACACCTGATGATCTCG 754

Db 641 TTTCTGGGGTTCCTGTGATCCCTCACCATCATCTGTCTTGTCTACCTGTTCATTATCATCA 700

QY GTCTCAAGAGCCTCCGGCTCTCTTTCGGGCTCCCGAAGAGAAGATGCGCACCTGCGTAGGA 814

Db 701 AGGTGAAGTCTCTGGAATCCGAGTGGGGCTCTCTTAAGAGAGAAGTCTGAGAGAAAG 760

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Db 821 TATTCACGTTCTTCCGTCCTCCATGCGCATAGCCCTCACCCCGACTTAAAGGATGT 880

QY ATTACTTTCGATGCGCTTAGGCTATACCAACAGTAGCCTGAATCCCATTTCTTAGCCT 994

Db 881 TTGACTTTGTGGTGTCTCACTATGCTAAACAGCTGTGCCAACCTATCTATAATGCTT 940

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LOCUS	linear EST 07-JAN-2002	LOCUS	linear EST 07-JAN-2002
DEFINITION	IMAGE:556221 5' similar to SW:ORF_HUMAN P4146 NOCICEPTIN RECEPTOR ;, mRNA sequence.	DEFINITION	IMAGE:556221 5' similar to SW:ORF_HUMAN P4146 NOCICEPTIN RECEPTOR ;, mRNA sequence.

ACCESSION	BM342951	GI:18079743
VERSION	BM342951.1	
KEYWORDS	EST	
SOURCE	Danio rerio (zebrafish)	
ORGANISM	Danio rerio	

REFERENCE

1 (pages 1 to 425)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (Pages 1 to 429)	Clark, M., Johnson, S. L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucada, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.	Washu Zedrafatish EST Project 1998	Unpublished (1998)	Contact: Stephen L. Johnson

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: zdrafi@watscon.wustl.edu
DNA Library construction by: Joe Barnes and Steve Johnson. DNA
Sequencing by: Washington University Genome Sequencing Center Clonal
distribution: Research Genetics web address:
<http://www.researchgenetics.com/>
Seq primer: T3 ET from Amersham
High quality sequence stop: 413.
Location/Qualifiers
1. .429

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FEATURES
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location/Qualifiers
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 5'-ggcgccgcatataagcattaccata-ctaggg-3'. Second strand
 synthesis was a 3-cycle PCR using the primers
 5'-ggcgccgcatataagcattaccata-ctaggg-3' and
 5'-aagcagctggtaacacagcagcagatctt-ctttttttttttt-3'. cDNA
 was subsequently amplified in a 7-cycle PCR with the
 following primers: 5'-ggcgccgcatataagcattaccata-ctaggg-3' and
 5'-aagcagctggta-accacagcag. Deoxy-UMP adaptors were added in
 a third PCR (5 cycles) and the primers
 5'-cauccaaccacgaugccgcatataagcattaccataaggg-3' and
 5'-ctacucacucacuaagcagctggtaacacagcagcagatct-3'. Ends were
 treated with uracil DNA glycosylase and product with 3'
 overhangs was annealed to complementary ends of PAMp1.
 Insert can be excised using EcoRI and NotI. Library
 constructed by Joe Barnes and Steve Johnson (Washington
 University)."

Query Match	18.5%	Score 214;	DB 12;	Length 429;
Best Local Similarity	69.8%;	Pred. No. 4.2e-31;		
Matches 289; Conservative	0;	Mismatches 125;	Indels 0;	Gaps 0

156 ccggccatccccgcatcacacggcgctactccgaagtgatcgggggctggtg 225
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Oy 226 GGCACCTCGTGTGATGTCGATCATCCGATACAAGATGAAGA CAGCAACC AAC 285
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DY
QY

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 Db 241 TCATTGTTACTATAACATGTTTACACGATGCGTTACCTGGCGGTATGAGATGAT 300
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||||| ||||| ||||| ||||| ||||| ||||| |||||
bh 361 AAGCGTCCATAAATACCTGCTGCCCTTTTGCCCTGCTATTCCTCCCCCTGCTGA 414
||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 29	
AK051189	2432 bp
LOCUS	mRNA linear HTC 20-SEP-2003
DEFINITION	Mus musculus 12 days embryo spinal ganglion cDNA, RIKEN full-length enriched library, clone:DL30013M04 product:somatostatin receptor 4, full insert sequence.
ACCESSION	

ACCESSION AK051189
VERSION AK051189.1 GI:26341779
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE	
AUTHORS	1 Carninci, P. and Hayashizaki, Y.
TITLE	High-efficiency full-length cDNA cloning
JOURNAL	Meth. Enzymol. 303, 15-44 (1999)
MEDLINE	99219253
PMID	10349636
REFERENCE	2

AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Komu, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PUBMED 11042159

REFERENCE AUTHORS 3

Shibata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P., Komu, H., Akiyama, J., Nishi, K., Katsunari, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

TITLE RIKEN integrated sequence analysis (RISA) system-384-format

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

REFERENCE AUTHORS 4

The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409, 685-690 (2001)

REFERENCE AUTHORS 5

The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE AUTHORS 6 (bases 1 to 2432)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Haseizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Komu, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Nunazaki, R., Ohno, M., Onisato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

TITLE Direct Submission

JOURNAL Submitted (16-JUN-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

PLEASE VISIT OUR WEB SITE FOR FURTHER DETAILS.

URL: http://genome.gsc.riken.go.jp/

URL: http://fantom.gsc.riken.go.jp/.

location/Qualifiers

1. 2432

feature

source

organism="Mus musculus"

molecule="mRNA"

strain="C57BL/6J"

db_xref="FANTOM DB:DI30013H04"

db_xref="MGI:241395"

db_xref="taxon:10090"

clone="DI30013H04"

tissue_type="spinal ganglion"

clone_lib="RIKEN full-length enriched mouse cDNA library"

dev_stage="12 days embryo"

130..1287

CDS

/note="unnamed protein product; putative somatostatin receptor 4 (MGDI MGI:105372, GB|NM_009219, evidence: BLASTN, 98%, match=1158)"

/protein_id="BAC34552.1"

/db_xref="GI:26341780"

/translation="MNAAPALPVGEDTTTPGINSANAPDEEEDAMGSDGTAGMVTIOCTVALVGLVGNALVFLVLRARAKMTATNIVLNLAVDELPMGLVFPVASAAALRHPRGAVLCRAVSVNGINMETSFCITLVSVRVYVAVRPAATVRRPVAKLINIGVWLASLTLPLPAVRADTPRAGGEVAVCNLHPHAKSAVPIYTFPLGFLLPVLAIGVCLYLVKMAVALRAGQORRREKKITRLVAVVTFVLCMPFVYQVLNLEFVGLDVTNHNVSILSYANGCAPILVGFSDNFRSFOVALCIRCLLETYTGAAEERPLVYATALKSRGAGGICPPLPCQDEPVOABPCQKQVPFKTKTTP"

ORIGIN

Query Match 18.5%; Score 213.8; DB 11; Length 2432;

Best Local Similarity 54.0%; Pred. No. 9.1e-31;

Matches 496; Conservative 0; Mismatches 402; Indels 21; Gaps 2;

108 CGACAGCAACGCGACGCGCGCTCGAGAGAGCGGACGCTGGAGCCGCGACATCTCCCC

192 CGCCAGCTGGGCTCCGAG

168 GGCATCCCGGCTCATCATCAGCGCGCTACTCCGTAAGTTCGTGCTGGGCTGGTGGG

252 AGCGGCGATGTCATCATCTCAGTGCATCTATCGCTCGTGTGCTGGGCTGGTGGG

228 CAATCGCTGTCATGTTGCTGTCATCATCCGATACCAAGAGTAAAGACAGCAACCAAT

312 AAACGCCCTGGTCATCTTCTGTCATCTGTCATCTGTCATCTGTCATCTGTCATCTG

268 TTACATATTATACCTGCTGTTGGAGAGCTTTACTTACTACCAACAGCCCTTTCAGAG

372 CTACTACTCAACCTGGCGCTGCGAGTAGCTTTCACTGCTGACGCTGCTGCTGCTG

348 TACGCTACTTATGATGAATTCCTGGCTTTGGGAGTGTGCTGCAAGATATATTC

432 CTCGGCGGCTGCGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTG

408 CATGATTAATCAACATGTTTACCAAGATCTTCACTTACCATGATGAGCTGGACCG

492 CGTGACGCGCTGACATGTTTACATGATGTTTCTTGCCTCACCGTCTGACGCTGACCG

468 CTACATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG

552 CTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG

528 GATCATCAATATCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG

612 GCTATCACTCACTGAGAGTGTGCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTG

588 TGGAGCAACCAAGTCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG

672 CGGTACACAGAGCGAGCTGCGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG

732 CCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG

708 GATCCCTGCTCATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG

783 ACTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG

768 CCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG

843 GGCCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG

828 CCGT

903 GCTATGT

888 GGAGGCTGTGGAGACACTCCACAGACAGAGCTCTCTCTACGCTATTAATCTGCTAT

Db 963 GAACCTGTTTGTACCAAGCGCTGATGCACTGT-----CAACATGTGTCCCT 1010

Qy 948 CGCGTTAGGCTATACCAAGCTGCTGATCCCATTTCTGTACGCTTTCTGTGATGAAA 1007

Db 1011 CATCTGAGCTATGCCAAGCTGTGCATCCCATCTCTATGCTCTCTCTGTACAA 1070

Qy 1008 CTTCAAGCGGTGTTCCGG 1026

Db 1071 CTTCCGCGCTCTTTCCAG 1089

RESULT 30
CNS02261
LOCUS
DEFINITION

CNS02261 836 bp DNA linear GSS 01-SEP-2000
Tetradon nigriviridis genome survey sequence T7 end of clone
227103 of library G from Tetradon nigriviridis, genomic survey
sequence.
AL177778.1 GI:7815835
GSS: genome survey sequence.
SOURCE
Tetradon nigriviridis
Tetradon nigriviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodontidae; Tetradon.

REFERENCE
AUTHORS
Roest Crolius, H., Jallion, O., Dasilva, C., Bouneau, L., Fischer, C.,
Bernot, A., Fizames, C., Winkler, P., Brotlier, P., Quetier, F.,
Saurin, W. and Weisenbach, J.
Estimate of human gene number provided by genome-wide analysis
using Tetradon nigriviridis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)

JOURNAL
MEDLINE
PUBMED
20296633
10835645

TITLE
Roest Crolius, H., Jallion, O., Dasilva, C., Ozouf-Costaz, C.,
Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F.,
Saurin, W., Bernot, A. and Weisenbach, J.
Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetradon nigriviridis
Genome Res. 10 (7), 939-949 (2000)

JOURNAL
MEDLINE
PUBMED
10899143
3 (bases 1 to 836)

REFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT
Direct Submission
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetradon nigriviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetradon.

FEATURES
source
1..836
/organism="Tetradon nigriviridis"
/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone="227103"
/clone_11b="G"
/note="Genoscope sequence ID : C0AG227AE02LPI-end : T7"

ORIGIN
Query Match 18.5%; Score 213; DB 29; Length 836;
Best Local Similarity 74.2%; Pred. No. 8.5e-31;
Matches 268; Conservative 1; Mismatches 92; Indels 0; Gaps 0;

Qy 257 GATACCAAGATGAGACAGCAACATTTATCATTTAACTGCTTTGGCAGATG 316

Db 270 GGTACCAAGATGAGACAGCAACATTTATCATTTAACTGCTTTGGCAGACG 329

Qy 317 CTTTAGTTACTACCAACATGCCCTTTGAGAGTACGCTCTACTTGAATTCCTGGCCTT 376

Db 330 CTTAGCCACAGCAACCTCCCTTCAGACGCCAAGTACTATGTAACAGTGCTGT 389

Qy 377 TTGGGATGTGTGTGCAAGATAGTATTTTCATTTACTATACAAACATGTTACAGCA 436

Db 390 TGGGAGACTGTGTGCAAACTGGTCACTGCGATTTGACTATACAAACATGTTACAGCA 449

Qy 437 TCTTACCTTGACCATGATGAGCGTGAACCGCTACATTTGCCGTGGCCACCCGTGAAG 496

Db 450 TCTTACCGCTACCACTGATGAGCGTGAACCGCTACATTTGCCGTGGCCACCCGTGGCG 509

Qy 497 CTTTGACCTTCGCGACACCTTTGAAGCAAGATCATCATATCTGCGTGGCTGT 556

Db 510 CGCTGACCTTCGCGACACCGCTTCGAGCAAGCAAAATCATCATCTTCACTTGATCCTCT 569

Qy 557 CGTCACTGTTGGCATCTCTGCAATAGTCTTTGAGGACCAACAGTCAAGGAGACGTCG 616

Db 570 CTTGACCGCTCGAGATCCCGTGTATGATGATGAGGACGACAGAGAGACGATTAATGTCG 629

Qy 617 A 617

Db 630 A 630

RESULT 31
LOCUS
DEFINITION

CD246184 866 bp mRNA linear EST 22-MAY-2003
AGENCOURT_14127005 NIH_MGC_145 Homo sapiens CDNA clone
IMAGE:6912766 5', mRNA sequence.
CD246184
CD246184.1 GI:1006648
EST.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strauberg, Ph.D.
Email: cgabs-romail.nih.gov
Tissue Procurement: GPCR Consortium
CDNA Library Preparation: GPCR Consortium
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: IRB101 row: b column: 09
High quality sequence stop: 559.
Location/Qualifiers
1..866
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6912766"
/tissue_type="mixed"
/lab_host="DH10B"
/clone_11b="NIH_MGC_145"
/note="Vector: pCDNA3.1; Site 1: varies by clone; Site 2:
varies by clone; ORFs were PCR-amplified and cloned into
pCDNA3.1 by the GPCR Consortium. Cloning sites vary by
clone and include the following: 5'-EcoRV-XbaI/XhoI-3',
5'-EcoRV-XbaI/NotI-3', EcoRV (TA cloned, non-directional).
For information about which gene each clones represents,
please visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearrayed_plates/IRB1_prev.dat
a Note: this is a NIH_MGC Library."

FEATURES
source
1..866
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6912766"
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/lab_host="DH10B"
/clone_11b="NIH_MGC_145"
/note="Vector: pCDNA3.1; Site 1: varies by clone; Site 2:
varies by clone; ORFs were PCR-amplified and cloned into
pCDNA3.1 by the GPCR Consortium. Cloning sites vary by
clone and include the following: 5'-EcoRV-XbaI/XhoI-3',
5'-EcoRV-XbaI/NotI-3', EcoRV (TA cloned, non-directional).
For information about which gene each clones represents,
please visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearrayed_plates/IRB1_prev.dat
a Note: this is a NIH_MGC Library."

ORIGIN
Query Match 18.5%; Score 213; DB 14; Length 866;
Best Local Similarity 66.4%; Pred. No. 8.6e-31;

Matches 306; Conservative 0; Mismatches 155; Indels 0; Gaps 0;

Qy	153	CGCGCAATCTCCCGGCATCCGGTATATACGGGGTCTACTCGTAGTGTCTG	212
Db	137	CGCCTTCTGCCCCCTCGGGCTCAAGGTACACATCGGGGGCTCTACTCGGCCGTGTGT	196
Qy	213	CGTGGGCTTGGTGGCAACTCGCTGGTCATGTTTCGTGATCATCCGATACCAAAAGTAA	272
Db	197	CGAGAGGCTCCCGGGGAACTGCCTGTCTATGACGTACATCCACAGCACCAAAATGAA	256
Qy	273	GACAGCAACCAACATTTACATATTTAACTGGCTTTGGAGATGCTTAGTTACTACAC	332
Db	257	GACACCCACCAATATTTTACATCTTTAACTGGCCCTGGCCGACACTGTGCTCTGAC	316
Qy	333	CATGCGCTTTCAGAGTACGGTCTACTGTGATGAAATTCCTGGCCTTTTGGGGATGTGCTGTG	392
Db	317	GCTGCCCTTCAGGGCAGGACATCCTCCTGGGCTTTCTGGCGCTTTGGGAATGGCGCTGTG	376
Qy	393	CAAGTATATTAATTTCCATTTGATTTACTACAAACATGTTCAACAGACATTTTACCTTGACCAT	452
Db	377	CAAGCACTCAATTTGGCATTGACTACTACAAACATGTTCAACACACACCTTACACCTTAATC	436
Qy	453	GATGAGCTGGAACCGCTACATTTGCCGTGGCCACCCCGTGAAGGCTTGTGAATTCGCGAC	512
Db	437	CATGAGTGTGATTCCTATGTAGCCATCTGCCACCCCAATCCGGGCCCTGAGGTCCGAC	496
Qy	513	ACCCTTGAAGGCMAAGATCATCAATATCTGCATCTGGACTGTGTGTCATCTGTTGGCAT	572
Db	497	GTCCAGCAAGGCCCAGGCTGTCAATGTGGCCATCTGGGCCCTGTGCTCTGTGTGTGTGT	556
Qy	573	CTTGGCAATATGTCCTTGGAGGCAACCAAGTCAGGGAAAGC	613
Db	557	TTCGGTGGCCATCATGTGGCTCGGCACAGGTCTAGAGTGAAG	597

RESULT 32	LOCUS	DEFINITION
CE517843	531 bp	DNA linear GSS 28-SEP-2001
CE517843	119r-gss-dog-17000311696913	Dog library Canis familiaris genomic, genomic survey sequence.

ACCESSION	CE517843
VERSION	CE517843.1
KEYWORDS	GI:36834624
SOURCE	GSS.
	Canis familiaris (dog)

REFERENCE
AUTHORS
Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Eutele
Mammalia; Euteria; Carnivora; Fissipedia; Canidae; Canis
1 (bases 1 to 531)
Kirkness, E. F., Bafna, V., Halpern, A. L., Levy, S., Remington,

TITLE The dog genome: survey sequencing and comparative analysis
JOURNAL Science 301 (5641), 1898-1903 (2003)

COMMENT Contact: Kirkness EF

The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.

FEATURES	Location/Qualifiers
SOURCE	1. .531

```

/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="nog Library"
/note="Site 1: Bactx; Libraries were prepared from
peripheral blood"

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ORIGIN

Query Match	18.3%	Score 211;	DB 29;	Length 531;
Best Local Similarity	88.4%	Pred. No. 1.7e-30;		
Matches 229;	Conservative 0;	Mismatches 30;	Indels 0;	Gaps 0;

Qy	1	ATGAGCTCCCCGATCCAATCTTTCGCGGGAGACGGGGCCTTACCTGCGCCCGGACGGC	60
Db	157	ATGAGATCCCCGGTCTCAATCTTTTCGCGGGAGACGGGGCCCACTGTCTCCGAGACAC	216
Qy	61	TGCTGCCCCCAACAGCAGCGCTGTGTTTCCCGCTGAGGCCGACAGCAACGAGC	120
Db	217	TGCTGTCTCCCAACGACGAGCGCTGTGCTGCCCGCTGGGCGGACGGAAGGCAACAC	276
Qy	121	AGCGCGGCTCGAGAGACGCGACGTGAGCCCGGCACATCTCCCGGCGCATCCCGGAC	180
Db	277	AGCGCGGCTCGAGAGCGCGACGTGAGTCCAGTCCGACATCTTCTCCGCAATCCCGGAC	336
Qy	181	ATCATCAACGGGGTCTACTCCGTAGTGTTCGTGAGGCTTGTGGGCAACTCGCTGGTC	240
Db	337	ATCATCAACGGGTGTCTACTCCGTGGTGTTCGTGAGGCTTGTGGGCAACTCCCTGGTC	396
Qy	241	ATGTTGATCATCATCCGAT	259
Db	397	ATGTTGATCATCATCCGAT	415

RESULT 33	
CNS028C2	
LOCUS	877 bp DNA
DEFINITION	linear GSS 01-SEP-2000
	Tetradon nigroviridis genome survey, sequence, PUC-ori end of clone

ACCESSION	AL211691
VERSION	AL211691.1
KEYWORDS	GSS; genome survey sequence
SOURCE	Tetraodon nigroviridis
ORGANISM	Tetraodon nigroviridis

Bukarjovca; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Acanthopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Actinopterygii; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodontidae; Tetraodon.

REFERENCE	1
Roest Croollius, H., Jallion, O., Daslva, C., Bouneau, J., Fisher, B., Bernin, A., Fizames, C., Wincker, P., Brottier, P., Quettier, F., Saurin, W., and Weissbach, J	
TITLE	Estimate of human gene number provided by genome-wide analysis using Tetradon nigroviridis DNA sequence
JOURNAL	Nat. Genet. 25 (2), 235-238 (2000)

MEDLINE	20296633
PUBMED	10835645

AUTHORS
Roest Crollius, H., Jailon, O., Dasilva, C., Ozouf-Costaz, C.,
Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F.,...

TITLE Characterization and repeat analysis of the compact genome of the freshwater pufferfish *Tetraodon nigroviridis*
JOURNAL Genome Res. 10 (7), 939-949 (2000)

MEDLINE	20359837
PUBMED	10899143
REFERENCE	3 (bases 1 to 877)

TITLE	Direct Submission
JOURNAL	Submitted (12-APR-2000) Genoscope - Centre National de Sequencage

COMMENT

FEATURES

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source
1. .877
/organism="Tetradodon nigroviridis"
/mol_type="genomic DNA"
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/db_xref="taxon:99883"
/clone="161H06"
/note="Genoscope sequence ID : C0AG161DD03SP1-end :
PUC-Or1"

Query Match 18.1%; Score 208.6; DB 29; Length 877;
Best Local Similarity 72.6%; Pred. No. 6.1e-30; Indels 0; Gaps 0;
Matches 262; Conservative 5; Mismatches 94; Indels 0; Gaps 0;

257 GATACACAAAGATGAGACGACGACCAACATTATTTAAGCTGGCTTGGCAGATG 316
349 GGTACACCAAGATGAGACGACGACCAACATTATTTAAGCTGGCTTGGCAGACG 408
317 CTTTGTATCTCAACACCATGCTTTGAGAGTACGCTTCTATGATGAATTCCTG 376
409 CTTTGTATCTCAACACCATGCTTTGAGAGTACGCTTCTATGATGAATTCCTG 468
377 TTGGGAGATGCTGTCAGATGATGATGATGATGATGATGATGATGATGATGATG 436
469 TGGGAGATGCTGTCAGATGATGATGATGATGATGATGATGATGATGATGATG 528
437 TCTTCACTTGAACATGATGATGATGATGATGATGATGATGATGATGATGATG 496
529 TCTTCACTTGAACATGATGATGATGATGATGATGATGATGATGATGATGATG 588
497 CTTTGTATCTCAACACCATGCTTTGAGAGTACGCTTCTATGATGAATTCCTG 556
589 CCGTGTATCTCAACACCATGCTTTGAGAGTACGCTTCTATGATGAATTCCTG 648
557 CGTGTATCTCAACACCATGCTTTGAGAGTACGCTTCTATGATGAATTCCTG 616
649 CCGTGTATCTCAACACCATGCTTTGAGAGTACGCTTCTATGATGAATTCCTG 708
617 A 617
709 A 709

RESULT 34
CNS02SKU/ 842 bp DNA linear GSS 01-SEP-2000
LOCUS
DEFINITION
Tetraodon nigroviridis genome survey sequence T7 end of clone
16218 of library G from Tetraodon nigroviridis, genomic survey
sequence.

AL212007.1 GI:7870826
GSS: genome survey sequence.
Tetraodon nigroviridis
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthopterygii; Acanthopterygii; Perciformes; Tetraodontiformes;
Tetraodontidae; Tetraodontidae; Tetraodon.

1 Roest Crolius, H., Jallou, O., Dasiya, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizes, C., Wincker, P., Brodier, P., Quetier, F.,
Saurin, W., Bernot, A., and Weissenbach, J.
Estimate of human gene number provided by genome-wide analysis
using Tetraodon nigroviridis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)

JOURNAL
MEDLINE
PUBMED
10835645

Roest Crolius, H., Jallou, O., Dasiya, C., Bouneau, L., Fisher, C.,
Fizes, C., Fisches, C., Bouneau, L., Billault, A., Quetier, F.,
Saurin, W., Bernot, A., and Weissenbach, J.

Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
Genome Res. 10 (7), 939-949 (2000)
JOURNAL
MEDLINE
PUBMED
10899143

REFERENCE 3 (bases 1 to 842)
AUTHORS
TITLE
JOURNAL
Direct Submission
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr -
Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/tetraodon.
Location/Qualifiers

FEATURES
source
1. 842
/organism="Tetraodon nigroviridis"
/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone="162B18"
/clone_11b="G"
/note="Genoscope sequence ID : C0AG162BC09LP1-end : T7"

Query Match 18.0%; Score 208.2; DB 29; Length 842;
Best Local Similarity 65.9%; Pred. No. 7.2e-30; Indels 6; Gaps 2;
Matches 323; Conservative 6; Mismatches 155; Indels 6; Gaps 2;

623 TTGAGTGTCTCTTCAAGTTCACAGATGATGATGATGATGATGATGATGATGATG 682
781 TGT 725
683 TGT 742
724 TGT 765
743 TGT 802
664 TGT 862
803 TGT 862
604 TGT 862
863 TGT 919
544 TGT 919
920 TGT 979
484 TGT 979
980 TGT 1039
424 TGT 365
1440 TGT 1099
364 TGT 305
1100 TGT 1109
304 TGT 295

RESULT 35
LOCUS
DEFINITION
697 bp mRNA linear EST 25-NOV-2002
60134091F1 CSFQHL24 Gallus gallus cdna clone CHEST15624 5', mRNA
sequence.
BUI39251
BUI39251
BUI39251.1 GI:25353599
EST.
Gallus gallus (chicken)
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

REFERENCE
1 (bases 1 to 697)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.U.
A Comprehensive Collection of Chicken cDNAs
JOURNAL
Curr. Biol. 12 (22), 1965-1969 (2002)
MEDLINE
2235534
PUBMED
12445392

COMMENT
Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.

FEATURES
SOURCE
1..697
Location/Qualifiers
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="White Leghorn, Hisex"
/db_xref="taxon:9031"
/clone="CHST115e24"
/dev_stage="16 day embryo"
/lab_host="DH10B"
/clone_1lb="CSBCHL24"
/note="Organ: Brain; Vector: pluescript II KS(+); Site 1:
EcoRI; Site 2: NotI; Modification of pluescript II KS(+)
[Stratagene] vector to accommodate cDNA produced with the
1-stranded protocol (Construction of uni-directionally
cloned cDNA libraries from messenger RNA for improved 3'
end DNA sequencing by Glenn Fu, et al. U.S. Patent #
6,387,624). Cut pluescript II KS(+) with NotI and EcoRI.
ligate in double stranded adaptor containing BspI and
BamHI sites [5'ggcgcgtgcagcccgatccgaaataag]
[5'aattcttttcggatccggcgctgcagc]"

ORIGIN
Query Match 18.0%; Score 207.8; DB 13; Length 697;
Best Local Similarity 66.5%; Pred. No. 86-30;
Matches 329; Conservative 0; Mismatches 162; Indels 4; Gaps 2;

664 TGGGACCTTCATGAAGATCGGCTTCATCTTGGCTTGATGCTCGT-CCTAT 722
Db TGGGACCAAGTGTGGCATCTGCGTTTCTCTTATATATCCCGCTGAT 66
723 CATCATCTGCTGCTACACCTGATGATCTCGCTCAAGAGCTCCGCTCTTCTG 782
Db CATCATCTGCTGCTACAGCTCATATGACAGCGCTCAAGAGCTCCGCTCTG 126
783 CTCCGAGAGAAATCGCACTCGGTGATGATCACAGACTGCTGCTGCTGCTG 842
Db CTCCAGAGAGAAAGCGGACCTGAGGCGATCACCCGATGCTGCTGCTGCTG 186
843 AGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 902
Db GCTTCCTATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 246
903 CACTTCCACAGACAGCTGCTCTCCAGCTATTACTTCTGATGCTGCTGCTG 962
Db CAAGGCGGAAAGCGAGCTGAGCTGAGCTGCTGCTGCTGCTGCTGCTGCTG 306
963 CACAGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1022
Db CAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 366
1023 CCGGAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1082
Db CAAGAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 426
1083 AATACAGTTCAGATCTGCTTA--CCTGAGGACATGATGGATGATTAACAGT 1139
Db CAGCATTCGCAAGAGATGCTGCTTATGCTCGAAGAACTCGAGGGGACATTAATCCGGC 486

Qy 1140 ATGACTAGCGCGGA 1154
Db 487 CTGACTAGCATGGA 501

RESULT 36
BU614716
LOCUS
DEFINITION
BU614716 757 bp mRNA linear EST 20-FEB-2003
UI-M-EV0-cdh-m-08-0-UI-r1 NIH_BMAP-EV0 Mus musculus cDNA clone
ACCESSION
BU614716
VERSION
BU614716.1 GI:23280931
KEYWORDS
EST
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 757)
NIH-MGC http://mgi.nci.nih.gov/
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bcr-mail.nih.gov
Tissue Procurement: Dr. James Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@iowa.edu
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
Seq primer: PYX-5,
Location/Qualifiers
1..757
/organism="Mus musculus"
/mol_type="mRNA"
/strain="CS7BL/6"
/db_xref="taxon:10090"
/clone="UI-M-EV0-cdh-m-08-0-UI"
/tissue_type="whole brain"
/dev_stage="embryo 15.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_1lb="NIH_BMAP EV0"
/note="Organ: brain; Vector: pYX-Anc, Site 1: EcoRI;
Site 2: NotI; The library was constructed according to
Bonaldi, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured mRNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with an
oligo-dT primer containing a NotI site. Double stranded
cDNA was size selected according to mRNA size fraction,
ligated with EcoRI adaptor, digested with NotI, and then
cloned directionally into pYX-Anc vector. The library tag
sequence located between the NotI site and the polyA
tail, is GTGCGTGGAA. This library was created for the
University of Iowa Mouse Brain Molecular Anatomy Project
(BMAP): 'Gene Discovery in the Developing Mouse Nervous
System', supported by National Institutes of Mental Health
(NIMH), Hemlin Chin, Ph.D., program coordinator."

ORIGIN
Query Match 18.0%; Score 207.8; DB 13; Length 757;
Best Local Similarity 60.3%; Pred. No. 8.3e-30;
Matches 382; Conservative 0; Mismatches 242; Indels 9; Gaps 2;

466 CGCTACATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 525
Db 1 CTTATGAGCTATCTGACACCTTATCCGCTGCTGCTGCTGCTGCTGCTG 60
526 AAGATCAATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 585
Db 61 CAGGCGCTTAATGTCGATATGGGCTGCTGCTGCTGCTGCTGCTGCTGCT 120

QY 586 CTGGAGGACCAAGTCAAGGAGAGAGTGTATCTTGGTCTCTTGCATCCCA 645
 Db 121 ATGGGCTCAGACAAAGTGGAGAGTAAAGAG-----ATCAGTGCCTGGAGATCCCC 174
 QY 646 GATGATGACTACTCTCTGGTGGACCTCTTCATGAAAGTGCCTTTCATCTTTGGCTTC 705
 Db 175 GCCCCTCAGAGACTATTGGG---CCCTGATTGGCCATCTGCATCTTCTTTTCTTC 231
 QY 706 GTATCTCTCTCTCATCATCATCATCTGTCTGTCAACCTTGATGATCTCGCTCAAGAC 765
 Db 232 ATCATCCCGGTCTGTATCATCTCTGTCTGTCTACAGCTCATGTATGACAGACTTCGTGT 291
 QY 766 GTCCGCTCTCTTCTGGCTCCCGAGAGAAAGATCGAACCTGGTGAATCACCAGAC 825
 Db 292 GTCCGCTCTTTCAGGCTCCCGAGAGAGACCGAAGCTGACAGCATCACACGGCTG 351
 QY 826 GTCTGT 885
 Db 352 GTACTGGTAGT 411
 QY 886 GTGAGAGCTCTGGGAGACCTCCACAGACAGCTGTCTCTCCAGCTATTACTTGTGC 945
 Db 412 GTTCAAGAGACTGGT 471
 QY 946 ATGCGCTTGAAGCTATACCAACAGTACCTGATCCCATCTTACAGCTTCTGTATGA 1005
 Db 472 ACAGCCTCTGGCTATGTCAACAGTGTGTCAATCCATCTCTATGCTTGTGTGTGTGT 531
 QY 1006 AACTTCAAGCGGT 1065
 Db 532 AACCTTCAAGCGCTGT 591
 QY 1066 AGCATAGACAGTCCGAAATACAGTTCAGGAT 1098
 Db 592 GTTTCGTATCTGT 624

RESULT 37
 LOCUS B1754749 785 bp mRNA linear EST 25-SEP-2001
 DEFINITION 603025465F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5195801 5',
 mRNA sequence.
 ACCESSION B1754749
 VERSION B1754749.1 GI:15746327
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE NIH-MGC http://mgc.nci.nih.gov/.
 1 (bases 1 to 785)
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cgabs-r@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNLN at:
 http://image.llnl.gov
 Plate: L1M11490 row: a column: 18
 High quality sequence stop: 785.
 Location/Qualifiers
 1..785
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5195801"
 /lab_host="DH10B"
 /clone_id="NIH_MGC_114"
 /note="Organ: Brain; Vector: pCMV-SPORT6; Site_1: NotI;

Site_2: EcorV (destroyed); RNA source anonymous pool of 6
 male brains, age range 23-27 yo. Library is oligo-dT
 primed and directionally cloned (EcorV site is destroyed
 upon cloning). Average insert size 1.5 kb, insert size
 range 1-3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 019. Note:
 this is a NIH_MGC Library."

Query Match 17.6%; Score 203.4; DB 12; Length 785;
 Best Local Similarity 69.5%; Pred. No. 6e-29; Indels 0; Gaps 0;
 Matches 276; Conservative 0; Mismatches 121;

QY 153 CGCGACATCTCCCGGACATCCCGATCATGACGCGGTCTTACCTCGTAGTTCGT 212
 Db 295 CGCCTTCTGCCCCCGGCTCAAGTATCAGCATGTGGGCTTACCTGGCCGTGTGT 354
 QY 213 CGTGGGCTTGGTGGCACTGCTGTGTATTTGTGTATCTCCGATACACAAAGTAA 272
 Db 355 CGAAGGCTCCTGGGAACTGCTGTGTATGTATGATCTCTCAGGACACCAAAATGAA 414
 QY 273 GACAGCAACCAATTTATATTTAACTGTGGCTTGGCAGATGCTTATTTACTACAC 332
 Db 415 GACAGCCACCAATTTATATTTAACTGTGGCTTGGCAGATGCTTATTTACTACAC 474
 QY 333 CATGCCCTTTCAGAGTACGCTTATTTATTTATTTATTTATTTATTTATTTATTTAT 392
 Db 475 GCTGCCCTTTCAGAGGACGACATCTCTGTGGCTTGTGGGATGGCTGTG 534
 QY 393 CAAGATGTATTTTCAATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 452
 Db 535 CAAGATGTATTTTCAATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 594
 QY 453 GATGAGGCTGACCGCTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 512
 Db 595 CATGATGTGTGATGTGTATGTATGTATGTATGTATGTATGTATGTATGTATGTATGT 654
 QY 513 ACCCTTGAAGGCAAAAGTATCATATATCTGCATCTGG 549
 Db 655 GTCCAGCAAGCCCAAGCTGTCAATGTGGCCATCTGG 691

RESULT 38
 LOCUS BM943972 810 bp mRNA linear EST 14-MAR-2002
 DEFINITION U1-M-BHOP-byp-c-24-0-UI.r1 NIH_BMAP_BHOP Mus musculus cDNA clone
 IMAGE:5695055 5', mRNA sequence.
 ACCESSION BM943972
 VERSION BM943972.1 GI:19427557
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE NIH-MGC http://mgc.nci.nih.gov/.
 1 (bases 1 to 810)
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cgabs-r@mail.nih.gov
 Tissue Procurement: Dr. James Lin, University of Iowa
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNLN at:
 http://image.llnl.gov
 This clone was contributed by the Brain Molecular Anatomy Project
 (BMAP)

FEATURES
 source
 1..810
 Location/Qualifiers
 Seq primer: pTX-5,
 _1..810

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/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:5695055"
/cisue_type="whole brain"
/dev_stage="embryo 18.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_1ib="NH_BMAP_EH0P"
/notes="Organ: Brain; Vector: pYX-Ase; Site_1: EcoR I;
Site_2: Not I; The library was constructed according to
Bonaldi, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured mRNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was size selected according to mRNA size fraction,
ligated with EcoR I adaptor, digested with Not I, and then
cloned directionally into pYX-Ase vector. The library tag
sequence located between the Not I site and the polyA
tail is CAGCCAGAC. This library was created for the
University of Iowa Mouse Brain Molecular Anatomy Project
(BMAP): 'Gene Discovery in the Developing Mouse Nervous
System', supported by National Institute of Mental Health
(NIMH), Hemin Chin, Ph.D., program coordinator."

```

ORIGIN

Query Match 17.6%; Score 202.8; DB 12; Length 810;
 Best Local Similarity 62.8%; Pred. No. 7.9e-29;
 Matches 369; Conservative 0; Mismatches 207; Indels 12; Gaps 3;

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154 GGCACATCTCCCGGCGCATCCGCGATCATCAGCGCGCTACTCCGAGTTCGTC 213
228 GCGTCTCTCCCTTGGACTCAAGTCAACATCTGGGCTCTACTTGGCTGTGTCATC 287
214 GTGGGCTTGTGGGCACTCGCTGATCTGTGATCATCCGATACCAAGATGAAG 273
288 GGGGGGCTCTGGGAACTGCGTCATGATGTCATCTCGGACACCAAGATGAAG 347
274 AAGCAACCAATTTACATTTTAACTGGCTTTGGCAGATGCTTTAGTACTACACC 333
348 ACTGCTACCAATTTACATTTTAACTGGCAGCTGCTGATPACCTGCTCTTGACA 407
334 ATGCCCTTCAAGTACGCTACTGATGAATTCCTGGCCTTTGGGATGTCGTGC 393
408 CTGCCCTTCAAGGACACACATCTTGGGCTTGTGGCATTTGGGATGATGATGTC 467
394 AAGATGATATTTCCATTTACTTACCAACATGTTCCAGCATCTTCACTTGACCATG 453
468 AAGAGGATGATGCTATGCTACATCAATGTTTACAGACATTTCACTTGAATGCGC 527
454 ATGAGCGTGGACCGCTACATTTGCGTGGCCACCCGTTGAAGCTTTGACCTTGCACA 513
528 ATGAGTGTAGACCGTATGATGATCTCCACCCCTATCCGCTTGTATGTTCCGACA 587
514 CCCTTGAAGGCAAGATCATATATCTGATCTGCTGCTGCTGATCTGTTGGCATC 573
588 TCCAGTAAAGCCAGGCGGTATATGTCGCAATATGGCCCTGCTGCTGCTGTTGTT 647
574 TCTGCAATAGTCTTGGAGGACCAAGTCAGGGAAGATGCTGATGCTTGAAGTCTCC 633
648 CCGTGTGTCATATGGGCTCAGACAAAGT-----GGAAGATGAAGATGAGTCTCCG 701
634 TTGCAAGTTCAGATGATGATCTCTGGTGGACCTTTCAATGAAGATGCTGCTTTC 693
702 GTGGAGATCCCGCC-----CTCAGGACTATTGGGGGCTGTATTGTCATCTGCACTTC 756
694 ATCTTGCCTGATCTGCTGCTGCTCATCATCATGCTGCTGATCACC 741
757 CTTTCTTT-CTTCAATATCCCGGTTTGAATCATCTCTGTCTGCTACGC 803

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RESULT 39
 BU219037

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LOCUS BU219037 649 bp mRNA linear EST 25-NOV-2002
DEFINITION 60375543F1 CSEQCHN04 Gallus gallus cDNA clone CHEST665F12 5', mRNA
sequence.
ACCESSION BU219037
VERSION BU219037.1 GI:25402920
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
1 (bases 1 to 649)
AUTHORS Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
TITLE A Comprehensive Collection of Chicken cDNAs
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
MEDLINE 2235534
PUBMED 12445392
COMMENT Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.

```

FEATURES

source
 1..649
 Location/Qualifiers

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/mol_type="mRNA"
/strain="White Leghorn, Hixex"
/db_xref="taxon:9031"
/clone="CHEST665F12"
/cisue_type="whole embryo"
/dev_stage="20-21"
/lab_host="DH10B"
/clone_1ib="CSEQCHN04"
/notes="Organ: whole embryo; Vector: pBluescript II KS(+);
Site_1: EcoRI; Site_2: NotI; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was bluntend, ligated to NotI adaptors, digested with
EcoRI, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldi et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."

```

ORIGIN

Query Match 17.3%; Score 199.2; DB 13; Length 649;
 Best Local Similarity 65.3%; Pred. No. 3.6e-28;
 Matches 308; Conservative 0; Mismatches 163; Indels 1; Gaps 1;

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664 TGGACCTTCTCATGAAGATCTGCGTTCATCTTTGCCCTTGATCCCTGCTCTCATC 723
24 TGGAAACCTTACTGAAATCTGTGTTGTTGCTTTCCTTATCATATGCAATGCGATC 83
724 ATCATCTGCTCTCAACCTGATGATCTGCTGTCAAGAGGCTCGGCTCTTTCTGGC 783
84 ATTACTGTGTGTATGGGCTGATGATTTTAACTTAAAGATGTCGCAATGTTATCTGGC 143
784 TCCCGAGAAAGATGCAACTGCGTAGATGATCAACAGATGCTGCTGGTGGTGGCA 843
144 TCTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 203
844 GTCTTGTCTGTGTGAATCCCATTCATATTCATCTGCTGGAGGCTTGGGGAGC 903
204 GTGTTCATCATCTGCTGAGCTCTCTATCCACATTTATGTCATATTAAGACCTGTCAC 263

```

QY 904 ACCTCCACGACAGACGCTGCTCTCCAGCATATTACTTCGATCCGCTTAGGCTATACC 963
 Db 264 ATCCCAAACTACTTTCAGACTGTCTCTGGACATTTGTATGTTAGGTATATA 333
 QY 964 AACAGTAGCTGAATCCCATTTCTTACGCTTTCTTGATGAAAACTTCAAGCGGTGTTTC 1023
 Db 324 AATAGCTGCTCAATCAGTCTCTGTATGATTTCTTAATGAGAAATTTCAAAAGTGTTC 383
 QY 1024 CGGACTCTGCTTTTCACTGGAAGATGAGATGAGCGGACAGACTTACAGATCCGA 1083
 Db 384 AGAGAGTTGTCATCTCCACCTCTCTCAATTTAGAGAGCAAACTCCACAG-GTCCGA 442
 QY 1084 AATACAGTTGAGATCTGCTTACCTGAGGACATGATGAGATGAATAAC 1135
 Db 443 CAAATATCTGTACCATCTTCTTCCACTGCAACACATCTGTGACAGACTAAC 494

RESULT 40
 BQ179148 816 bp mRNA linear EST 30-APR-2002
 LOCUS UI-M-EMO-bmw-i-19-0-UI.r1 NIH_BMAP_EMO Mus musculus cDNA clone
 DEFINITION IMAGE:5703258 5', mRNA sequence.
 ACCESSION BQ179148
 VERSION BQ179148.1 GI:20354640
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 816)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-x@mail.nih.gov
 Tissue Procurement: Dr. James Lin, University of Iowa
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 This clone was contributed by the Brain Molecular Anatomy Project
 (BMAP)

FEATURES
 source Location/Qualifiers

1..816
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE:5703258"
 /tissue_type="whole brain"
 /dev_stage="embryo 15.5 dpc"
 /lab_host="DH10B (T1 phage resistant)"
 /clone_11b="NIH_BMAP_EMO"
 /note="Organ: brain; Vector: pYX-Asc; Site 1: Ecor I,
 Site 2: Not I; The library was constructed according to
 Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
 1996. Denatured mRNA was size fractionated on a 1% agarose
 gel. First strand cDNA synthesis was primed with an
 oligo-dT primer containing a Not I site. Double stranded
 cDNA was size selected according to mRNA size fraction,
 ligated with Ecor I adaptor, digested with Not I, and then
 cloned directionally into pYX-Asc vector. The library tag
 sequence located between the Not I site and the polyA
 tail, is GTGCGTGAA. This library was created for the
 University of Iowa Mouse Brain Molecular Anatomy Project
 (BMAP): 'Gene Discovery in the Developing Mouse Nervous
 System', supported by National Institutes of Mental Health
 (NIMH), Hemlin Chin, Ph.D., program coordinator."

ORIGIN

Query Match 16.9%; Score 195.6; DB 13; Length 816;
 Best Local Similarity 63.9%; Pred. No. 2e-27;
 Matches 294; Conservative 0; Mismatches 166; Indels 0; Gaps 0;

QY 154 GGCACATCTCCCGGCCATCCGGTCAATCATACGGGGGTCTACTCCGTAGTGTGTC 213
 Db 290 GCTTCTCGCCCTTGAGACTCAAGGTACACCATCGTGGGGCTCTACTGGCTGTGTGATC 349
 QY 214 GTGGCTTGTTGGGCACTCGTGTGATGTTCTGATCATCCGATACCAAGATGAAG 273
 Db 350 GGGGGGCTCTGGGAACTGCTGTGATGATGATGATGATGATGATGATGATGATGATG 409
 QY 274 AAGCAACCAATTTAATATTAACTGCTTGGCAGATGCTTTAGTTACTCAACC 333
 Db 410 ACTGTACCAACATTTAATATTAACTGCTGACATGCTGATATCCGTGTTCGTGCA 469
 QY 334 ATGCCCTTTCAGAGTACGCTGCTACTTGTGATGATTCCTGGCTTTGGGATGTGCTGTC 393
 Db 470 CTGCCCTTCAGGGGACAGACATCTTCTGGGCTTCTGGCCATTTGGAAATGCACTGTGC 529
 QY 394 AAGATGATATTTTCATTTGATTAATCAACATGTTTCAACAGCATCTTCACTTGAACATG 453
 Db 530 AAGAGGTCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 589
 QY 454 ATGAGCGTGAACCGTATCATTTGCGGTGACACCCCGGAAAGCTTTGACTTCCGACA 513
 Db 590 ATGAGTGTAGACCGTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 649
 QY 514 CCTTGAAGGCAAGATCATCATATATGATGATGATGATGATGATGATGATGATGATGATG 573
 Db 650 TCCAGTAAAGCCCAAGGCGGTATGATGATGATGATGATGATGATGATGATGATGATG 709
 QY 574 TCTGATATGCTTGTGAGGACCAACAAAGTCAGGGAAGC 613
 Db 710 CCGTGTCCATCATGCGCTCAGCAAGTGAGGATGAAG 749

RESULT 41
 LOCUS BX228633 787 bp DNA linear GSS 29-JAN-2003
 DEFINITION BX228633
 ACCESSION BX228633
 VERSION BX228633.1 GI:28062783
 KEYWORDS GSS.
 SOURCE Danio rerio (zebrafish)
 ORGANISM Danio rerio

REFERENCE 1 (bases 1 to 787)
 AUTHORS Humphray, S.J., Huckle, E. and Durham, J.L.
 JOURNAL Direct Submission
 COMMENT Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome
 Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
 humphray@sanger.ac.uk Unpublished
 This sequence was generated from the SP6 end of BAC 244F17. 244F17
 is part of the Daniokey BAC library created by R. Plasterk and N.V.
 Keygene. Further details:
 http://www.sanger.ac.uk/Projects/D_rerio/.

FEATURES
 source Location/Qualifiers

1..787
 /organism="Danio rerio"
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 /clone="DKEY-244F17"
 /tissue_type="Testis"
 /note="vector pindigobAC-536"

ORIGIN

Query Match 16.8%; Score 194; DB 29; Length 787;
 Best Local Similarity 71.8%; Pred. No. 3.9e-27;
 Matches 254; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

QY 251 TCATCCGATACACAAAGATGAAGACAGCAACCAATTACATATTAACTGGCTTGG 310
 DB 82 TGTGAGATACACCAAGCTGAAAGCTGCCACCAACATCTACATCTTCAATTTGGCCCTG 141
 QY 311 CAGATGCTTTAGTACTACACCAATGCCCTTTCAAGTACGGTCTACCTTGATGAATTCCT 370
 DB 142 CAGATGCACTGGCTACTAGTACATCTCCATCCAGAGCACAAGATATTAAATGAACACT 201
 QY 371 GGCCTTTGGGGATGCTGCTGACAGATAGTAAATTTCCATTGATTAATCAACATGTTCA 430
 DB 202 GGCCTTTGGGGATGCTGCTGACAGATAGTAAATTTCCATTGATTAATCAACATGTTCA 261
 QY 431 CCAGATCTTCACTTACCATGATGAGGGTGAACCGCTACATGTCGGTGGCCACCCCG 490
 DB 262 CCAGATCTTCACTTACCATGATGAGGGTGAACCGCTACATGTCGGTGGCCACCCCG 321
 QY 491 TGAAGCTTTGGACTTCCGACACCCCTTGAAGGCAAAAGATCATCAATATCTGCATCTGGC 550
 DB 322 TGAGAGCACTGAGATTGCTGATCCCGATCAAGGCCAAATTAATCAATGTCATCTGGA 381
 QY 551 TGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 604
 DB 382 TCCCT 435

RESULT 42

B0571737

LOCUS B0571737 746 bp mRNA linear EST 19-JUN-2002
 DEFINITION UI-M-FCO-byc-k-12-0-UI.r1 NIH BMAP_FCO Mus musculus cDNA clone
 IMAGE:571635 5', mRNA sequence.

ACCESSION

B0571737

VERSION B0571737.1 GI:21475054
 KEYWORDS EST.

SOURCE

ORGANISM

Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaab@rmail.nih.gov
 Tissue Procurement: Dr. James Lin, University of Iowa
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/BLN at:
 http://image.llnl.gov
 This clone was contributed by the Brain Molecular Anatomy Project
 (BMAP)

FEATURES

SOURCE

1..746

Location/Qualifiers

/organism="Mus musculus"
 /mol_type="mRNA"
 /strain="CS7BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE:571635"
 /tissue_type="whole brain"
 /dev_stage="embryo 12.5 dpc"
 /lab_host="DH10B (T1 phage resistant)"
 /clone_lib="NIH-BMAP_FCO"
 /note="Organ: brain; Vector: pYX-Aac; Site 1: EcoR I;
 Site 2: Not I; The library was constructed according to
 Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
 1996. Denatured mRNA was size fractionated on a 1% agarose
 gel. First strand cDNA synthesis was primed with an
 oligo-dT primer containing a Not I site. Double stranded
 cDNA was size selected according to mRNA size fraction,
 ligated with EcoR I adaptor, digested with Not I, and then
 cloned directionally into pYX-Aac vector. The library tag

ORIGIN

Query Match 16.7%; Score 192.8; DB 13; Length 746;
 Best Local Similarity 65.0%; Pred. No. 6.5e-27;
 Matches 284; Conservative 0; Mismatches 153; Indels 0; Gaps 0;

sequence located between the Not I site and the polyA
 tail, is TGAGAGACC. This library was created for the
 University of Iowa Mouse Brain Molecular Anatomy Project
 (BMAP); "Gene Discovery in the Developing Mouse Nervous
 System", supported by National Institutes of Mental Health
 (NIMH), Hemlin Chin, Ph.D., program coordinator."

QY 154 GGCACATCTCCCGCCCATCCCGTCAATCAACAGCGGCTACTCCGTAAGTGTGTC 213
 DB 307 GCTTCTCTGCCCCCTTGGACTCAAGGTACACATCGTGGGCTTACTTGGCTGTGCAATC 366
 QY 214 GTGGCTTGTGTGGGCACTCGTGTGATGTTGATGATCGATCCGATACAAAGATGAAG 273
 DB 367 GGGGGGCTCTGGGAACTGCTCGTCAATGATGATGATCCTCAGGACACCAAGATGAAG 426
 QY 274 ACAGCAACCAATTTACATATTTAATCTGCTGGAGATGCTTACTTACTACAAAC 333
 DB 427 ACTGTACCAACATTTACATATTTAATCTGCTGGAGATGCTTACTTACTACAAAC 486
 QY 334 ATGCCCTTTCAGAGTACGGTCTACTGATGATGATGATGATGATGATGATGATGATGATG 393
 DB 487 CTGCTCTTTCAGAGGACAGACATCTCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTT 546
 QY 394 AAGATGATGATTTTCCATGATTTACTTACAAACATGTTTACACAGCATCTTCACTTGAAC 453
 DB 547 AAGAGGATCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 606
 QY 454 ATGACCGTGGACCGCTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 513
 DB 607 ATGAGTGTAGACCGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 666
 QY 514 CCTTGAAGGCAAAAGATCATCAATATGATGATGATGATGATGATGATGATGATGATGATG 573
 DB 667 TCCAGTAAAGCCAGGCGCTTATGATGATGATGATGATGATGATGATGATGATGATGATG 726
 QY 574 TCTGCAATATGCTTGG 590
 DB 727 CCTGTGCAATCATGG 743

RESULT 43

AY410421

LOCUS

DEFINITION

AY410421

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

1 (bases 1 to 954)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,

Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B.,

Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Snihsy, J.J.,

Adams, M.D. and Cargill, M.

Inferring nonneutral evolution from human-chimp-mouse orthologous

gene trios

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

2 (bases 1 to 954)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,

Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B.,

Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Snihsy, J.J.,

Adams, M.D. and Cargill, M.

Direct Submission

Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,

COMMENT
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES
Location/Qualifiers
source
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
<1..>954
/gene="SSSTR4"
/locus_tag="HCM3885"

ORIGIN
Query Match 16.5%; Score 190.6; DB 29; Length 954;
Best Local Similarity 55.8%; Pred. No. 1.9e-26;
Matches 436; Conservative 0; Mismatches 324; Indels 21; Gaps 3;

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QY 246 CGTGCATCATCCGATACCAAGATGAAGACGACCAACATTTACATATTTAACTGGC 305
DB 1 CGTGATCTCTCGCTACGCCAAGATGAAGACGCTACCAATCTACCTGCTCACTGGC 60
QY 306 TTGGAGATGCTTAACTAACAACATGCCCTTCAGAGTACGCTCTACTATATGA 365
DB 61 CGTAGCCGACGAGCTCTTACGTGAGCGCTTCGTGCGCTCGTGGCGCGCTCGG 120
QY 366 TTCCCTGGCTTTGGGAGATGCTGTGCAAGATGATGATTTCCATTTGATTAACAACAT 425
DB 121 CCACTGGCCCTTGGCTCGGTGCTGTCGCGCGCGCTGCTCAGGTGACAGGCTCAACAT 180
QY 426 GTTACACAGATTTTACCTTGAACATGATGAGCGTGACCGGTACATTTCCGTGTGCA 485
DB 181 GTTACACAGATTTTCTGTCTACCTGTGTCAGCGTGACCGGTACATGTCGCTGTGCA 240
QY 486 CCCCGTGAAGGCTTTGAGCTTCGCGACACCCCTTGAAGGCAAGATCATATATCTGAT 545
DB 241 CCTCTGGCGCGCGGACCTACCGGCGCGCTGCGCAAGCTCATTAACCTGGGCT 300
QY 546 CTGGCTGCTGTGCTCATCTGTGGCATCTCTGCAATATGCTTGGAGGACCAAGTCAAG 605
DB 301 GTGGCTGGGATCCCTGTGTGCTCATCTCCCATCCGATCTTGGAGACACAGACCGGCG 360
QY 606 GGAAGACGTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 665
DB 361 TCGCGCGCGCGCGCGCGCTGCGCAACCTGCAAGTGGCCA-----CACCGCGCTGTGTC 414
QY 666 GGAACCTCTCATGAAGATCTGCGCTCTTCACTTTTGGCTTGGATCCGTCCTCATCAT 725
DB 415 GCGAGCTTCTGTG---TCTACACTTCTCTGCTGGCTTCTGTGCTGCTGCTGCTGCTGCT 471
QY 726 CATGCTGTGCTACACCTGATGATCTGTGCTGTCAAGACGCTCGGCTCTTCTGTGCTGTC 785
DB 472 TGGGCTGTGCTACCTGCTCATCTGTGGGCAAGATGCGCGCGCTGCGCGCTGCGCTG 531
QY 786 CCGAAGAAAGATCCGACCTGCGATGATGATGATGATGATGATGATGATGATGATGATGAT 845
DB 532 GAGAGCGCGCGCGCGCTGCGAAGAAATACAGCGCTGCGTGAATGCTGTGTGTGTGT 591
QY 846 CTTCGTGTGCTGTGAGACTCCCATTCACATATTTCACTGAGGAGGCTGTGGGAGGAC 905
DB 592 CTTCGTGTGCTGTGAGTGTGCTTCTAC-----GTGGTGTGAGTGTGCTTAACT 639
QY 906 CTCCACAGACAGCTGCTCTCTCAAGCTATTAATCTGTGATCGCTTAAAGCTATACCA 965
DB 640 CTTCGTGTGACAGCTTGTGATGACACGCTCAACACAGCTGTATCTTAACTATGCA 699
QY 966 CAGTGGCTGATATCCCATTTCTTAGCTTTTATATGAAATCTTCAAGCGGTGTTCCG 1025
DB 700 CAGTGGCGCAACCCCATTTCTATGCTTCTCTGCAACAATTCGCGCATCTTCA 759
QY 1026 G 1026
DB 760 G 760

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RESULT 44
AZ226406
LOCUS
DEFINITION
RPCT-23-80H6.TV RPCT-23 Mus musculus genomic clone RPCT-23-80H6,
genomic survey sequence.
AZ226406
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

546 bp DNA linear GSS 14-JUN-2000
Mus musculus
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 546)
Zhao, S., Niemman, W., Feldblum, T., Malek, J., Shateman, S.,
Akinret, B., Levin, M., McGinn, S., Teegaye, G., Geer, K., Krol, M., de
Jong, P. and Fraser, C.M.
Mouse BAC End Sequences from Library RPCT-23
Unpublished (1999)
Other GSSs: RPCT-23-80H6.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCT-23. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.htm>)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac/ends/mouse/bac_end_intro.html
Plate: 80 row: H column: 6
Seq primer: SP6
Class: BAC ends.

FEATURES
source
Location/Qualifiers
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/mol_type="genomic DNA"
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/db_xref="taxon:10090"
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/sex="Female"
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/clone_lib="RPCT-23"
/note="Organ: Kidney/Brain; Vector: pBAC3.6; Site 1:
EcoRI; Site 2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBAC3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies)."

ORIGIN

Query Match 16.4%; Score 189.8; DB 28; Length 546;
Best Local Similarity 90.2%; Pred. No. 2.2e-26;
Matches 203; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

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QY 386 TGTGTGCAAGATGATGATTTCCATTTGATTTACTTCAACATGTTACACGATCTTCACT 445
DB 1 TGTATATCAAGATGATGATTTCCATTTGATTTACTTCAACATGATTTTACGATATTCACCT 60
QY 446 TGACATGATGAGGCTGACCGCTACATTTGCGGTGCGCACCCCGTGAAGCTTTGGACT 505
DB 61 TGACATGATGAGGCTGACCGCTACATTTGCGGTGCGCACCCCGTGAAGCTTTGGACT 120
QY 506 TCGGACACCTTTGAAGGCAAGATCATCATATTTGATGATGATGATGATGATGATGATGAT 565
DB 121 TCGGACACCTTTGAAGGCAAGATCATCATATTTGATGATGATGATGATGATGATGATGAT 180
QY 566 TTGGCATCTCTGCAATGCTCTTGGAGGACCAAGTCAAGGAG 610

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Db 181 TTGTATATACGAGTAGTCTTGAGAGCACCAGTACAGGAG 225

RESULT 45
AK03151 2848 bp mRNA linear HTC 19-SEP-2003
LOCUS Mus musculus adult male hypothalamus cDNA, RIKEN full-length
DEFINITION enriched library clone:A230102K24 product:weakly similar to opioid
receptor, kappa 1, full insert sequence.

ACCESSION
AK03151
VERSION AK03151.1 GI:26086975
KEYWORDS HTC, CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS Carninci, P. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PubMed 10349636

REFERENCE
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PubMed 11042159

REFERENCE
AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Teshiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Yuijwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, B., Matsubara, S.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsubara, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A. and Hayashizaki, Y.
TITLE RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PubMed 11076861

REFERENCE
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the
PANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
MEDLINE 11076861

REFERENCE
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
MEDLINE 11076861

REFERENCE
AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hirao, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kigawa, I., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Konda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, C., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
TITLE Direct Submision
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Teurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@sc.riken.go.jp,

COMMENT
URL: <http://genome.gsc.riken.go.jp/>, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)
CDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: <http://genome.gsc.riken.go.jp/>
URL: <http://fantom.gsc.riken.go.jp/>,
location/Qualifiers

FEATURES
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/strain="C57BL/6J"
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/clone="A230102K24"
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/tissue_type="hypothalamus"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
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/note="weakly similar to opioid receptor, kappa 1
(MGI:MGI:97439, GB|L11065, evidence: BLASTN, 100%,
match=273)"

ORIGIN
Query Match 15.8%; Score 182.2; DB 11; Length 2848;
Best Local Similarity 81.5%; Pred. No. 1.3e-24;
Matches 211; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
1 ATGAGTCCTCCGATCCAGATCTTCCGCGGAGCGCGCCCTTACTCGCCCCGAGCGCC 60
2 585 ATGAGTCCTCCGATCCAGATCTTCCGCGGAGCGCGCCCTTACTCGCCCCGAGCGCC 644
3 61 TGCCTGCCCCCAAGAGAGCGCGCTTTCCTGCGGCTGGCGCGAGCGAGCAAGCGCC 120
4 645 TGCCTTCTCCCAAGAGAGCGCGCTTTCCTGCGGCTGGCGCGAGCGAGCAAGCGAGTATGGCC 704
5 121 AGCGCGGCTCGAGAGAGCGCGAGCGCGCGCGAGCGCGAGCGCGAGCGCGAGCGCGCG 180
6 705 AGTGTGGGCTCAGAGAGATCAGACGCTGAGCTCGCGGCAATCTCTCGGCAATCCCTGTT 764
7 181 ATCATCAGCGCGCTTACTCTCGTGTGCTGCTGCGGCTTGTGGCGCAATCGCTGCTGTC 240
8 765 ATCATCAGCGCGCTTACTCTGTGTATTTGGTGGGCTGTAGTGGGCAATCTCTGCTGTC 824
9 241 ATGTCGATCATTCGCGAT 259
10 825 ATGTTGTATCATTCGCGAT 843

RESULT 46
CG536117 318 bp DNA linear GSS 01-OCT-2003
LOCUS OS1123712 Mus musculus 1295V/5V Mus musculus genomic clone
DEFINITION OS1123712, genomic survey sequence.
ACCESSION
CG536117
VERSION CG536117.1 GI:37322689
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Zambrowicz, B.P., Abuln, A., Ramirez-Solis, R., Richer, L.J.,
Piggott, U., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A.,
Fridde, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jai, C.,
Key, B.W., Jr., Klupp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D.,
Payne, R., Porter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,
Sparkes, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N.,

TITLE	JOURNAL	COMMENT
Zhu Q., Person C. and Sands A.T.		
Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention	Proc. Natl. Acad. Sci. U.S.A.	100 (24) , 14109-14114 (2003)
Contact: Zambrowicz BP		
OmitBank		
Lexicon Genetics Incorporated		
4000 Research Forest Drive, The Woodlands, TX 77381, USA		
Email: materials@lexgen.com		
Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature, 1998 Apr 9;392(6676):608-11)		
Class: Gene Trap.		
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1.318		
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Query Match	15.8%;	Score 181.8; DB 29; Length 318;
Best Local Similarity	77.4%;	Pred. No. 6.2e-25;
Matches 233; Conservative	0;	Mismatches 67; Indels 1; Gaps 1;
Db	257	GATPACAAAGATGAAAGACGACCAACATTTACATATTTAACTGCTTTGGCAGATG 316
Qy	317	CTTTAGTTACTCAAAACCATGCGCTTTGACAGTACCGGTCTACTGTGATTCCTGCGCCTT 376
Db	67	CCCTGGCCACGACGACGCGTCCCTTCCAGAGGCCAAGTACTGATGGAACGTGCGCT 126
Qy	377	TTGGGGATGCTGTGGCAAGATGATTAATTCATTGATTACTACAACATGTTACCACGACA 436
Db	127	TTGGCGAGCTGTGTGGCAAGGCTGTGCTCTCCATTGACCTACTACAACATGTTACTACACA 186
Qy	437	TCTTCACCTTGCATCATGATGAGCGTGGACCGGCTACATTCGCGTGTGACACCCCGTGAAG 496
Db	187	TCTTCACCTTGCATCATGATGAGCGTGGACCGGCTACATTCGCGTGTGACACCCCGTGAAG 496
Qy	497	CTTTGGACTTCCGACACCCCTTGAAGGCAAGATCATCATATTCGATCTGCTGCTGT 556
Db	247	CCCTGACCTTCGACACCCGACGCAAGGCAAGCTGATCATATATATGACATCTGGGCTTGG 306
Qy	557	C 557
Db	307	C 307
RESULT 47		
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LOCUS	AGNCNC0IRT_15592335 NIH_ZGC_4	Danio rerio cdna clone IMAGE:7014015
DEFINITION	5', mRNA sequence.	
ACCESSION	CF550026	
VERSION	CF550026.1	GI:34886858
KEYWORDS	EST.	
SOURCE	Danio rerio (zebrafish)	
ORGANISM	Danio rerio	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS	Actinopterygii; Neopterygii; Teleostei; Ostariophysi;	
TITLE	Cypriniformes; Cyprinidae; Danio.	
JOURNAL	1 (bases 1 to 776)	
COMMENT	NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics National Cancer Institute / NIH Bldg. 31 Rm10A07 Bethesda, MD 20892	

		Email: cgaabs-remail.nih.gov Tissue Procurement: John Ngai, Univ of CA, Berkeley cDNA Library Preparation: Dr. Sumio Sugano cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNI) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNI at: http://image.llnl.gov Plate: LLAM14726 row: 1 column: 13 High quality sequence stop: 726.
FEATURES		location/Qualifiers
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ORIGIN		
Query Match	15.7%	Score 181.2; DB 14; Length 776;
Best Local Similarity	56.1%	Pred. No. 1.2e-24;
Matches	403; Conservative	0; Mismatches 308; Indels 7; Gaps 3;
Dn	171	CATCCCGTCATCATCAGGCGGTCTACTCCGATGTTCGTGGCGTTGATGGCAA 230
Oy	40	CAGGCGCAATTTCCTTCCTCATCTACCTCGTGCTAGTAGTAATGTGGAA 99
Dn	221	CTCGGTGATGTTCGATGATGCCAATCACAAAATGAAGAACAACAATTTA 290
Oy	100	CTCATGTGATATATGTATGTATCTTCAAGTATGCAAAATGAAATCTGACCAATACTA 159
Dn	291	CATATTTAACCTGGCTTTGGCAATGCTTTAGTTACTACAAACCATGECCTTTGAGATAC 350
Oy	160	TATTTGAACTTGGCGATCGCGATGTAGTTACTCATGTGAGCGGTCTTCTTGTCAC 219
Dn	351	GGTCTACTGTATGAAATTCCTGGCTTTTGGAGATGCTGTCAAAATAGTAATTTCCAT 410
Oy	220	CTCTCTTTACTTACACAACGCGCGTTTGGTCTCTCTGTGCTGGTTTTMAAGT 279
Dn	411	TGATTTACTACAACATGTTTACACAGATCTTCACCTTGACATGATGACGTGACGCTTA 470
Oy	280	TGATGCAATTAATATGTTCACACAGATCTATGTCACCGTGTGTAGCATCGATCGTTA 339
Dn	471	CATTGCCGTGCCACCCCGTGAAGCTTTTGAACCTTCCGACACCCCTTGAAGCAAGAT 530
Oy	340	CATCTCGGTGATGCCATCAAAAGCTGCCGCTACCGGAGACCCATCGCTAAAT 399
Dn	531	CATCAATATTCGATCTGGCTGTGCTGTGATCATCGTTGGACATCTGCAATTAATCCTGG 590
Oy	400	GGTCACTTGACAGTCTGATGTT---CTCACTCTGATATTTCTCCCATCATCTT 456
Dn	591	AGGCACCAAAATCAGGAGAACGTGATGTCATTGATGTCTCTTSCAGTITCCAGATGA 650
Oy	457	CTCCACCACTGCCCCCAACTGTATGGATCTAGAGGTGCAACATGCAAGTCAAGGCC 516
Dn	651	TGACTATCTCTGTGGGAAGCTCTTCAATGAAGATCTGGCTTTATCTTTGCTGAT 710
Oy	517	CGAGCGCAAGTATGCGCGTTTGT---GATATACGCTTTCTATGAGGCTTTCTCT 573
Dn	711	CCCTGTCATCATGATCGTCTGTACACCCGATGATCTCGTCAAGAGCGTCCG 770
Oy	574	CCCTGTCATGCAATCTGATGTCATCAATCTCATTCAATGTCATCAATGCAAGTGTGGC 633
Dn	771	GCTCTTTTGGTCTCCCGAAGAAATGCAACTCTGCTAGATCACAGACTGCTCT 830
Oy	634	GCTCAAAAGCGGCTGGCAAGCGCAAAAAGTCCGAGAGAAAAATCACCTGATGTGAT 693
Dn	831	GGGTGTGTGTGAGAGTCTTGTGTGTGTGTGATCTCCATTTCAATTTATCTGTGTG 888
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RESULT 48
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 LOCUS Pan troglodytes SSTR1 gene, VIRTUAL TRANSCRIPT, partial sequence.
 DEFINITION genomic survey sequence.
 ACCESSION AY400828
 VERSION AY400828.1 GI:39756817
 KEYWORDS GSS.
 SOURCE Pan troglodytes (chimpanzee)
 ORGANISM Pan troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pan.
 REFERENCE 1 (bases 1 to 1176)
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejaritwal,A., Todd,M.A., Tanenbaum,D.M., Civeallo,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,J.J., Adams,M.D. and Cargill,M.
 Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
 JOURNAL Science 302 (5652), 1960-1963 (2003)
 PUBMED 14671302
 AUTHORS 2 (bases 1 to 1176)
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejaritwal,A., Todd,M.A., Tanenbaum,D.M., Civeallo,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,J.J., Adams,M.D. and Cargill,M.
 Direct Submission
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
 COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.
 FEATURES
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 1..1176
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 /mol_type="genomic DNA"
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 Beel Local Similarity 47.2%; Pred. No. 2e-24;
 Matches 448; Conservative 0; Mismatches 484; Indels 18; Gaps 3;
 QY 75 CAGCAGCGGCTGTTCCCGGCTGGGCGAGCCCGACAGCAACGCGCGGCTCGGA 134
 DB 72 CGCGGCGACAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGA 131
 QY 135 GGACGCGCAGCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 194
 DB 132 TCGGCTCCGAGAACGGGACCTTGAGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCTT 191
 QY 195 CTACTCCGTAAGTGTCTGTGGGCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 254
 DB 192 CTACTCCGTAAGTGTCTGTGGGCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 251
 QY 255 CGGATACACAAGATGAAGACAGCAACCAATTATTAATTAACCTGGCTTGGCACA 314
 DB 252 GCGGCTATGCGAAGATGAAGACAGCAACCAATTATTAATTAACCTGGCTTGGCACA 311
 QY 315 TGCTTAGTTACTACAAACGATGCTTTCAGAGTACGATCTTCTGATGAATTCCTGGCC 374
 DB 312 TGAGCTGCTCATGCTCAGGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 371
 QY 375 TTTTGGGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 434
 DB 372 NNN 431
 QY 435 CATCTTCACTTGCACATGATGAGCGGTGACCGCTACATTTGCGCTGCGACCCGCTGAA 494

DB 432 NNN 491
 QY 495 GCGTTGACCTTCCGACACCTTTGAAGCAAGATCATATATGTGATCTGGCTGCT 554
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 QY 555 GTGCTCATCTGTTGGATCTGCAATAGTCTGGAGGACCAAGTACGGAGGACGCT 614
 DB 552 ATGCTGCTGCTCATCTGCTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 611
 QY 615 CGATGCTCATGAGTGTCTCTGCAAGTCCAGATGATGATCTCTCTGCTGCTGCTGCT 674
 DB 612 CACGG---TGGCTTGAACATCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 668
 QY 675 CATGAAGATCTGCTGCTTCTCATCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 734
 DB 669 CGT---GCGTGTACATTTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 725
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 DB 726 CTACGCTCTCATCTATCTTCTAAGATGCGCATGCTGCTGCTGCTGCTGCTGCTGCTG 785
 QY 795 AGATGCGCAACTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 854
 DB 786 CAAAGGCTGCGAGCGGCAAGATCACCTTATGATGATGATGATGATGATGATGATGATG 845
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 DB 846 CTGCTGAGTCCCATTCATCTGCTGAGGCTCTGGGAGACCTCCACAG 905
 QY 915 CACAGCTGCTCTCTCAGATATTTACTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 974
 DB 906 CACGCTGAGCC-----AGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 953
 QY 975 GATCCCATCTCTACGCTTCTTCTGATGAAACTTCAAGCGGCTTTCC 1024
 DB 954 CAAACCATCTCTATGCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1003
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 BU366266 735 bp mRNA linear EST 28-NOV-2002
 LOCUS 603567880P1 CSEQCHN72 Gallus gallus CDNA clone CHEST523019 5', mRNA
 DEFINITION sequence.
 ACCESSION BU366266
 VERSION BU366266.1 GI:25874267
 KEYWORDS EST.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 REFERENCE 1 (bases 1 to 735)
 Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E., Pong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
 A Comprehensive Collection of Chicken cDNAs
 JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
 MEDLINE 22355534
 PUBMED 12445392
 COMMENT Contact: Simon Hubbard
 Department of Biomedical Sciences
 University of Manchester Institute of Science and Technology
 (UMIST)
 PO Box 88, Manchester, M60 10D, UK
 Tel: 01612008930
 Fax: 01612360409
 Email: Simon.Hubbard@umist.ac.uk.
 FEATURES
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/notes="Organ: brain; Vector: pBluescript II KS(+); Site_1:
EcoRI; Site_2: NotI; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was bluntended, ligated to NotI adapters, digested with
EcoRI, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."
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ORIGIN

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Query Match      15.5%; Score 179.2; DB 13; Length 735;
Best Local Similarity 70.1%; Pred. No. 2.8e-24;
Matches 255; Conservative 0; Mismatches 108; Indels 1; Gaps 1;

QY 249 GATCATCCGATACAAAGATGAGACGACCAACATTATTTAACTGGCTTT 308
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DB 372 GCTTACCGGATTCACCAAGATGAGACGACCAACATTATTTAACTGGCTTT 431
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QY 309 GGCAGATGCTTATGATCTACCAACATGCGCTTTCAGAGTACGCTACTTGATGAAATTC 368
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 422 GGTACACACGCTGTGTGATGACCTTACCTTCCAGGTTACAGACAGCTTCTGGGCTT 491
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 369 CTGGCTCTTTGGGAGATGCTGTGCAAGATGAAATTTTCATGATTAACACATGTT 428
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    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 429 CACGACATCTTACCATGACATGATGAGCGGTGA-CGGCTACATTTGCCGTGCCAC 487
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 552 CACAGACACTTACGCTGACATGATGAGCGGTGACCGCTTACATCGCTATCTGCCATC 611
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 488 CCGTGAAGGCTTTGACCTTCCGACACCTTGAAGGCAAGATCATATATCTGCATCT 547
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 612 CTATCAAGGCTGTGACATTCGCACTCTCATTAAGGCAAGTGTGAACGTCGCACTCT 671
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 548 GCGTCTGTCTGATCTGTGGCATCTCTGCAATAGTCTTTGGAGGACCAAGTCAGGG 607
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DB 672 GGGCGCTGCTTCTGTCTTTGGCATCCGACGATGATGGAGTCTGCCAGATATGAG 731
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QY 608 AAGA 611
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DB 732 AACA 735
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RESULT 50
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LOCUS       Homo sapiens GPR7 gene, VIRTUAL TRANSCRIPT, partial sequence.
DEFINITION  Homo sapiens GPR7 gene, VIRTUAL TRANSCRIPT, partial sequence.
ACCESSION   AY401571
VERSION     AY401571.1 GI:39757560
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 987)
AUTHORS     Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
            Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
            Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sinsky,J.J.,
            Adams,M.D. and Cargill,M.
            Inferring nonneutral evolution from human-chimp-mouse orthologous
```

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gene trio
Science 302 (5652), 1960-1963 (2003)
PUBMED      14671302
REFERENCE   2 (bases 1 to 987)
AUTHORS     Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
            Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
            Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sinsky,J.J.,
            Adams,M.D. and Cargill,M.
            Direct Submission
            Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
            This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
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FEATURES

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Best Local Similarity 51.8%; Pred. No. 3.7e-24;
Matches 452; Conservative 0; Mismatches 417; Indels 3; Gaps 2;

QY 154 GCGCATCTCCCGGCGCATCCGATCATCAACGCGGCTTACTCCGATGTTGCTC 213
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DB 148 GTGGCTTTGGGCACTGCTGTGATGTTGTTGATCATTCGATACCAAGATGAAG 207
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DB 208 ACCGTACCAACCTGTTATCTCACTGACCTGACCTGACCTGACCTGACCTGAC 267
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QY 334 ATGCCCTTCAAGATGAGTCTTACTTATGATGAAATCTCGGCTTTTGGGAGTGTGTC 393
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DB 268 CTGCCATCAACATTCGCGCACTTCTGCTGCGGAGTGGCGCTTCGGGAGCTCATGTGC 327
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QY 394 AAGATGAAATTTTCATGATTAACATGATTAACATGATTAACATGATTAACATGAT 453
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DB 328 AAGCTATCGTGTGATGACAGTATCAACACTTCTCAAGCTTCTCAAGCTTCTCA 387
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QY 454 ATGACGTGACCGCTCACTATTTGCGGTGACACCCGCTGAAGGCTTTGACCTTCGACA 513
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DB 388 ATGACGTGACCGCTCACTATTTGCGGTGACACCCGCTGAAGGCTTTGACCTTCGACA 445
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QY 514 CCTTTGAAGGCAAGATCATATATCTGATCTGCTGCTGTCTGTATCTGTTGGATC 573
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DB 446 GCCGCACTTACAGCGCGCGCGCGCGGTGAGCTTGCGGCG--TGTGGGAGATGTACATC 504
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DB 505 GTCTGTGCTGCTTTCGAGATCTTTCGCGCGCTACAGACAGAGGCGCGCGCACTGC 564
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QY 634 TTGCACTTCCAGATGATGATCTCTGTGAGGAGCTTTCAATGAAGTGTGCTTC 693
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QY 694 ATCTTTCCTTTGATGATCTGTCTGTATATATATATATATATATATATATATATAT 753
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DB 625 GTGCTGAGCTTTCGCACTCCCGTGTCCACCATCTGTCTCTTATACCACTCTGTGC 684
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DB 685 CGGCTGATGCTATGCGCTGAGACGACGACGACGACGACGACGACGACGACGACGAG 744
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QY 814 ATCAACGAGCTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 873
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Qy 874 AATATTCCTGCTGGAGGCTCTGGGGAGACCTCCACAGCAGCTCTCTTCACG 933

Db 805 CTGAGCAGCGTGTGCGCTCACACGACCTCCCGACACGCCGTGTCTCATCGCTATC 864

Qy 934 TATTACTTGTGATCGCCTTTAGGCTATACCAACAGAGCTGATCCATCTCTTACGCG 993

Db 865 TCTTACTTATATCACGAGCCTGAGCTACGCGCAACAGCTGCTTCAACCTCTCTTACGCC 924

Qy 994 TTTCTTGATGAAACTTCAAGCGGTGTTCCG 1025

Db 925 TTCTGTGACGCCAGCTTCCGACGAACCTCCG 956

RESULT 51
BC033145/c 2724 bp mRNA linear HTC 04-MAR-2003

LOCUS Homo sapiens, clone IMAGE:4040710, mRNA.

DEFINITION BC033145

ACCESSION BC033145.1 GI:23138699

VERSION BC033145.1 GI:23138699

KEYWORDS HTC.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2724)

AUTHORS Strausberg, R.

JOURNAL Direct Submision
Submitted (25-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT Contact: MGC help desk
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca

Steven Jones, Jennifer Asano, Ian Boedert, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Leticia Heiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeay, Steven Ness, Pawan Pandoh, Anna-Lissa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smalhu, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Teal, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: <http://image.linl.gov>
Series: IRAL Plate: 43 Row: c Column: 19
This clone has the following problem: retained intron.

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ORIGIN
Query Match 15.5%; Score 178.8; DB 11; Length 2724;
Best Local Similarity 51.8%; Pred. No. 5,6e-24;
Matches 452; Conservative 0; Mismatches 417; Indels 3; Gaps 2;

154 GGGCAGATTCGGCGGCATCCGGCATCATCAGCGCGGTACTCCGTAGGTTCCG 213
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Db 1123 GCGCCGTCGCGGCGCCGCTGAGCGGTGTACCAAGTTGTACGCGGTATTCGCGC 1064

Qy 214 GTGGCTTGATGGGCAATCGCTGTGATGTTCTGTGATCATCCGATACCAAGATGAAG 273

Db 1063 GTGGGTCTGGCGGGAATCCCGCGTGTGATGTTGTGCTCGCGCGCGCGCAAGA 1004

Qy 274 ACAGAACCAATTTACATATTTTAACCTGCGTTTGAGAGATGCTTTAGTTACTAACAC 333

Db 1003 ACCGTACCAACTGTTTATCTCTCAACTGGGCATTCGCGAGAGCTCTTACGCTGG 944

Qy 334 ATGCCCTTACAGATGATCGCTACTGATGATGAAATTCCTGCGCTTTTGGGATGTGCTGC 393

Db 943 CTGCCCATCAATCGCGCGAATCTCTGCTGCGGAGTGCCCTTGGGGAGCTCATGTGC 884

Qy 394 AAGATGTAATTTCCATTGATTTACTACCAATGTTTACACGATCTTACCTTGACATG 453

Db 883 AAGCTCATGTGTGCTATGACACAGATCAACACCTTCTCCAGCTTACTTCTCCACCGTC 824

Qy 454 ATGACGTGGAACCGCTACATTTGCGTGTGCCACCCCGTGAAGGCTTTGAGCTTCCGACA 513

Db 823 ATGAGCGCGACCGCTTACTGTGTGTGTGTGACCTGCGAG--TGGCGCGGTGCGCG 766

Qy 514 CCTTGAAGGCAAGATCATCAATATCTGCATCTGCTGTCTGTCTCATCTGTGGCATC 573

Db 765 GCGGACCTACAGCGCGCGCGCGGCGGTGAGCTGGCG--TGTGGGGATGTCAACATC 707

Qy 574 TCTGCAATATGTCCTTTGAGGACCAAGTCAAGGAAGCTGATGTCTATTAGTCTCC 633

Db 706 GTGTGTGTCGCTTGTGCGAGTCTTCCCGGCTGACGACGACGAGCGCGCGCGCAATGC 647

Qy 634 TTGCAATTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 693

Db 646 GTGTGATGTTTCCGACCGCGAGCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 587

Qy 694 ATCTTGTGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 753

Db 586 GTGTGTGTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 527

Qy 754 GGTCTCAAGAGCGTGTGCTCTTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 813

Db 526 CGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 467

Qy 814 ATCAGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 873

Db 466 GTACCTTCTGT 407

Qy 874 AATATTCCTGCTGGAGGCTCTGGGGAGACCTCCACAGCAGCTCTCTTCACG 933

Db 406 CTGAGCAGCGTGTGCGCTCACACGACCTCCCGACAGCCCGCTGTCTATCGCTATC 347

Qy 934 TATTACTTGTGATCGCCTTTAGGCTATACCAACAGAGCTGATCCATCTCTTACGCG 993

Db 346 TCTTACTTATATCACGAGCCTGAGCTACGCGCAACAGCTGCTTCAACCTCTCTTACGCC 287

Qy 994 TTTCTTGATGAAACTTCAAGCGGTGTTCCG 1025

Db 286 TTCTGTGACGCCAGCTTCCGACGAACCTCCG 956

RESULT 52
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LOCUS UI-M-BH3-ssd-d-09-0-UI.81 NIH_BMAP_M_S4 Mus musculus CDNA clone

DEFINITION UI-M-BH3-ssd-d-09-0-UI 3', mRNA sequence.

ACCESSION AM489031

VERSION AM489031.1 GI:7059301

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 433)

AUTHORS Bonaldo, M.F., Lennon, G. and Soares, M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 97044477
 PUBMED 8889548
 COMMENT

Contact: Chin, H
 National Institute of Mental Health
 6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
 20892-9643, USA
 Tel: 301 443 1706
 Fax: 301 443 9890
 Email: mstremail.nih.gov
 Oligo-dt track not found, Not I site shown in beginning of sequence
 is likely internal to the message. cDNA library Preparation: M.B.
 Soares Lab Clone distribution: Researchers may obtain BMAP cDNA
 clones from RESEARCH GENETICS. It should be noted that Bento Soares
 is generating a small number of additional specialized
 non-redundant arrays of BMAP cDNAs whose availability will be
 considered under appropriate and limited collaborative arrangements
 Seq primer: M13 Forward
 POLYA=No.

FEATURES

Location/Qualifiers
 1..433
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UI-M-BH3-asd-g-09-0-UI"
 /dev_stage="27-32 days"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="NIH_BMAP_M_S4"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified
 polylinker; Site 1: Not I; Site 2: Eco RI; The
 NIH_BMAP_M_S4 library is a subtracted library of a series,
 ultimately derived from a mixture of individually tagged
 normalized libraries from ten regions of the mouse brain
 (cerebellum, brain stems, olfactory bulbs, hypothalamus,
 cortex, amygdala, basal ganglia, pineal gland, striatum,
 hippocampus) after a series of subtractions to reduce the
 representation of cDNAs from which ESTs had already been
 generated. The following serially subtracted libraries
 were generated in this process: NIH_BMAP_M_S4,
 NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, NIH_BMAP_M_S3.1,
 NIH_BMAP_M_S2, NIH_BMAP_M_S1. The subtracted library
 (NIH_BMAP_M_S4) was constructed as follows: PCR amplified
 cDNA inserts from NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, and
 NIH_BMAP_M_S3.1 clones from which 3' ESTs had been derived
 was used as a driver in a hybridization with a pool of
 the NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, and NIH_BMAP_M_S3.1
 libraries in the form of single-stranded circles. The
 remaining single-stranded circles (subtracted library)
 was purified by hydroxyapatite column chromatography
 converted to double-stranded circles and electroporated
 into DH10B bacteria (Life Technologies) to generate the
 NIH_BMAP_M_S4 library. This procedure has been previously
 described (Bonaldi, Lennon and Soares, Genome Research
 6:791-806, 1996)
 TAG_TISSUE=cerebellum
 TAG_LIB=NIH_BMAP_M_S4
 TAG_SEQ=CGGNA"

ORIGIN

Query Match 15.5%; Score 178.4; DB 10; Length 433;
 Best Local Similarity 68.5%; Pred. No. 3.2e-24;
 Matches 261; Conservative 0; Mismatches 117; Indels 3; Gaps 1;
 QY CTCCTGGGAGACCTCTTCATGAAAGATCTGGCTCTTATCTTTGGCTTCGATCCTGT 716
 Db CTGGTACTGGAGACACTGACCAAGATCTGGCTCTTCTCTTGGCTTCGATCCGAT 340
 QY CCTCATCATCATCGCTCTGTACACCTGATGATCTCGGCTCTCAAGAGCGTCCGGCTCT 776
 Db CCTCATCATCATCGGCTGTCTATGCGCTCATCTACTGCGCTGCGCAGCGTCTGCT 280

QY 777 TTCTGCTCCGAGAGAAATTCGCACTTCGTAAGATACCAAGACTGCTCTGTGGGT 836
 Db TTTCTGCTCCGAGAGAAATTCGCACTTCGTAAGATACCAAGACTGCTCTGTGGGT 220
 QY 837 GGTGACGCTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 896
 Db GTTGGGCGCTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 160
 QY 897 GGGG---AGCACTCCACACGACAGCTGCTCTCTCCAGCTATTACTTGTGATCGCTT 953
 Db GGTGACATCATATCGGCGCGACCCACATCTGTGTGGCGGACATGACCTGTGCGCT 100
 QY 954 AGGCTATTCACACGATGACCTGATTCATTCATCTTACGCTTTTGTATGAAACTTCAA 1013
 Db GGGCTACGCGCAACGACGACCTCAACCGGTTCTTACGCTTCTGACGAGAACTTCAA 40
 QY 1014 GCGGTGTTTCCGGGACTTCTG 1034
 Db 39 GCGCTGCTTCCGCCAGCTCTG 19

RESULT 53
 BUE13017 741 bp mRNA linear EST 20-FEB-2003
 LOCUS BUE13017
 DEFINITION UI-M-FR0-cbd-m-06-0-UI.r1 NIH_BMAP_FRO Mus musculus cDNA clone
 UI-M-FR0-cbd-m-06-0-UI.5, mRNA sequence.
 ACCESSION BUE13017
 VERSION BUE13017.1 GI:23279232
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE 1
 AUTHORS Mammalia; Butcheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 TITLE NIH-MGC http://mgc.nci.nih.gov/.
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Unpublished (1999)
 Contact: Robert Strauberg, Ph.D.
 Email: egads-remail.nih.gov
 Tissue Procurement: Dr. Jim Lin, University of Iowa
 DNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be obtained
 from Dr. M. Bento Soares, bento-soares@uiowa.edu
 This clone was contributed by the Brain Molecular Anatomy Project
 (BMAP)

FEATURES

Location/Qualifiers
 1..741
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="UI-M-FR0-cbd-m-06-0-UI"
 /tissue_type="whole brain"
 /dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
 /lab_host="DH10B (TI phage resistant)"
 /clone_lib="NIH_BMAP_FRO"
 /note="Organ: Brain; Vector: pYX-Asc; Site 1: EcoR I;
 Site 2: Not I; The library was constructed according
 to Bonaldi, Lennon and Soares, Genome Research, 6:791-806,
 1996. Denatured RNA was size fractionated on a 1% agarose
 gel. First strand cDNA synthesis was primed with oligo-dT
 primer containing a Not I site. Double strand cDNA was
 size selected according to mRNA size fraction, ligated
 with EcoR I adaptor, digested with NotI and then cloned
 directionally into pYX-Asc vector. The library tag
 sequence located between the Not I site and the polyA tail
 is AGCGAGACG. This library was created for the University
 of Iowa Brain Anatomy Project (BMAP). 'Gene Discovery in the
 Developing Mouse Nervous System', supported by National

ORIGIN

Institute of Mental Health (NIMH), Hemlin Chin, Ph.D.,
program coordinator."

Query Match 15.5%; Score 178.4; DB 13; Length 741;
Best Local Similarity 64.3%; Pred. No. 4e-24;
Matches 283; Conservative 0; Mismatches 156; Indels 1; Gaps 1;

QY 660 CTGGTGGGACCTCTTCATTAAGATCGGCTTT-CATCTTGGCTTCGGATCCCTGTC 718
DB 42 CTATTGGGGCCCTGATTTGGCCATTCGATCTTCTTTTCTTCATCATCCCGGTTTC 101
QY 719 TCATCATCTGCTGCTACCGCTGATGATCCTGGCTCAAGAGCGTCCGGCTCTTT 778
DB 102 TCATCATCTGCTGCTACCGCTGATGATGATGATGATGATGATGATGATGATGAT 161
QY 779 CTGGCTCCCGAGAGAAAGATCCCAACCTGAGATCAACAGACTGCTCTGAGTGG 838
DB 162 CAGGCTCCCGAGAGAAAGACCGGACCTGAGATCAACAGGCTGTAAGTGG 221
QY 839 TGGCAGCTCTTCTGCTGCTGAGCTCCCATTCATATTCATCTGCTGAGGCTTGG 898
DB 222 TGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 281
QY 899 GAGAGACCTCCCAAGACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 958
DB 282 GTGCTCAGCAGAGTGTAGAGCTGAGTACGATGCTGCTGCTGCTGCTGCTGCTGCT 341
QY 959 ATACCAACAGTACCTGATTCCTGATTCCTGATTCCTGATTCCTGATTCCTGATTC 1018
DB 342 ATGTCACAGCTGTGCTCAATCCCATCTCTATGCTTTCTGATGAGATTCAGAGGCT 401
QY 1019 GTTTCGGGACCTTCTGCTTCCATGAGATGAGATGAGATGAGATGAGATGAGATG 1078
DB 402 GCTTGAAGAAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 461
QY 1079 TCCGAATTCAGTTCAGAT 1098
DB 462 TCCGACGATTCAGAT 481

RESULT 54
B1753905 720 bp mRNA linear EST 25-SEP-2001
LOCUS 603022907P1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5193768 5',
DEFINITION mRNA sequence.
ACCESSION B1753905
VERSION B1753905.1 GI:15745483
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 720)
TITLE NIH-MGC http://mgi.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Place: LAM1484 row: m column: 01
High quality sequence stop: 716.
Location/Qualifiers

FEATURES
source
1..720
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"

/clone="IMAGE:5193768"
/lab_host="DH10B"
/clone_lib="NIH_MGC_114"
/note="Organ: brain; Vector: pCMV-SPORT6, Site_1: NotI;
Site_2: EcoRV (destroyed); RNA source anonymous pool of 6
male brains, age range 23-27 yo. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.5 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 019. Note:
this is a NIH_MGC Library."

ORIGIN

Query Match 15.4%; Score 177.8; DB 12; Length 720;
Best Local Similarity 56.0%; Pred. No. 5.1e-24;
Matches 378; Conservative 0; Mismatches 292; Indels 5; Gaps 2;

QY 166 CCGGCGATCCGGATCATCAAGGCGGTCTCTCGATGCTGCTGCTGCTGCTGCTGCTG 225
DB 49 CAGGCGAGCGCATCTGATCTTTTCACTACCTCGGTGCTGCTGCTGCTGCTGCTGCTG 108
QY 226 GCGAATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 285
DB 109 GGGAACTGATGCTATCTAGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 168
QY 286 ATTTACATATTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 345
DB 169 ATCTACATCTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 228
QY 346 AGTACGCTACTGATGATGATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 405
DB 229 GTACCTTCACCTTTTGGCCATGAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 288
QY 406 TCCATTTGATTTACATGATTTTCAACAGATCTTCACTTCACTTCACTTCACTTCACT 465
DB 289 AGCGTGAAGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 348
QY 466 CGCTACATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 525
DB 349 CGCTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 408
QY 526 AAGATCATCAATATCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 585
DB 409 AAGTATGATTAACCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 468
QY 586 CTGGAAGCACAAGTACAGGAGAGAGCTGATGCTGATGCTGCTGCTGCTGCTGCTGCTG 645
DB 469 TTCTCTGCAACCGGCGGCAACGCAAGGCAAGG---TGGCTTGAACATGCTCATGCCA 525
QY 646 GATGATGACTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 705
DB 526 GAGCCCGCTCAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 585
QY 706 GTGATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 765
DB 586 CTG---CCCGTGGGGCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 643
QY 766 GTCCGCTCTCTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 825
DB 644 GTGGGCTCTCAAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 703
QY 826 GTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
DB 704 GTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 718

RESULT 55
BX843850 828 bp mRNA linear EST 11-DEC-2003
LOCUS BX843850
DEFINITION BX843850 NICHD XGC Emb2 Xenopus laevis cDNA clone IMAGE998C1410117
ACCESSION ; IMAGE:4404805 5', mRNA sequence.
BX843850

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VERSION      BX843850.1  GI:39734073
KEYWORDS     EST.
SOURCE       Xenopus laevis (African clawed frog)
ORGANISM     Xenopus laevis
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
              Xenopodinae; Xenopus.
              1 (bases 1 to 828)
REFERENCE    Heil, O., Neubert, P., Peters, M., Radelof, U., Schneider, D.,
AUTHORS      Schrott, A., Korn, B. and Landgrebe, J.
TITLE        Xenopus laevis UniGene Set 1 (RZPDLIB No.988)
JOURNAL      Unpublished (2003)
COMMENT      Contact: Ina Rolfs
              RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
              Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
              RZPD: IMAGP988C1410117.
              RZPDLIB: I.M.A.G.E. cDNA Clone Collection (amp- resistant) (RZPDLIB
              No.988) http://www.rzpd.de/cgi-
              bin/products/showlib.pl.cgi/response?libNo=988 RZPDLIB: Xenopus
              laevis UniGene Set 1 (RZPDLIB No.988) http://www.rzpd.de/cgi-
              bin/products/showlib.pl.cgi/response?libNo=988 Contact: Ina Rolfs
              RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
              Heidenweg 6, D-14059 Berlin, Germany
              Tel: +49 30 32639 101
              Fax: +49 30 32639 111
              www.rzpd.de
              This clone is available royalty-free from RZPD.
              Contact RZPD (clone@rzpd.de) for further information. Seq primer:
              SP6, 5' ATTTAGGTACACTAATG 3'.
FEATURES     location/Qualifiers
source       1..828
              /organism="Xenopus laevis"
              /mol_type="mRNA"
              /db_xref="taxon:8355"
              /clone="IMAGP988C1410117 ; IMAGE:4404805"
              /tissue_type="embryo, stage 17/19"
              /lab_host="DH10B (phage-resistant)"
              /clone_lib="NICHD XGC Emb2"
              /note="Vector: pCMV-sPORT6; Site_1: NotI; Site_2: SalI;
              Cloned unidirectionally. Primer: Oligo dt. Average insert
              size 2.1 Kb. Constructed by Life Technologies."
ORIGIN
Query Match      15.3%; Score 176; DB 13; Length 828;
Best Local Similarity 71.0%; Pred. No. 1.2e-23;
Matches 247; Conservative 0; Mismatches 100; Indels 1; Gaps 1;
OY      253 ATCCGATACACAAAGATGAGACAGCAACCAATTACATATTTACCTGGCTTTGCA 312
DB      469 ACCAGATACACCAAGATGAGAAACAGCAACCAATCTACATCTTCACCTTGGCT 528
OY      313 GATGCTTAACTTACACCAACCATGCTTTCAGATGAGTACTGATGTAATTCCTGG 372
DB      529 GATGCTCTTCCACATGACACCTCTTCCATTCAGATGCTAAGTATCTTAAGAACTTGG 588
OY      373 CTTTGGGGAGATGCTGTGCAAGATGATTAATTTCCATTGATTACTTACAAAGTTTACC 432
DB      589 CCTTTGGGAGAGCCCTCTGCAAGTGTCTTACGATATGACTTACTTACAAAGTTTACC 648
OY      433 AGCATCTTACCTTACCATGATGAGCGTGAACCGCTACATTCGCGTGTGCCACCCCGTG 492
DB      649 AGTATTTTACACATGACATGATGAGCGTGAATGCTGCTACATGCTGATATGACCTTATA 708
OY      493 AAGGCTTTGAGCTTCCGACACCTTTGAAGGC-AAAGATCATCAATATTCGATCTGGCT 551
DB      709 CGAGCACTGAGATTTTCGAATCCCTCTAAGGCTAAGGTTAATAAGTCTGATTTGGAT 768
OY      552 GCTGTCATCTGTTGGCATCTGCAATAGTCCCTGGAGGACACAA 599
DB      769 CTGTCTTCTGCAATGGGTTCAATTAATGTTTAATGCAATACAA 816
RESULT 56

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CONSULT1IBD 1307 bp  mRNA  linear  HTC 18-JUN-2003
LOCUS        human full-length cDNA 5-PRIME end of clone CS0DK011YG11 of Hela
DEFINITION   human full-length cDNA 5-PRIME end of clone CS0DK011YG11 of Hela
ACCESSION    BX248780
VERSION      BX248780.1  GI:28375508
KEYWORDS     HTC.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
              1 (bases 1 to 1307)
REFERENCE    Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
AUTHORS      Full-length cDNA libraries and normalization
TITLE        Unpublished
JOURNAL      Contact: Feng Liang Email : fliang@lifetech.com URL :
              http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
              Faraday Avenue
              2 (bases 1 to 1307)
COMMENT      Genoscope.
              Direct Submission
              Submitted (13-FEB-2003) Genoscope - Centre National de Sequencage :
              BP 191 91006 Evry cedex - FRANCE (E-mail : seqre@genoscope.cns.fr
              - Web : www.genoscope.cns.fr)
              1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
              end enriched, double-strand cDNA was digested with Not I and cloned
              into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library
              was normalized. Library was constructed by Life Technologies, a
              division of Invitrogen.
FEATURES     location/Qualifiers
source       1..1307
              /organism="Homo sapiens"
              /mol_type="mRNA"
              /db_xref="taxon:9606"
              /clone="CS0DK011YG11"
              /tissue_type="Hela Cells"
              /note="end : 5-PRIME-Cot 25-normalized-vector pCMVSPORT_6"
              332..661
              /note="unnamed protein product"
              /codon_start=1
              /protein_id="CAD66587.1"
              /db_xref="GI:28375509"
              /translation="MAVPCGAPTSWPLSTVACARAPRSCLQSPGNMAVAPAGAR
              SRAPSGCALPGAGRLMAAGKRSRGGRRRVREKAPALAPLAPLSDVDPQMR
              LSLFLS"
CDS
ORIGIN
Query Match      14.9%; Score 171.6; DB 11; Length 1307;
Best Local Similarity 57.1%; Pred. No. 1e-22;
Matches 312; Conservative 0; Mismatches 234; Indels 0; Gaps 0;
OY      75 CAGCAGCGCGTGTTCCTCCGCTGGGCGGAGCCGACAGCAACGACCGCGGCTCGGA 134
DB      689 CGGCGGACGAGCGGCGCCCGGGGCGGCGTGCAGCGCATGAGAGCGACGAGCGAAA 748
OY      135 GAGCGGAGCGTGAAGCGCGGACATCTCCCGGACATCCCGGTCATCATCGAGCGGT 194
DB      749 TCGTCCAGAACGAGACTTGAAGCGAGGCGCAGGCGCATCTGATCTTTTCAT 808
OY      195 CTACTCCGTAGTGTTCGTGCTGTGAGCTTGTGTGGGCACTCGCTGTGTCATGTTGATCAT 254
DB      809 CTACTCCGTGTGTGTGCTGTGAGCTGTGTGTGGAACTCTATGTGATCTAGTGATCTT 868
OY      255 CCGATACCAAAAGATGAAAGACGACACCAACATTTATTAATTTAACTGCGCTTTGGCAGA 314
DB      869 GCGGTATGCGCAAGATGAAAGCGGACCAACATCTTAATCTTGAATGCGCATTTGCGA 928
OY      315 TGCTTTAGTTTCTAACCAACCATGCGCTTTCAGAGTACGCTACTTGAATTTCTGGCC 374
DB      929 TGAAGTGTCTATGCTCAGCGTGCCTTCTAGTACCTCCACGTTGTCGCGCACCTGGCC 988
OY      375 TTTTGGGAGATGTGCTGTGCAAGATGATTAATTTCCATTGATTACTTACCAACATGTTCCACG 434

```


Db 989 CTTGGGCGCTGCTCTGCGCGCTGCTGCTGACGCGGCTCAACATGTTACACAG 1048
 Qy 435 CATCTTCACTTGACCATGATAGAGGTGAGACCGCTTACATTTGCGGTGACCCCGTGA 494
 Db 1049 CATCTACTGTCTGACGTGCTGAGCGTGAGCCGTACCGGCGGTGTCATCCATCA 1108
 Qy 495 GGCCTTGGACCTTCCGACACACCTTTGAAGGCAAGATCATCAATTCATCTGAGTGTCT 554
 Db 1109 GCGGCGCGGCTACCGCGCGGCTCAAGGTAGTAACTGAGCGGTGTGGTGTCT 1168
 Qy 555 GTGCTCATCTGTGGCATCTCTGCAATAGTCTTGGAGGACCAAGTCAAGGAAGAGCT 614
 Db 1169 ATGCGTGTCTGTCATCTCTGCGCATGCTGTCTTCTCTGACCGGCGCAACAGGAGCG 1228
 Qy 615 CGATGT 620
 Db 1229 CACGGT 1234

RESULT 57
 AM373832 654 bp mRNA linear EST 04-FEB-2000
 LOCUS AM373832
 DEFINITION QV3-BT0537-221299-048-h10 BT0537 Homo sapiens cDNA, mRNA sequence.
 VERSION AM373832.1 GI:6878486
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 654)
 HCCP <http://www.judwig.org.br/ORESTES>.
 TITLE The FAPESP/LICR Human Cancer Genome Project
 JOURNAL Unpublished (1999)
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@judwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (<http://www.judwig.org.br/scripts/gethtml2.pl?cl=QV3&c2=QV3-BT0537-221299-048-h10&t3=1999-12-22&t4=1>)
 Seq primer: puc 18 forward
 High quality sequence start: 639.
 Location/Qualifiers

FEATURES
 source 1..654
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_11b="BT0537"
 /note="Organ: Breast; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 14.7%; Score 170.2; DB 10; Length 654;
 Best Local Similarity 69.3%; Pred. No. 1.5e-22;
 Matches 232; Conservative 0; Mismatches 103; Indels 0; Gaps 0;
 Qy 153 GCGGACATCTCCCGGCGCATCCGGTATCATCAAGCGGCTTACTCGTAGTGTCT 212
 Db 320 CGCTTCTCGCCCTCGGCGCTCAAGGTACATCGGCGGCTTACTCGCGGTGTGT 379

Qy 213 CTTGGGCTTGGTGGGCAACTCGCTGATGATGTTCTGTATCATCCGATACAAAGATGA 272
 Db 380 CGAGAGGCTCTCGGGGAATCGCTTGTATGATGATCTTCAAGGACACAAATGA 439
 Qy 273 GACAGCAACCAATTATCATATTTTAACTGGCTTTGGAGATGCTTTAGTACAAAC 332
 Db 440 GACAGCCACCAATATTTATCATCTTTAACTGGCCCTGGCCGACACTGTGTCTGTGAC 499
 Qy 333 CATGCCCTTTAGAGTACAGGTCTACTTATGAAATTCCTGGCCCTTTTGGGAGATGCTGTG 392
 Db 500 GCTGCCCTTCCAGGCGACGAGCATCTCTCTGGCTTCTGGCCGTCTGGAAATGCGCTGTG 559
 Qy 393 CAAGATAGTAATTTCTATGATTTACTAACAAGTTTACACAGATCTTACCTTACCAT 452
 Db 560 CAAGACATGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 619
 Qy 453 GATGAGCGTGAACCGCTACATTCGCGTGTCCACC 487
 Db 620 CATGAGTGTGATCGGTATGTAGCATCTGCGAAC 654

RESULT 58
 AY401573 990 bp DNA linear GSS 15-DEC-2003
 LOCUS AY401573
 DEFINITION Mus musculus GPR7 gene, VIRUAL TRANSCRIPT, partial sequence,
 genomic survey sequence.
 VERSION AY401573.1 GI:39757562
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 990)
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.
 Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
 JOURNAL Science 302 (5652), 1960-1963 (2003)
 PUBMED 14671302
 REFERENCE 2 (bases 1 to 990)
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.
 Direct Submision
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
 This sequence was made by sequencing genomic exons and ordering them based on alignment.
 COMMENT
 LOCATION/Qualifiers
 source 1..990
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10090"
 /gene="GPR7"
 /locus_tag="HGM0935"

ORIGIN

Query Match 14.7%; Score 170.2; DB 29; Length 990;
 Best Local Similarity 50.3%; Pred. No. 1.7e-22;
 Matches 446; Conservative 0; Mismatches 438; Indels 3; Gaps 1;
 Qy 145 GCGAGCCCGGACATCTCCCGGCGCATCCGGTATCATCAAGCGGCTTACTCGGA 204
 Db 85 CTGACTCTCTGCGCGCTGCGGCGGCTGCGGAGAGAGTCTGTCTACGGGGTA 144
 Qy 205 GTGTCGTGTCGTGGCTTGGTGGGCAACTCGCTGATCTGTCGTGATCATCCGATACA 264
 Db 145 ATTGCGCGGTGGAGCTGGCGGCAACTCTGGCGGTGTGTAGTACTGTGCGGACGCG 204

QY 265 AAGATGAAGACAGCAACCAATTACATTTTAACTGGCTTTGGCAGATGCTTAACT 324
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 Db 205 CGCATTAAGACTGTACCAACGCTTTCATCTCAACCTGGCTATCCCGATGAAGCTCTTC 264
 325 ACTACAAACATGCGCTTTGAGAGTACGCTTCTATGTAATTTCTGGCTTTGGGAGT 384
 265 ACCCTGCTGCTGCCCATCAACATCGCGAGCTTCTGCTGAGGGGCGCTGGCTTCGGGAG 324
 QY 385 GTGCTGTGAAGATAGTAAATTTTCATTTACTATACATATGTTACCGACATCTTACAC 444
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 Db 325 GTCATGTGAAGTCAATGTAGCCGTGACCAAGTAAACATTTCTTGAAGCTTCACTTC 384
 445 TTGACCATGATGAGCGTGAAGCGCTACATTTGCGGTGGCCACCGCGTGAAGGCTTTGAC 504
 385 CTGCGCTGATGAGCGCGGACCGATACCTGGTGTCTTGGCCACAGAGATCGCGCG 444
 QY 505 TTCCGACACCTTTGAAGCAAAAGATCAATCAATATCTGATCTGGCTGTCTGATCT 564
 445 GTGTCCGGGCGACATTAAGGTGACGCGCTGCTGATGCTGAGCTGAGGCTGGCTGGTG 504
 QY 565 GTTGGATCTGCAATAGTCTCTTGAAGGACCAAGTCAAGGAAAGACTGATGCTACT 624
 505 ACGCTGTGTGCTGCTGCTTTCGCTATTCGCTGAGTGAAGAGAGAGAGGCTGCGCG 564
 QY 625 GAGTGTCTTGTGCAAGTCCAGATGATGACTACTCTGCTGGGAGCTCTTCTTGAAGATC 684
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 Db 565 CAGTGTGTGTGTGTCTTCCGAGCGCGAGGCTTCTGTGTG---GATGCCAGCGCTCTC 621
 685 TGGCTTCTATCTTGTGCTTGTGATCTGCTGCTCATCATCATGCTGTCTTACACCTTG 744
 622 TACACACTGATGTGGCTTTGCTTCCATCCGCTGACCAACATCTGATCTTATACACT 681
 QY 745 ATGATCTGCTGCTCAAGAGCGTCCGCTCTTCTGCTGCTCCGAGAGAAATGTCAC 804
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 Db 682 CTGCTGTGCGAGTGGCTGCTATCCAGCTAATAGCAGCAGCGCAAGCGCTGATGTGCT 741
 805 CTGCTGATGATCAAGACAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 864
 742 AAGAAAGCGGTGATCTGT 801
 QY 865 CCCATTCATATTTATCTGT 924
 |||||
 Db 802 CTTATTCACCTGAGTACATAGTGGCTTCCACCAACCGCTCCCAACCGCGCTGTGCT 861
 925 CTCTCAGCTATTACTTGTGATGCTGCTTGAAGCTTATCCACAGTAAAGCTGATCCCAT 984
 862 ATGCGATCTCTTACTTATCTACACAGCTGAGCTAATGCTAAGCTGCTCAACCTTTC 921
 QY 985 CTCTACGCTTCTTGTATGAAATCTTCAAGCGGTGTTCCGGGACTT 1031
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 Db 922 CTCTATGCTTCTCTGAGCAGAGCTTCCGCAAGACCTCCGGCAATT 968

RESULT 59
 AY400986 1095 bp DNA linear GSS 15-DEC-2003
 LOCUS AY400986 Homo sapiens SSTR5 gene, VIRUAL TRANSCRIPT, partial sequence,
 DEFINITION genomic survey sequence.
 ACCESSION AY400986
 VERSION AY400986.1 GI:39756975
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1095)
 AUTHORS Clark,A.G., Ghanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.
 TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene titles

JOURNAL Science 302 (5652), 1960-1963 (2003)
 PUBMED 14671302
 REFERENCE 2 (bases 1 to 1095)
 AUTHORS Clark,A.G., Ghanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.
 TITLE Direct Submission
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 COMMENT This sequence was made by sequencing genomic exons and ordering
 them based on alignment.
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 source location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
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ORIGIN
 Query Match 14.6%; Score 169; DB 29; Length 1095;
 Best Local Similarity 52.1%; Pred. No. 3.1e-22;
 Matches 463; Conservative 0; Mismatches 405; Indels 21; Gaps 3;

QY 140 CGCAGCTGAGACCGCGCCACATCTCCCGGATCCCGGCTCATGATGACGGGCTTAACT 199
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 Db 83 CGCTGTGGGGCCGCGCCCTCGGCAAGGGCCCGGGGCTGTGTGCTCCGTGTGACC 142
 QY 200 CCGATGT 259
 143 TGT 202
 QY 260 ACACAAAGATGAGACAGCAACCAATTTATATTTAACTGCTTTGGCAGATCTT 319
 203 TCGCAAGATGAAAGACCGTCAACCAATTTATTTCAACTGCGCAGTGGCCGACCTCC 262
 Db 320 TAGTTATCAACCAATCCCTTTCAGAGTACGGTCTTCTTGAATTTCTGCGCTTTG 379
 263 TGTATATGCTGGGGCTCTCTTCTGCGCAGCAGAAAGCGCGCTCTTCTGCGCTTGC 322
 QY 380 GGGATGTCTGTGCAAGATAGTAAATTTCAATTTACTTAAACATGTTACAGCATCT 439
 323 GCCCGCTCTGTGTGCGCTGCTGTATGACGCTGAGACGGCGTCAACAGTTACACAGTGTCT 382
 Db 440 TCACCTTGACCATGATGAGGTGAGCCGCTTACATTTGCTGTGTGCAACCCGTGAAGCTT 499
 383 TCTGCTGACAGTATGAGGTGAGCCGCTTACCTGCGAGTGTGCAACCCGTGAGCTCGG 442
 QY 500 TGAAGTCCGCAACCTTTGAAGGCAAGATCAATATCTGATCTGGCTGTGTGCT 559
 443 CCGCTGCGCGCGCGCGCGGTGTGCGCAAGCTGGCGAGCGCGCGCTGGGCTCTG--- 498
 Db 560 CATCTGTGGCATCTTCAATAGTCTTGTGAGGACCAAAAGTCAGGAGAGAGCTGCATG 619
 499 --TCTGTGTGATGTGCTGCGCTGCTGTGTTTGTGCGACGTGTGAGAGAGGGGTAACT 556
 QY 620 TCATTTAGTGTCTTCTTCAAGTTCACAGTATGACTACTCTGCTGTGGAGCTCTTATGA 679
 557 GCAACGCAACCTGTGCGGACCGCGTGGGCT-----GTGGGGGCGCGTCTTCA 604
 Db 680 AGATCTGCGCTTCAATCTTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 739
 605 TCATTTCAACGCGCGT 664
 QY 740 CCGTGTATGATCTGCGCTCAAGAGCGTCCGCTCTTCTTGTGCTCCGAGAGAAAGATC 799
 665 TGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 721
 QY 800 GCAACTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 859
 722 GCTGTGAGCGGAAGTGAACGCGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 781

QY 860 GGACTCCCATTCATATTCATCTGAGAGCTCTGGGGAGACACTCCACAGACAG 919
 DB 782 GCGTCCCTCTTTCACACCTGATCTCAACCTGGCCGCTGGCCCGACAGACCCG 841
 QY 930 CTGCTCTCTCAGACTTATTCCTTCGATCGCCTTAGCTATACCAACAGTACCTGATTC 979
 DB 842 CCGCCGCGGGCCCTTACTTCTTGATGTCATCTCTTACGCAACAGCTGTGGCAAC 901
 QY 980 CCATTCCTACGCTTCTTGTATGAAACTTCAGGCGGTCTTCCGGGA 1028
 DB 902 CCGCTCTACGCGCTTCTCTGACACTTCGCGCAGACTTCCAGAA 950

RESULT 60
 BI919235 627 bp mRNA linear EST 17-OCT-2001
 LOCUS 603181578P1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5245602 5',
 DEFINITION mRNA sequence.
 ACCESSION BI919235
 VERSION BI919235.1 GI:16200355
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 627)
 NIH-MGC http://mgi.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT Robert Strausberg, Ph.D.
 EMAIL: cgarbes@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Place: LBL/LLNL row: 1 column: 19
 High quality sequence start: 4
 High quality sequence stop: 624.
 Location/Qualifiers

FEATURES
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/organism="Homo sapiens"
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 /db_xref="taxon:9606"
 /clone="IMAGE:5245602"
 /lab_host="DH10B"
 /clone_1ib="NIH_MGC_121"
 /note="Organ: brain; Vector: pCMV-SPORT6, Site_1: NotI;
 Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
 fetal brains, female age 20 weeks, female age 24 weeks,
 and male age 26 weeks. Library is oligo-dT primed and
 directionally cloned (EcoRV site is destroyed upon
 cloning). Average insert size 1.7 kb, insert size range
 0.7-3.5 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 017. Note:
 this is a NIH_MGC Library."

ORIGIN

Query Match 14.6%; Score 168.4; DB 12; Length 627;
 Best Local Similarity 71.0%; Pred. No. 3.2e-22;
 Matches 237; Conservative 0; Mismatches 96; Indels 1; Gaps 1;
 153 GCGGACATCTCCCGGACATCCCGGTATCATACCGGGGTCTCTCCGTAGTGTGGT 212
 DB 295 GCGCTTCTCTCCCTCGGCTCAAGGTACCAATCGGGGCTCTTACCTGGCCGTGTGT 354
 QY 213 CGTGGGCTTGTGTGGCACTCGCTGTGTCTGTTCGTATCATCCGATACCAAGATGAA 272
 DB 355 CGGAGGCGCTCTGGGGAATGCGCTTGTATGTACGTATCTCAGGCAACCAATGAA 414

QY 273 GACAGAACCAATTATACATTTTAACTGCTTGGCAGATGCTTAGTACTACAC 332
 DB 415 GACAGCACCAATTATTTATCTTTTAACTGGCCCTGGC-GACATCTGTGCTGTGC 473
 QY 333 CATGCCCTTTCAGAGTACGCTTACTGTATGTAATTCCTGGCCCTTTGGGATGTGTG 392
 DB 474 GCTGCGCTTCCAGGGCAGGACATCTCTCTGGGCTTCTGGCCGTTGGGAATGCGCTGTG 533
 QY 393 CAAGTATGTAATTTCCATTGATTACTACAAATGTTTACACAGACATCTTACCTGACAT 452
 DB 534 CAAGCAGTCATTTGATGATGACTACTACAAATGTTTACACAGACATCTTACCTGAC 593
 QY 453 GATGAGCGTGGACGCTCATTTGCGGTGGCCAC 486
 DB 594 CATGATGTGATCGCTATGTAGCCATCTGCAC 627

RESULT 61
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 LOCUS YJ04b04.r1 Soares placenta Nb2HP Homo sapiens cDNA clone
 DEFINITION IMAGE:147727 5' similar to gb:U25119 MU-TYR OPDIO RECEPTOR
 (HUMAN);, mRNA sequence.
 ACCESSION R81583
 VERSION R81583.1 GI:858186
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 183)
 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
 Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
 Parsons, J., Rifkin, B., Rohlfing, T., Soares, M., Tan, F.,
 Trevasakis, E., Waterston, R., Williamson, A., Wohldmann, P. and
 Wilson, R.

TITLE The Washu-Merck EST Project
 JOURNAL Unpublished (1995)
 COMMENT Contact: Wilson RK
 Washington University School of Medicine
 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.edu

Insert Size: 1518
 High quality sequence starts: 1
 High quality sequence stops: 1
 Source: IMAGE Consortium, LLNL
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Trace considered overall poor quality
 Insert Length: 1518 Std Error: 0.00
 Seq primer: M13RP1
 High quality sequence stop: 1.
 Location/Qualifiers

FEATURES
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 /db_xref="taxon:9606"
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 /sex="female"
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 /lab_host="DH10B (ampicillin resistant)"
 /clone_1ib="Soares placenta Nb2HP"
 /note="Organ: placenta; Vector: pRTT3D (pharmacia) with a
 modified polylinker. Site 1: Not I. Site 2: Eco RI; 1st
 strand cDNA was primed with a Not I - oligo(dT) primer [5'
 AACTGGAAGAATTCGCGCGCGCAGAGATTTTCTTTTCTTTT 3'],
 double-stranded cDNA was ligated to Eco RI adaptors
 (pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pRTT3 vector. Library

gene
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/db_xref="taxon:10090"
<1..>945
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ORIGIN

Query Match 14.3%; Score 165; DB 29; Length 945;
Best Local Similarity 53.2%; Pred. No. 1.7e-21;
Matches 410; Conservative 0; Mismatches 340; Indels 21; Gaps 2;

QY 256 CGATACACAAAGATGAAGACAGACCAACATTTACATTTTAACTGGCTTTGGCAGAT 315
DB 2 CGCTATGCCAAGATGAAGACAGACCAACATCTACTACTCACTGCGCCGCGCGCAT 61
QY 316 GCTTATGTTACTACAACATGCCCTTTTCAAGAGTACCGCTTACTGTATGTAATTCCTGGCT 375
DB 62 GAGCTCTTCATCTCAGCGCTGCCATTCGTGGCTCCGCGCGCTGCCGCACTGGCGCG 121
QY 376 TTTGGGAGATGCTGTGCAAGATGATTAATTTCCATGATTACTACAAATGTTCCACGAC 435
DB 122 TTGGGAGCGGTGCTGTGTGCGCAGTGTCTTACGTGGACGGCTGAAACATGTTCACTAGT 181
QY 436 ATCTTACCTTGACATGATGAGCGGTGACCGCTACATTTGCCGTGGCCACCCCGTGAAG 495
DB 182 GTCTTGTGCTCAGCGGTGCTCAGCGGTGACCGCTATGTTGGCTGTGTGTGACACCTCTGCGC 241
QY 486 GCTTGGACCTCCGACACCTTTGAAAGCAAGATCATATATCTGCATCTGGCTGCTG 555
DB 242 GCCGCGACCTTACCGCGCGCGCCAGCGGTGCGCAAGCTAATCACTGGAGATGTGGCTAGCA 301
QY 556 TGTGATCTGTTGGATCTCTGCAATAGTCTTGGAGGACCAAAATGTCAGGAAGACGTC 615
DB 302 TCTTGTGCTGTGATCCTGCCCATTCGACATCTTGTGCTGACACCAAGCGCAGCTGCTGGGCGC 361
QY 616 GATGTCATGATGATGCTCTTGTGAGTCCAGATGATGATCTCTGCTGGAGACCTCTTC 675
DB 362 GAGGCGGTGCTGTCGACCTGCTGACCTGCTCACCGCGCTGTGTGTGCGG-----TC 412
QY 676 ATGAAGATCTGCGCTCTTCACTTTTGTGCTGTGATCCGCTGCTCTCATCATCTGCTGC 735
DB 413 TTTGATCTATATCTTTTGTGTGGGCTTCTACTCCCGCTTCTGGCCATCGGATATATGC 472
QY 736 TACACCTGATGATCTCTGCTCTCAAGAGCGTCCGGCTCTTTTGTGGCTCCGAGAGAA 795
DB 473 TACCTGTTATGTGTGGCAAGATGCGCGCTGTGGCCCTGCGGCTGGCTGGCAACAAACG 532
QY 796 GATCGCAACCTGCTGATGATCAACAGATGATCTGCTGTGGTGTGAGCTTTCGTCGTC 855
DB 533 AGCGCTGCAAGAAAGATCACTAGGCTGCTGTCTATATGTGTGACCGTCTTTTGTGCTA 592
QY 856 TGTGAGTCTCCGATTCATATTCATCTGTGTGAGAGCTTGGGAGACCTCCCAACAGC 915
DB 593 TGTGAGTCTCCGATTCATATTCATCTGTGTGAGAGCTTGGGAGACCTCCCAACAGC 915
QY 916 ACAGCTGCTCTCTCCAGCTATTAATCTGTGATGCTTGGCTTATACCAACAGTACCTG 975
DB 653 ACTGT-----CAACATGTGTCTCTATCTCTAGCTATGCAACAGCTGTGTC 700
QY 976 AATCCATCTCTACGCTTTCTGTGATGAATACTCAACGCGGTGTTCCGG 1026
DB 701 AATCCATCTCTATGCTTCTCTGTGCAACCTTCGCGGCTCTTTCCAG 751

RESULT 64
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LOCUS BX280512 NIH_MGC_114 Homo sapiens cDNA clone IMAGE998M0111484 ;
DEFINITION IMAGE:5193768, mRNA sequence.
ACCESSION BX280512
VERSION BX280512.1 GI:28613890
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 502)

AUTHORS

Ebert,U., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,
Radelof,U., Schneider,D. and Korn,B.

TITLE

Human Unigeneset - RZPD3

JOURNAL

Unpublished (2003)

COMMENT

Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAGE998M0111484.
RZPDLIB; I.M.A.G.E. cDNA Clone Collection:
Human Unigeneset - RZPD3 (RZPDLIB No.972)
http://www.rzpd.de/CloneCards/cgi-bin/showLib.pl.cgi?responseLibNo=972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
M13u, Primer sequence: GGTGTAAACGACGCGCAGT.

FEATURES

source

1..502

/organism="Homo sapiens"

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/clone="IMAGE998M0111484 ; IMAGE:5193768"

/lab_host="DH10B"

/clone_lib="NIH_MGC_114"

/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: EcoRV (destroyed); RNA source anonymous pool of 6
male brains, age range 23-27 yo. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.5 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 019. Note:
this is a NIH_MGC library."

ORIGIN

Query Match 14.2%; Score 164; DB 13; Length 502;
Best Local Similarity 59.0%; Pred. No. 2.1e-21;
Matches 281; Conservative 0; Mismatches 195; Indels 0; Gaps 0;

QY 140 CGCAGCTGAGCGCGGCGACATCTCCCGGCATCCCGCTCATCATCAGCGCGCTACT 199
DB 25 CCCAAGACGGGACCTTTGAGCGAGGGCGAGGGACGCCATCTGATCTCTTTCATCTACT 84
QY 200 CCGTAGTGTCTGTGCTGTGGCTTGTGTGGCACTCGCTGTGATGTTGTGTGATCATCCGAT 259
DB 85 CCGTAGTGTCTGTGCTGTGGCTTGTGTGGCACTCGCTGTGATGTTGTGTGATCATCCGAT 259
QY 260 AACAAAGATGAAGACAGCAACCAATTAATATTTAACTGGCTTGGAGAGGCTT 319
DB 145 ATGCCAAGATGAAGACGGCGACCAATCTAATCTTAATCTGGCATTTGATGAGAC 204
QY 320 TAGTACTACACCAATGCGCTTTACAGAGTACGATCTATGATGTAATCTCGGCTTTTG 379
DB 205 TGTCTATGCTACGCTGCGCTCTTCTAGTACCTCCACGTTGTGTGGCCACTGGCCTTGG 264
QY 380 GGAATGTGCTGTGCAAGATGATTAATTTTCATGATTAATCAACATGTTTACCAAGATCT 439
DB 265 GTGCGCTGTGTGCGCGCTCGTGTGAGCGGTGGAACGCGGTCAACATGTTTACCAAGATCT 324
QY 440 TCACTTGAACATGATGAGCGGTGAGCGGTATGATGCTGCTGCGACCCCGTGAAGGCTT 499
DB 325 ACTGTCTGACTGTGCTCAGCGGTGAGCGGTATGATGCTGCTGATCCATCAAGGCGG 384
QY 500 TGAAGCTCCGACACCCCTTGAAGCAAGATCATCAATATCTGCAATCTGGCTGTGCT 559

Db 385 CCCGCTACCGCCGCCACCGGTGGCCAAAGTAGTAAACTGGGCGTGTGGTGTACTGCG 444
 QY 560 CATCTGTGGCATCTCTGCATAATAGTCTTGGAGGACCAAGTCAGGGAAGAGTGC 615
 Db 445 TGTCTGTCATCTCCCATCTGTGTCTTCTTCGACCCGGCCCAACAGGACGGC 500

RESULT 65
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 ACCESSION AY400332
 VERSION AY400332.1 GI:39756321
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 1257)
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejaritwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriere,S., Wang,G., Zheng,X.H., White,T.J., Smitsky,J.J., Adams,M.D. and Cargill,M.
 TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
 JOURNAL Science 302 (5652), 1960-1963 (2003)
 PUBMED 14671302
 REFERENCE 2 (bases 1 to 1257)
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejaritwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriere,S., Wang,G., Zheng,X.H., White,T.J., Smitsky,J.J., Adams,M.D. and Cargill,M.
 TITLE Direct Submission
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
 COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.
 FEATURES
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ORIGIN
 Query Match 14.1%; Score 162.2; DB 29; Length 1257;
 Best Local Similarity 51.2%; Pred. No. 6.7e-21;
 Matches 436; Conservative 0; Mismatches 403; Indels 12; Gaps 2;

QY 178 GTGATCATCAGCGGGCTCTACTCCGATGTTGTCGTGCGTGGTGGGCACTCGCTG 237
 Db 133 GTTCTGATGCCCTGCTACTCTGTGGTGGTGGGCGTGGTGGTGGTGGTGGTGGTGG 192
 QY 238 GTGATGTTGTCATCTCGATACCAAGATGAAGAGCAACCAATTTACATATT 297
 Db 193 GTGATCTATGTGTGCTCTGGGACACGGCCGCTTCACTGACCAAGTCACTCTCTC 252
 QY 258 AACCTGGCTTTGGGAGATGCTTAACTACACCAATGCCCTTTCAAGATGCTTAC 357
 Db 253 AACCTGGGCTGGCGGACGAGCTCTTCAATGCTGGGCTGCTCTTCTGGCCGACAAAC 312
 QY 358 TTGATGAATCCCTGGCTTTTGGGGAGTGGCTGTGCAAGATAGTAATTTCCATTTATAC 417
 Db 313 GCCCTGCTTACTGCGCTTGGCTCCCTCATGTGCGCGCTGTGATGCGGTGATGCGC 372
 QY 418 TACAACATGTTTACACGATCTTTCATCTTGAACATGATAGAGCGTGAACCGCTAATTGCC 477
 Db 373 ATCAACAGTTTACACGATATTTGCTGCTGACTGTCAATGAGCGTGAACCGTCTGGCC 432
 QY 478 GTGTGCCACCCCGTGAAGGCTTTGGACTTTCGACACACCTTTGAAGGCAAGATCATCAT 537

Db 433 GTGTGATCATCCACCCGCTCGGCGCGCTGGGCGACAGCTCCGATGCCCGACGCTACG 492
 QY 538 ATCTGCATCTGAGCTGCTGTGTCATCTGTGGATCTGTGCAATATCTCTTGAAGACAC 597
 Db 493 GCGGCTGTGTGGGTGGCTTACGCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 552
 QY 598 AAAGTCAGGAAAGAGCTGATGTCTATTAGTCTCTTGCAGTTCCAGATGATGACTAC 657
 Db 553 CCCCGGCGATGAGACCTTGCACATGACATGAGCCGCGCGCGCGCGC-----C 603
 QY 658 TCTGTGGGAGACCTTTGATGAAGATCTGCGCTTCACTTTGCTGCTGATGCTGCTGTC 717
 Db 604 TGGCGAGCGGCTTATATATATACACGCGCCGACCTGGGCTTCTTGGGCGCGCTGTC 663
 QY 718 CTGATCATCATCTGTCTGACACCTGATGATCTGCTGTCAGAGCGCTCGCTCTT 777
 Db 664 ATCTGCTCTTCTGCTACTCTCTCATCTGATGATGATGATGATGATGATGATGATGAT 723
 QY 778 TCTGCTCCGAGAGA---AGATGCGAACCTGGGTGATGATGATGATGATGATGATGATGAT 834
 Db 724 GCACCTGTGTCAGCG 783
 QY 835 GTGTGGGAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 894
 Db 784 GTGTGGGAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 843
 QY 895 CTGGGAGACCTCTCCACAGACAGCTGCTCTCTCAAGTATTAATTCTGATGCGCTTA 954
 Db 844 GTGTGCCACATGCG 903
 QY 955 GGCATATACCAAGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1014
 Db 904 CCTATGCAACAGCTGTGCAACCCATCTTATGAGCTTCTCTTACCGCTTCAAG 963
 QY 1015 CGGTGTTTCG 1025
 Db 964 CAGGCTTCG 974

RESULT 66
 CD559493/C
 LOCUS
 DEFINITION AGENCOURT 14496636 NIH MGC 195 Homo sapiens cDNA clone
 IMAGE:6971825 5', mRNA-sequence.
 ACCESSION CD559493
 VERSION CD559493.2 GI:38453543
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 798)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT On Jun 10, 2003 this sequence version replaced gi:31585561.
 Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgabs-r@mail.nih.gov
 Tissue Procurement: Narayan Bhat
 cDNA Library Preparation: Bhat Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
 http://image.llnl.gov
 plate: IRB82 row: d column: 04
 High quality sequence start: 8
 High quality sequence stop: 749.
 Location/Qualifiers

FEATURES

source

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 /note="Vector: pDNR-Dual; Site_1: loxp-Sall; Site_2: loxp-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxp sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat a Note: this is a NIH_MGC Library."

ORIGIN

Query Match 14.0%; Score 162; DB 14; Length 798;
 Best Local Similarity 54.1%; Pred. No. 6.1e-21;
 Matches 399; Conservative 0; Mismatches 327; Indels 12; Gaps 3;

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 766 ATCTGAACCTGGCAGCTGCGACGAGGCTCTTCAAGCTGTAAGCTCTGTAACATGCGCGA 707
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 354 CTACTTGATGAATTCCTGGCTTTTGGGATGCTGTCAGATAGTAATTTCCATTGA 413
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 706 GCACCTGCTGCAAGTACTGGCCCTTGGGGAGCTGCTCTGCAAGCTGCTGCTGCGA 647
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 828 CTTGT 887
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 888 GGAGGCTGTGGGAGGAGCTCCACAGCAGAGCTGTCTCTCAGCTATTACTTGTGAT 947
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Qy 948 GGCCTTGGCTTATACCAAGATGAGCTGATATCCATCTCTTACGCTTTCTGATGATAAA 1007
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RESULT 67
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 VERSION
 AY400988.1 GI:39756977
 KEYWORDS
 SOURCE
 ORGANISM
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 1089)
 Clark A.G., Gianowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
 Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
 Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shtinsky, J.J.,
 Adams, M.D. and Cargill, M.
 Direct Submission
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 This sequence was made by sequencing genomic exons and ordering
 them based on alignment.

FEATURES
 source
 location/Qualifiers
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 360 GATGAATTCCTGCTTTTGGGAGT 419
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Db      354 CAACAGTTTCAACAGATCTTCTGCGTGTGATGATGATGATGATGATGATGATGATGATGAT 413
Qy      480 GTGCGACCCCGTGAAGGCTTTGAGCTTCCGACACCCCTTGAAGGCAAAATATCATATAT 539
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Qy      540 CTGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 599
Db      474 TGCCTGCTGGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 533
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Qy      660 CTGTGTGGACCTCTTTCATGAAGATGCTGCTTTCATCTTGTGCTTGTGATCCCTGTCT 719
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Db      699 GGGGCTCTCAAGCGGAGGCGCTCAAGAAAGCAAGGACTCGCATGCTGCTGCTGCTGCT 758
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Db      879 TCCCAATAGCTTGCACACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 938
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DEFINITION BB631900 RIKEN full-length enriched, adult male hypothalamus Mus
ACCESSION BB631900
VERSION   BB631900.1 GI:16468581
KEYWORDS
ORGANISM Mus musculus (house mouse)
SOURCE   Mus musculus
          Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
          Eumetazoa; Muridae; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS  Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T.,
          Hara,A., Hiimoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J.,
          Kono,M., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K.,
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          Sugabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
          Takeda,Y., Tanaka,T., Toyota,T., Muramatsu,M., and Hayashizaki,Y.
          RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
          Unpublished (2001)
TITLE    JOURNAL
COMMENT  Contact: Yoshinori Hayashizaki
          Laboratory for Genome Exploration Research Group, RIKEN Genomic
          Sciences Center (GSC), Yokohama Institute

```

FEATURES

source

The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suenho-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gsr.riken.go.jp,
 URL: http://genome.gsc.riken.go.jp/
 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
 Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M., and Hayashizaki,Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)
 wagi,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
 Matsubara,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
 Matsura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
 and Hayashizaki,Y.
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.
 10 (11), 1757-1771 (2000)
 Kono,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P.,
 Sugahara,Y., and Hayashizaki,Y.
 Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I.,
 Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K., and
 Hayashizaki,Y.
 Computational Analysis of Full-length Mouse cDNAs Compared with
 Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
 Please visit our web site (http://genome.gsc.riken.go.jp) for
 further details.
 e mouse tissues.

location/Qualifiers

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Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5',
GAGGAGAGAGATCCAGAGCTTTTCTTTTCTTTTCTTTT 3']. cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 20.0 and subtraction to Rot = 459.0. Second
strand cDNA was prepared with the primer adapter of
sequence [5' GAGGAGAGATTCGAGTTAATTAATTAATCCCCCCCCC
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modified pluscript KS(+) after bulk excision from Lambda
FLC I."

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ORIGIN

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Query Match      13.94; Score 160; DB 10; Length 714;
Best Local Similarity 65.84; Pred. No. 1.4e-20;
Matches 229; Conservative 0; Mismatches 119; Indels 0; Gaps 0;

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DEFINITION	BF193020 550 bp mRNA linear EST 02-NOV-2000
ACCESSION	Bf193020
VERSION	Bf193020.1
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SOURCE	Sus scrofa
ORGANISM	Sus scrofa (pig)
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus. 1 (bases 1 to 550) Fahrenkrug,S.C., Smith,T.P.L., Feking,B.A., Cho,J., White,J., Vallet,J., Wise,T., Rohrer,G.A., Perrea,G., Sultana,R., Quackenbush,J. and Keele,J.W. Porcine gene discovery by normalized cDNA-library sequencing and EST cluster assembly Mamm. Genome 13 (8), 475-478 (2002)
JOURNAL	Mamm. Genome 13 (8), 475-478 (2002)
MEDLINE	22213789
PUBMED	12326715
COMMENT	Contact: smitch tpl

DOOH, and US Neac Rumin Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smtlth@mail.marc.usda.gov
Single pass sequencing. Bases called and alt crimed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
-mismatch 12 options.
PCR primers
FORWARD: AGGAACAGCTATGACCT
BACKWARD: GTTTCACAGTACGACG
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							Gaps
Qy	153	CGCGGACATCTCCCGCGCCATCCCGCATCATCA	CGCGGCTTCACTCCGATGTTCTG	212			
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OY	393	CAAGATAGTATTTCCATGATGTTACTCTCAACATGTGTAACGAGCATCTTCAACCTTGAC	449
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									Clark,A.G., Glatowski,S., Nilsson,R., Thomas,P., Kejarival,A.,

TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL	Science 302 (5652), 1960-1963 (2003)
PUBMED	14671302
REFERENCE	2 (bases 1 to 987)
AUTHORS	Clark, A.G., Gnanowaki, S., Nielson, R., Thomas, P., Kejaritwal, A., Todd, M.A., Tenenbaum, D.M., Civiello, D.R., Lu, F., Murphy, B., Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shinkov, J.J., Adams, M.D. and Carroll, M.
TITLE	Direct Submission
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.

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Qy	214	GTGGGCTTGTGTGGCAACTCGCTGTGATGTTCTGTATCATCCGATACACAAAGATGAAG	273		
Db	148	GTGGGTCTGGGGGCAACTCCGGCTGCTGACTGTGTCGGGGGGCCCCGATGAAG	207		
Qy	274	ACAGCAACCAACATTATTAATTAACCTGGCTTTGGCAGATGCTTTAGTTACTACAAC	333		
Db	208	ACCGTCAACCAACGTGTTCATCTCAACCTGGCCATCGCCGAGANNCTTCACNCTGGTG	267		

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QY 394 AAGATGTAATTTTCATGTAATTAACAACATGTTGACGACGATCTTCACTTGAACATG 453
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RESULT 71
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 VERSION BU18522.1 GI:25826523
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 ORGANISM Gallus gallus
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 Phasianinae; Gallus.
 Boardman, P.B., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
 Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A., and Hubbard, S.J.,
 A Comprehensive Collection of Chicken cDNAs
 Curr. Biol. 12 (22), 1965-1969 (2002)
 MEDLINE 22355334
 PUBMED 12445392
 CONTACT: Simon Hubbard
 Department of Biomolecular Sciences
 University of Manchester Institute of Science and Technology

(UMIST)
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 Tel: 01612008930
 Fax: 01612360409
 Email: Simon.Hubbard@umist.ac.uk.

FEATURES
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 /note="Organ: heads; Vector: pBluescript II KS(+); Site_1: EcoRI; Site_2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunt-ended, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

ORIGIN
 Query Match 13.8%; Score 159.2; DB 13; Length 768;
 Best Local Similarity 65.4%; Pred. No. 2.1e-20;
 Matches 233; Conservative 0; Mismatches 123; Indels 0; Gaps 0;

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QY 202 GTAAGTTCGTCGTGAGGCTGTGAGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 261
    |||||
Db 1 GTGAGTGTGCTGCTGAGGGGCTGTGGAACCTCATGTCATCTACGATGCTACGCTAC 60
QY 262 ACAAGATGAAGACAGACCAACATTTACATTTAACTGGCTTTGGAGATGCTTTA 321
    |||||
Db 61 GCCAAGATGAAGAGGCGCACCAACATCTTAACTTTGAGCATTTGGCATTTGGAGAGACTG 120
QY 322 GTTACTCAACCAATGCCCTTTCAGAGTACGGTCTACTTGAATTCCTGAGCTTTGGG 381
    |||||
Db 121 CTGATGCTTACGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
QY 382 GATGCTGTGCAAGATGATGATTTTCATTGATTACTACAAACATGTTACACAGATCTTC 441
    |||||
Db 181 TCTCTGCTGTGCGCGCTGTGCTCAGCGTGGATGCATCAACATGTTACCAAGATATCTAC 240
QY 442 ACCTTGACCATGATGACCGGTGACCGCTTACATTTGCGGTGCCACCCCGTGAAGGCTTTG 501
    |||||
Db 241 TGCTGACTGTGCTGACCGGTGACCGCTTACATGCGCGGTGTGACCCCATCAAGAGCGGCC 300
QY 502 GACTTCCGACACCCCTTGAAGGCAAGATCATCAATATCTGCACTGTGGCTGTGCTG 557
    |||||
Db 301 AGTATCCGCGCGGCCACCGGTGCTAAGATGTCAACTCGGTGTGTGGTGTCTTC 356

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RESULT 72
 CD559491/c 795 bp mRNA linear EST 19-NOV-2003
 LOCUS CD559491
 DEFINITION IMAGE:6971827 5', mRNA sequence.
 ACCESSION CD559491
 VERSION CD559491.2 GI:38453539
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 (bases 1 to 795)


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Db      1 TACCTGCTCANNCTGGCCGCTAGCCGATGAGCTCTTATGCTGAGCGCTTCGTCGCC 60
Qy      349 AGGCTTACTTATGATGATTCCTGGCTTTGGGATGCTGTGCAAGATGATTAATTC 408
Db      61 TCGTCGGCGCCCTGCGCCACTGGCCCTTCGCTCGCTGTGCGCGGTGGTCTCAGC 120
Qy      409 ATTGATTACTACAAAGTTCACACACATCTTACCTTACCTGATGATGAGCGTGGAC 468
Db      121 GTTCAGGCGCTCAACATGTTACACACAGCTTCTGTCTCAAGTGTCTNNNGAGACCC 180
Qy      469 TACATTCGCGTGTGCCACCCGCTGAGAGGCTTTGAGCTTCGCAACACCTTTGAAGCA 528
Db      181 TAGTGGCGCTGTGATGACCTCTGCGCGGAGAGACCTACCGGCGCCACGCTGGCAAG 240
Qy      529 ATCATTAATATCTGCATCTGCTGTGTGTATCTGTTGGCATCTTGCATATGCTCTT 588
Db      241 TTCTATCACTGGGCGCTGTGCTGGCGTCCCTGTTGTGATCTTCCCATCCCATCNN 300
Qy      589 GGAGGACCAAGTCAAGGAGACGTCATGATGATGATGCTCTTGGAGTTCCAGAT 648
Db      301 GAGACACTAGAACCGACTGCGCGGCGGCGGCGCTGCAACCTGCAAGTGGCA--- 357
Qy      649 GATGACTACTCTCTGTGTGGAGACCTCTTATGAGATCTGCGTCTTATCTTGCCTTCTG 708
Db      358 ---CACCGGCGCTGTGCGGAGCTTCGT---GCTTACACTTCTGCTGGGCTTCTCTG 411
Qy      709 ATCCCTGTCTCATCATCTGCTGTGTCAACCTGTGATGATCTGCGTCTCAAGAGCTC 768
Db      412 CTGCGCGCTGTGCTGAGCTGTGCTGTCTGATGATGATGAGGAGAGTGGCGCGCG 471
Qy      769 CGGCTCTTCTGTGCGTCCCGAGAGAAATGCGAACCTGCGATGAGATCCAGACTGTC 828
Db      472 GCGCTGCGGCTGTGCTGTGAGAGAGCGGAGCGGCTGTGAGAGAGAGAGAGAGAGAG 531
Qy      829 CTGTGTGTGTGTGAGCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 888
Db      532 CTGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 579
Qy      889 GAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 948
Db      580 GTGCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 639
Qy      949 GCTTATGCTATACCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1008
Db      640 ATCTCAGTATGCGCAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 699
Qy      1009 TTCAAAGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1026
Db      700 TTCCGCGCATCTTCCAG 717

RESULT 74
AY400334      1287 bp      DNA      linear      GSS 15-DEC-2003
LOCUS      Mus musculus SSTR3 gene, VIRUAL TRANSCRIPT, partial sequence,
DEFINITION      genomic survey sequence.
ACCESSION      AY400334
VERSION      AY400334.1 GI:39756323
KEYWORDS
SOURCE
ORGANISM      Mus musculus (house mouse)
MUS musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS      Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
              Todd,M.A., Tanenbaum,D.M., Civeallo,D.R., Lu,F., Murphy,B.,
              Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
              Adams,M.D. and Cargill,M.
              Inferring nonneutral evolution from human-chimp-mouse orthologous
              gene trios
JOURNAL      Science 302 (5652), 1960-1963 (2003)
PUBMED      14671302

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REFERENCE      2 (bases 1 to 1287)
AUTHORS      Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
              Todd,M.A., Tanenbaum,D.M., Civeallo,D.R., Lu,F., Murphy,B.,
              Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
              Adams,M.D. and Cargill,M.
              Direct Submission
JOURNAL      Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
              Rockville, MD 20850, USA
COMMENT      This sequence was made by sequencing genomic exons and ordering
              them based on alignment.
FEATURES
source
1..1287
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
<1..>1287
/gene="SSTR3"
/locus_tag="HGM0522"

ORIGIN
Query Match      13.5%; Score 156.2; DB 29; Length 1287;
Best Local Similarity 50.8%; Pred. No. 9.8e-20;
Matches 439; Conservative 0; Mismatches 408; Indels 18; Gaps 2;

Qy      179 TCATCATACGCGGCTACTCCGAGTTCCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 238
Db      137 TCTGATCTCTGTGTGATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 196
Qy      239 TCATGTTGTATCATCCGATACCAAAAGATGAGACAGCAACCAATTATATATTA 298
Db      197 TGATCTAGTGTGTCTGTGGGACACGTCCACCATCATGATACAGTGTCTATATCTCA 256
Qy      299 ACTGTGCTTGTGAGTCTTGTAGTACTACACATGATCCCTTTGAGTACGCTTACT 358
Db      257 ACTGTGCTTGTGAGTCTTGTAGTACTACACATGATCCCTTTGAGTACGCTTACT 316
Qy      359 TGATGATTCCTGTGCTTGTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 418
Db      317 CCTGTCTACTGTGCTTGTGATCTCTATGTGTGTGTGTGTGTGTGTGTGTGTGTGT 376
Qy      419 ACAACATGTTACAGACATCTTCACTTGAACATGATGAGCGTGAACCGCTACATTCG 478
Db      377 TCAACAGTTACACGAGATCTTGTGCTCACGTCATGATGATGAGCGCTATCTGTG 436
Qy      479 TGTGCAACCCGCTGAAAGCTTGTGACTTTCGCAACCTTGAAGCAAAATATCAATA 538
Db      437 TGTGCAACCCGCTGAAAGCTTGTGACTTTCGCAACCTTGAAGCAAAATATCAATA 496
Qy      539 TGTGATCTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 594
Db      497 CAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 556
Qy      595 ACCAAAGTCAAGGAGAGCTGTGATGTATGAGTCTCTTGAAGTCCAGATGATGAC 654
Db      557 CCGGAGCATAGACAGCTGTGCAATGAGTGGCCAGACGACGCGGTGCGGAGAACAG 616
Qy      655 TACTCTGTGTG-----GGAACCTTTCAAGAGATGTGCTTCACTTTTG 700
Db      617 CTTTATCATCTTACACGCGCGCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 676
Qy      701 CTTTGTGATCCCTGTCTCATCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 760
Db      677 GCTATCTGTCTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 736
Qy      761 AGAGCGTGGGCTCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 820
Db      737 GTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 796
Qy      821 GATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 880
Db      797 GATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 856
Qy      881 TCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 940

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Dd	857	ACATGCTAAATGTGGTGTGTCGCCCGCTGCAGAGAACCCCGCTTTCTTGCGGCTTAATCC	916
Oy	941	TCTGCATCGCCTTAGCTAATACCAACAGTAGCCTGAATCCCATTTCTTACGCTTTCTTG	1000
Dd	917	TGTGTGTGGGCGCTGCCTTAAGCGCAACACTGTGGGAAACCACATCTCTAGGCTTCTCT	976
Oy	1001	ATGAATACTTCAAGCGGTGTTCGG	1025
Dd	977	CCTACCGCTTCAAGCAGGCGTTTTCG	1001
RESULT 75			
CP147827 701 bp mRNA linear EST 25-JUL-2003			
LOCUS CP147827			
DEFINITION AGNCOURT_14740147 NIH MGC 145 Homo sapiens cDNA clone			
ACCESSION CP147827			
VERSION CP147827.1 GI:33244095			
KEYWORDS EST.			
SOURCE Homo sapiens			
ORGANISM Homo sapiens (human)			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE 1 (bases 1 to 701)			
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.			
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)			
JOURNAL Unpublished (1999)			
COMMENT Contact: Daniela S. Gerhard, Ph.D.			
Office of Cancer Genomics			
National Cancer Institute / NIH			
Bldg. 31 Rml10A07 Bethesda, MD 20892			
Email: csapbs@email.nih.gov			
Tissue Procurement: GPCR Consortium			
cDNA Library Preparation: GPCR Consortium			
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)			
DNA sequencing by: Agencourt Bioscience Corporation			
Clone distribution: MGC clone distribution information can be			
found through the I.M.A.G.E. Consortium/LNL at:			
http://image.lnl.gov			
Plate: IRBI02 row: b column: 01			
High quality sequence scop: 430.			
Location/Qualifiers			
1..701			
/organism="Homo sapiens"			
/mol_type="mRNA"			
/db_xref="taxon:9606"			
/clone IMAGE:6971894"			
/tissue type="mixed"			
/lab host="DHI08"			
/note="Vector: pcdNA3.1; Site 1: varies by clone; Site 2:			
varies by clone; ORFs were PCR-amplified and cloned into			
pcDNA3.1 by the GPCR Consortium. Cloning sites vary by			
clone and include the following (5'-ScorV-Xmni/XhoI-3',			
5'-ScorV-Xmni/Nci-3', ScorV-TTA cloned, non-directional).			
For information about which gene each clones represents,			
please visit our anonymous ftp site at			
ftp://image.lnl.gov/image/rearrayed_plates/IRBI_presv.dat			
a Note: this is a NIH_MGC library."			
ORIGIN			
Query Match 13.5%; Score 156; DB 14; Length 701;			
Best Local Similarity 57.6%; Pred. No. 8.4e-20;			
Matches 279; Conservative 0; Mismatches 205; Indels 0; Gaps 0;			
Oy	75	CAGACGCGCTGTGTTCCCGCTGGCGCGAGCCCGACAGCAACGCGAGCGCGCTCGGA	134
Dd	81	CGGGGCGACGAGGGGCCCCGGGGCGGCGTGCAGACGACATGAGAGCGACGAGGGCGAAA	140
Oy	135	GGAAGCGAGCTGAGAGCCCGCGCACATATCCCGGCGCATCCCGGTATCATCAGCGCGT	194
Dd	141	TGCGTCCAGAACGGGACCTTGAGCGAGGGCGAGGGCGAGCGCCCATTCGATCTCTTCAT	200

QY	195	CTACTCCGTA	GTGTTCCGTGCGTGGGCTTG	GTGGGCACTCGTGTCATGTTCTGATCAT	254
Db	201	CTACTCCGTA <th>GTGTTCCGTGCGTGGGCTTG</th> <th>GTGGGCACTCGTGTCATGTTCTGATCAT</th> <th>260</th>	GTGTTCCGTGCGTGGGCTTG	GTGGGCACTCGTGTCATGTTCTGATCAT	260
QY	255	CCGATPACAA <th>GAAGTGAAGACAGACACCAATTTACATATTTAAACCGCTTGGCGAGA</th> <th>314</th> <td></td>	GAAGTGAAGACAGACACCAATTTACATATTTAAACCGCTTGGCGAGA	314	
Db	261	GGCGATAGCC <th>AAAGTGAAGACAGGCGACCAACATCTAACATCTTAATCTGGGCGCATTTGCTGA</th> <th>320</th> <td></td>	AAAGTGAAGACAGGCGACCAACATCTAACATCTTAATCTGGGCGCATTTGCTGA	320	
QY	315	TGCTTTAGTT <th>ACTCAACACCATGCGCTTTTCAGAGTAGCGGTCTACTTGTGATGAAATTCCTGGCC</th> <th>374</th> <td></td>	ACTCAACACCATGCGCTTTTCAGAGTAGCGGTCTACTTGTGATGAAATTCCTGGCC	374	
Db	321	TGAGCTGCTA <th>TGCTCAGCGGTGCGCTTCTTAGTACCTCCACGTTGTTGGCGCATGGCC</th> <th>380</th> <td></td>	TGCTCAGCGGTGCGCTTCTTAGTACCTCCACGTTGTTGGCGCATGGCC	380	
QY	375	TTTTGGGGAG <th>TGCTGTGCAAGATAGTAATTTCAATTGATTACTACAAACATGTTCCACAG</th> <th>434</th> <td></td>	TGCTGTGCAAGATAGTAATTTCAATTGATTACTACAAACATGTTCCACAG	434	
Db	381	CTTGCGTGCG <th>CTGCTCTGCGCGCTCTGCGTCAAGCGTGGACCGCGGTCAACATGTTCCACAC</th> <th>440</th> <td></td>	CTGCTCTGCGCGCTCTGCGTCAAGCGTGGACCGCGGTCAACATGTTCCACAC	440	
QY	435	CATCTTCAC <th>CTTTCAGTCATGATGAAGACCGTGGACCGCTTAATTTGGCGTGGCCACCCCGTGA</th> <th>494</th> <td></td>	CTTTCAGTCATGATGAAGACCGTGGACCGCTTAATTTGGCGTGGCCACCCCGTGA	494	
Db	441	CATCTACCT <th>GTCTGACTGTGCTCAGCGTGGACCGGTACATGGCCGTGTGTCATCCCATCTA</th> <th>500</th> <td></td>	GTCTGACTGTGCTCAGCGTGGACCGGTACATGGCCGTGTGTCATCCCATCTA	500	
QY	495	GCGCTTTGGA <th>CTTCCGCGACACCCCTTGAAGAGCAAAATCATCAATATTCGATCTGGCTGCT</th> <th>554</th> <td></td>	CTTCCGCGACACCCCTTGAAGAGCAAAATCATCAATATTCGATCTGGCTGCT	554	
Db	501	GGCGGCGCC <th>GTACCGCGCGGTCTTCTGTGGACATAGCAGTACACTGGCGCGTATGTCCT</th> <th>560</th> <td></td>	GTACCGCGCGGTCTTCTGTGGACATAGCAGTACACTGGCGCGTATGTCCT	560	
QY	555	GTCG	558		
Db	561	ATAG	564		
RESULT 76					
B0057593					
LOCUS					
DEFINITION	B0057593	688 bp	mRNA	linear	EST 26-AUG-2002
	UI-M-FRO-caj-c-15-0-UI.x1 NIH BMP_FRO		Mus musculus	CDNA clone	
ACCESSION	B0057593				
VERSION	B0057593.1	GI:22497882			
KEYWORDS	EST.				
SOURCE	Mus musculus	(house mouse)			
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
TITLE	NIH-MGC http://mgc.nci.nih.gov/.				
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)				
COMMENT	Unpublished (1989)				
	Contact: Robert Strausberg, Ph.D.				
	Email: cgabbs-remail.nih.gov				
	Tissue Procurement: Dr. Jim Lin, University of Iowa				
	CDNA library preparation: Dr. M. Bento Soares, University of Iowa				
	CDNA library Arrayed by: Dr. M. Bento Soares, University of Iowa				
	DNA Sequencing by: Dr. M. Bento Soares, University of Iowa				
	Clone Distribution: MGC clone distribution information can be				
	found through the I.M.A.G.E. Consortium/LNL at:				
	http://image.lnl.gov				
	This clone was contributed by the Brain Molecular Anatomy Project				
	(BMAP)				
Seq primer: pyx-5.					
FEATURES					
source	Location/Qualifiers				
	1..688				
	/organism="Mus musculus"				
	/mol_type="mRNA"				
	/strain="C57BL/6"				
	/db_xref="taxon:10090"				
	/clone="IMAGE:6413126"				
	/tissue_type="whole brain"				
	/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"				
	/lab_host="DH10B (T1 phage resistant)"				
	/clone_lhb="NIH BMAP FRO"				
	/note="Organ: Brain; Vector: pyx- Aes; Site_1: Ecor I;				
	Site_2: Not I; The library was constructed according				
	Bonaldi, Lennon and Soares, Genome Research, 6:791-806,				
	1996. Denatured RNA was size fractionated on a 1% agarose				

gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGCGAGACAG. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemlin Chin, Ph.D., program coordinator."

ORIGIN

```
Query Match      13.5%; Score 155.4; DB 13; Length 688;
Best Local Similarity 64.7%; Pred. No. 1,1e-19;
Matches 231; Conservative 0; Mismatches 126; Indels 0; Gaps 0;

QY 252 CATCCGATACACAAAGATGAAGACAGCAACCAATTTACATTTTACCTGGCTTGGC 311
DB 331 CAGCAGGACACACCAAGATGAAGACTCTACCAACATTTTACATTTTACCTGGCACTGGC 390
QY 312 AGATGCTTAGTACTACCAACCATGCGCTTGAAGATGAGTCTACTTGAATTCCTG 371
DB 391 TGAATACCTGGTCTTCTCTGACACTGCGCTTCAAGGACAGACATCTTCTGGCTTCTG 450
QY 372 GCGTTTGGGAGATGCTGCTGCAAGATAGTAATTTTCATTGATTAACAAGTTCAC 431
DB 451 GCCATTGGGAATGACCTGTGCAAGACGCTCATGTGATCGACTACTACCAACATGTTTAC 510
QY 432 CAGCATCTTACCTTGAACCATGATGAGCGTGACCGCTACATTCGCGTGCACCCCGT 491
DB 511 CAGCATCTTACCTTGAACCATGATGAGCGTGACCGCTTATGATCTGACACCCAT 570
QY 492 GAAGGCTTGAACCTTCCGACACCCCTGAAGGCAAGATCATCATATGATCTGCT 551
DB 571 CCGTCCCTTGAATGTTTGGACATCAAGTAAGCCAGGCGCTTAATGCGCATATGCGC 630
QY 552 GCTGTGCTATCTGTGGCATCTCTGCAATAGTCTTGGAGGACCAACCAAGTCAAGGA 608
DB 631 CCGTCCCTTGAATGTTTGGATGTTCTGTGCTTGCATCATGCGCTCAAGCAAGTGAAGA 687
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RESULT 77      916 bp mRNA linear EST 15-MAY-2003
BX433241/c     BX433241 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
LOCUS          CS0DF038YK09 3-PRIME, mRNA sequence.
DEFINITION     BX433241
ACCESSION      BX433241.1 GI:30773198
VERSION        EST.
KEYWORDS       Homo sapiens (human)
SOURCE         Homo sapiens
ORGANISM       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE      1 (bases 1 to 916)
AUTHORS        Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE          Full-length cDNA libraries and normalization
JOURNAL        Unpublished (2001)
COMMENT        Contact: Genoscope
                Genoscope - Centre National de Sequencage
                BP 191 91006 EVRY cedex - France
                Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
                Library was constructed by Life Technologies, a division of
                Invitrogen. This sequence belongs to sequence cluster 8778.f For
                more information about this cluster, see
                http://www.genoscope.cns.fr/
                cgi-bin/cluster.cgi?seq=CS0BA1015ZB06_CS01389_2&cluster=8778.f.
                Contact : Feng Liang Email : fliang@lifestech.com URL :
                http://fulllength.invitrogen.com/invitrogen Corporation 1600
                Faraday Avenue Genoscope sequence ID : CS0BA1015ZB06_CS01389_2.
                Location/Qualifiers
                1..916
                /organism="Homo sapiens"
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ORIGIN

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Query Match      13.3%; Score 153.4; DB 13; Length 916;
Best Local Similarity 49.3%; Pred. No. 3e-19;
Matches 413; Conservative 0; Mismatches 417; Indels 7; Gaps 3;

QY 217 GGCCTTGGGGCAATCCGCTGATCATGTTCTGTATCATCCGATACACAAAGATGAAGACA 276
DB 915 GNGTGTGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 856
QY 277 GCACCAATTTACATATTTTAACTGGCTTGGCAAGTCTTAACTTAAACCATG 336
DB 855 TNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 796
QY 337 CCGTTTGAAGTAGG-GTCTACTGATGAATTCCTGGCCTTTGGGATGCTGTGCA 395
DB 795 GCTTCTTNNCTTAAAGAGTGGGCTGTGTTCACCTGCCCCCTTGGCAAGNCATTTTCCG 736
QY 396 GATAGTAAATTTCCATTTGATTTACTTAAACATGTTTCAACAGCATCTTCACTTGAACATGAT 455
DB 735 GGTGTATATGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 676
QY 456 GAGGTGAGCCGCTACATTTGCGGTGTCACCCCGTGAAGGCTTGGACCTTCCGACACC 515
DB 675 GAGATGAGCCGCTACATTTGCGGTGTCACCCCGTGAAGGCTTGGACCTTCCGACACC 616
QY 516 CTTGAAGCAAAAGATCATCATATATCTGATCTGGCTCTGTCGTCATCTGTGGCATCTG 575
DB 615 CCGAGCGGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 559
QY 576 TGCAATAGTCTTGGAGGACCAAAAGTCAAGGAAAGATGATGATGATGATGATGATGATGAT 635
DB 558 GCCCATCATGATATATATCTGCGGCTCCGAGCAACCAAGTGGGGAGAAAGACGTGACCAT 499
QY 636 GCAATTCGCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 695
DB 498 CAATGCGCCAGTGAATCTGGGGCTTGTGTAACAAGGTTTAT--CATCTACACTTTTCA 442
QY 696 CTTTGCCTGCTGATCCCTGCTCATCATCATGCTGTGCTACACCTGATGATGATGATGATGAT 755
DB 441 TCTGGGGTCTCTGTATACCCCTACACATCATCTGTCTTGTACTCTGTATCATCA 382
QY 756 TCTCAAGAGGCTCGGCTCTCTTCTGCTGCTCCGAGAGAAAGATGCAACTGCGTGAAGAT 815
DB 381 GGTGAATCTCTGGAATCCGAGTGGGCTCTCTTGAAGAGAAAGATGGAAGAGAT 322
QY 816 CACGAGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 875
DB 321 CACCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 262
QY 876 ATTTCATCTGATGAGGCTTGGGAGACCTCCACAGACAGACAGCTCTCTCCAGCTA 935
DB 261 ATTTCATGTTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 202
QY 936 TTAATCTGATGCTTGAAGCTTAAACCAAGTGAAGCTTGAATCCATTTCTTACCGCTT 995
DB 201 TGAATTTGTGTGTCTCTCACTATGCTTAAAGCTGTGCCAACCTTATCTTATATGCTT 142
QY 996 TCTTGAATGAACCTTGAAGGCTTTCGGGGCTTCTGTTTCCACTGAAGATGAG 1052
DB 141 CTGTGTGACACTTCAAGAAAGCTTCCAGAAATGCTCTGCTGCTGCTGCTGCTGCTGCTGCT 85
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RESULT 78
LOCUS AZ966515 702 bp DNA linear GSS 27-APR-2001
DEFINITION 2M0237H04F Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0237H04 F, genomic survey sequence.
ACCESSION AZ966515
VERSION AZ966515.1 GI:13837742
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 702)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weis,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
TITLE Unpublished (2000)
JOURNAL
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 1000 Std Error: 0.00
Plate: 0237 row: H column: 04
Seq primer: CGTCTAAACGACGCGCCAGT
Class: Plasmid ends
High quality sequence stop: 702.
Location/Qualifiers
1..702
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0237H04"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: FMD42Nv, Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 13.3% Score 153.2; DB 28; Length 702;
Best Local Similarity 74.8%; Pred. No. 2.9e-19;
Matches 205; Conservative 0; Mismatches 68; Indels 1; Gaps 1;
242 TGTTCGTATCATCCGATACACAAAGATGAAGACGACCAACATTTACATATTTAAC 301
429 TGCTCTCTCTCCATGACGATACCAATATGAAGACCGCCACCAACATCTACATCTTCAATC 488

QY 302 TGGCTTTGGACAGATGCTTTAGTTACTACAAACGATGCCCTTTGAGATGAGTACTTGA 361
|||||
DB 489 TGGCTTTGGCTGATCGCTGGCCACGACGCTGCTTCCAGAGCCGCAAGTACTTGA 548
|||||
QY 362 TGAATTCCTGGCTTTTGGGAGATGCTGTGTGCAAGATAGTAAATTTCCATGATTA 421
549 TGGAAACGAGCGCGTTTGGCGAGCTGCTGTGCAAAAGCTGTCTTCATATGACTATA 608
|||||
QY 422 ACATGTTACACGACATCTTACCTTGACCATATG-AGGCTGAGCCGCTACATTTGCCG 480
DB 609 ACATGTTACATGACATCTTACCTTACCATATGATAGAGCTGAGCCGCTCATTTGCTGTC 668
|||||
QY 481 TGGCAACCCGATGAAGCTTTGAGACTTCCGACAC 514
669 TGGCATCTCTGACAAAGCCCTGACATTCGAGACAC 702
|||||

RESULT 79
LOCUS B1224313 741 bp mRNA linear EST 11-JUL-2001
DEFINITION 602940621P1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5103821 5', mRNA sequence.
ACCESSION B1224313
VERSION B1224313.1 GI:14677752
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 741)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@p5-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: L1M11250 row: 1 column: 06
High quality sequence stop: 599.
Location/Qualifiers
1..741
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5103821"
/tissue_type="cervical carcinoma cell line"
/lab_host="DH10B"
/clone_lib="NIH MGC 12"
/note="Organ: cervix; Vector: PCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.4 kb. Library prepared by Life Technologies."

ORIGIN

Query Match 13.3% Score 153; DB 12; Length 741;
Best Local Similarity 61.8%; Pred. No. 3.3e-19;
Matches 243; Conservative 0; Mismatches 150; Indels 0; Gaps 0;
166 CCGGCATCCGATCATCATCGCGGCTACTCTCGATGTTGTCGTGGCTTGGTG 225
DB 136 CAGGCAAGCGCATCTGATCTTTGATCTACCTCGGAGTGTGCTGGGGCTGTGT 195
|||||
QY 226 GCGAATCGCTGCTATGTTGTGATCATCGGATACAAAGATGAAGACGACCAAC 285
DB 196 GGGAACTTAATGCTATCTAGATGATCTGCGGCTATGCAAGATGAAGACGACCAAC 255
286 ATTACATATTTAACCTGCTTTGGCAGATGCTTTAGTTACTACAAACGATGCCCTTTGAG 345
|||||

Db 256 ATGTACATCTTAATCTGGCCATTGCTGATGAGCTGCTCATGCTCAGCGCTTCCTTA 315
QY 346 AGTACGCTTACTTGTATGAAATTCCTGACCTTTTGGAGATGCTGTGCAAGATGTAAT 405
Db 316 GTACCTCCACGCTGTGTGGCCACCTGCGCTTGGCGCTGCTGCGCTCGGCTC 375
QY 406 TCCATGATTTATACAAACATGTTTACCAGACCTTCCACCTGACCATGATGAGCGGAGC 465
Db 376 AGGTGAGAGCGGCTCAACATGTTTACACAGCATCTACTGTCTGCTGTGCTCAGCGTGAAC 435
QY 466 CGTACATTTGCGCTGTGCGCACCCCGTGAAGGCTTTTGACTTCGACACCTTTGAAGGCA 525
Db 436 CGCTACGTGGCGGTGTGATGATCCCATCAAGGCGCGCGCTACCGCTGCCACCGTGAAC 495
QY 526 AAGATCATTAATCTGTCATCTGCTGCTGCTGCTG 558
Db 496 AAGGTAGTAAACCTGGGCGTGTGGGTGCTATCG 528

RESULT 80
BB656301 663 bp mRNA linear EST 26-OCT-2001
LOCUS BB656301 RIKEN full-length enriched, 12 days embryo spinal ganglion
DEFINITION Mus musculus cDNA clone D130013H04 5', mRNA sequence.
ACCESSION BB656301
VERSION BB656301.1 GI:16490129
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 663)
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Hara, A., Hiramoto, K., Hori, F., Fukuda, S., Furuno, M., Hanagaki, T.,
Arakawa, T., Carninci, P., Itoh, M., Kawai, J.,
Kono, H., Konda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K.,
Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K.,
Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T.,
Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,
Takeda, Y., Tanaka, T., Toyota, T., Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
Unpublished (2001)
CONTACT Yoshihide Hayashizaki
LABORATORY for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
E-mail: genome-res@gs.c.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
Wegli, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
Matsuhira, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T.,
Matsunura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A.
and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Kono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P.,
Sugahara, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo, S., Shingawa, A., Saito, T., Kiyosawa, H., Yamanaka, I.,
Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
Hayashizaki, Y.
Computational Analysis of Full-length Mouse cDNAs Compared with
Human Genome Sequences. Mamm. Genome 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for

FEATURES
source
e mouse tissues
location/Qualifiers
1..663
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="D130013H04"
/tissue_type="spinal ganglion"
/dev_stage="12 days embryo"
/lab_host="VDH10B"
/clone_lib="RIKEN full-length enriched, 12 days embryo
spinal ganglion"
/note="Site 1: SalI; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAGCGCGCGCAACTCGAGTGTGTTTTTTTTTTTNN 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. Second strand cDNA was prepared with the
primer adapter of sequence [5'
GAGAGAGAGTTCGAGTTTAATTAATTAATCCCCCCCCC 3']. cDNA
was cleaved with BamHI and XhoI. Vector: a modified
pBluescript KS(+) after bulk excision from lambda PhiC 1."

ORIGIN

Query March 13.2%; Score 152.8; DB 10; Length 663;
Best Local Similarity 59.0%; Pred. No. 3.4e-19;
Matches 262; Conservative 0; Mismatches 182; Indels 0; Gaps 0;

QY 108 CGACGAGACGCGCAGCGCGCTGCGAGAGCGCGCACTGAGCCCGGACATCTTCCCC 167
Db 192 CGCCAGCTGGGCTCCGAGCGAGAGGAGATGCGATGGGTCGACGCGACAGGAGAC 251
QY 168 GGCATCCCGGTATATACAGCGGGGTCTACTCGTATGTTGTTGTCGTGGCTTGGTGG 227
Db 252 AGCGGGATGGTCACTATCCAGTGCATCTATGCGCTGTGTGTGTTGGGCTGTGGG 311
QY 228 CAATCGCTGGTCACTGTTGCGATCATCCGATACAAAGATGAGAGACGACCAACAT 287
Db 312 AAAGCGCTGTATCTTCTGTATCTTACGCTATGCGAATGAGACACACCAACAT 371
QY 288 TTACATATTTAACCCTGGCTTTGGCAGATGCTTTAGTTACTACCAACATGCCCTTTCAGAG 347
Db 372 CTACCTACTCAACCTGGCGCTGGCCATGAGCTTTCATGCTCAGGCTGCATTCGGG 431
QY 348 TAGGTTACTTATGAAATTCCTGGCTTTTGGGATGTGCTGTGCAAGTATTAATTC 407
Db 432 CTGGCGCGCTGCCCTGGCCACTGGCGGTTCGGGGGCGGTGTGTGCGCAATGCTTAG 491
QY 408 CATTTGATTTACAAACATGTTTACACAGCATCTTCACTTGACCATATGAGCGTGAACG 467
Db 492 CGTGAAGGCGCTGAACATGTTTACTATGCTTCTTCTGCTACCGTGTGAGCGG 551
QY 468 CTACATTTCCGTGTGCCACCGCGTGAAGGCTTTGACCTTCCGACACCTTTGAAGCAAA 527
Db 552 CTATGTGGCTGTGTGTGACCTCTTGGCGCGCCACCTACCGGCGGAGCGTGGCCAA 611
QY 528 GATCATCAATATCTGATCTGGCT 551
Db 612 GCTAATCACTGGAGTGTGGCT 635

RESULT 81
CNS04RP2/c
LOCUS CNS04RP2 927 bp DNA linear GSS 01-SEP-2000
DEFINITION Tetradodon nigroviridis genome survey sequence pUC-ori end of clone
003122 of library H from Tetradodon nigroviridis, genomic survey
sequence.

ACCESSION	AL304175
VERSION	AL304175.1 GI:8190656
KEYWORDS	GSS; genome survey sequence.
SOURCE	Tetradodon nigroviridis
ORGANISM	Tetradodon nigroviridis Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostei; Acanthopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodontidae; Tetradodon.
REFERENCE	1 Rosset Crollius,H., Jalllon,O., Daeilya,C., Bouneau,L., Fisher,C., Bernot,A., Filames,C., Minck,P., Brottier,P., Quettier,F., Saurin,W. and Weissenbach,J. Estimate of human gene number provided by genome-wide analysis using Tetradodon nigroviridis DNA sequence Nat. Genet. 25 (2), 235-238 (2000)
JOURNAL	20296633
MEDLINE	10835645
PUBMED	
AUTHORS	2 Roset Crollius,H., Jalllon,O., Daeilya,C., Ozouf-Costez,C., Filames,C., Fischer,C., Bouneau,L., Billault,A., Quettier,F., Saurin,W., Bernot,A. and Weissenbach,J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetradodon nigroviridis Genome Res. 10 (7), 939-949 (2000)
TITLE	
JOURNAL	20359837
MEDLINE	10899143
PUBMED	
REFERENCES	3 (bases 1 to 927) Genoscope. Direct Submission Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seque@genoscope.cns.fr - Web : www.genoscope.cns.fr) This sequence is a single read and was generated as part of a large scale clone-and-sequencing project of the Tetradodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetradodon .
COMMENT	
FEATURES	Location/Qualifiers 1..927 /organism="Tetradodon nigroviridis" /mol_type="genomic DNA" /db_xref="taxon:99883" /clone="003b22" /clone_1lb="H" /note="Genoscope sequence ID : COBH003DF1XEI-end ; FUC-Ori"
ORIGIN	
Query Match	13.2%; Score 152.2; DB 29; Length 927;
Best Local Similarity	70.0%; Pred. No.5,1e-19;
Matches 219; Conservative 0; Mismatches 93; Indels 1; Gaps 1,	
OY	219 CTGTGGGCACTCGTCGCATGTTGTGATTCATCCGATCACAAAGTAGAACAGC 278
DB	313 CTTCTTGTAATGATCTTTCAAACAACCCTTTTAGATACACCAAAATAAGAAGC 254
OY	279 AACCAACTTTACATATTAACTGGCTTTGGCAGATGCTTAGTTACTACAAACATGCC 338
DB	253 CACAACATCTACATCTTCAACCTGGCCCTGGCCGACGCCCTGGTCAACAGACCGCTTCC 194
OY	339 CTTTCAGAGTACGGTCTACTTGATGAATTCCTGGCCCTTTGGGAGATGTCGTGCAAGT 398
DB	193 CTTCCAGAGCGTCACTACCTGATGGGACGTCGGCC-TTCGGCGACGTCGTGCAAGT 135
OY	399 AGTATTTCCATGATTTACTAACAATGTTACACAGCATCTTCAACCTGACCATATAG 458
DB	134 CGTCAATGTCACGACTACAAACATGTTCACTTCACATCTTCAACGCTCACCAATGAG 75
OY	459 CGTGAACGCTACATTTGCGTGGCACCCCGTGAAGCTTTGGACTTCGACACCCCTT 518
DB	74 CGTGACCGCTACGTCGGCGTGTGCATCCGCTCAAAAGCGCTGACCTTCAGAACCCCGCA 15
OY	519 GAAGGCAAGATC 531

Db	14	CACACCACTTTC	2
RESULT 82			
CNS03JCN/c			
LOCUS	CNS03JCN	881 bp	DNA linear
DEFINITION	Tetradodon nigroviridis genome survey sequence T7 end of clone 03JC21 of library G from Tetradodon nigroviridis, genomic survey sequence.		
ACCESSION	AL246704		
VERSION	AL246704.1	GI:7967716	
KEYWORDS	GSS; genome survey sequence.		
SOURCE	Tetradodon nigroviridis		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.		
REFERENCE	1 Roest Crolius,H., Jalllon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizesse,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J. Estimate of human gene number provided by genome-wide analysis using Tetradodon nigroviridis DNA sequence Nat. Genet. 25 (2), 235-238 (2000)		
TITLE	Tetradodon nigroviridis DNA sequence		
JOURNAL	Nat. Genet. 25 (2), 235-238 (2000)		
MEDLINE	20296633		
PUBMED	10835645		
REFERENCE	2 Roest Crolius,H., Jalllon,O., Dasilva,C., Ozouf-Coataz,C., Fizesse,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetradodon nigroviridis Genome Res. 10 (7), 939-949 (2000)		
AUTHORS	3 Roest Crolius,H., Jalllon,O., Dasilva,C., Ozouf-Coataz,C., Fizesse,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetradodon nigroviridis Genome Res. 10 (7), 939-949 (2000)		
TITLE	Tetradodon nigroviridis DNA sequence		
JOURNAL	Nat. Genet. 25 (2), 235-238 (2000)		
MEDLINE	20296633		
PUBMED	10835645		
REFERENCE	3 Roest Crolius,H., Jalllon,O., Dasilva,C., Ozouf-Coataz,C., Fizesse,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetradodon nigroviridis Genome Res. 10 (7), 939-949 (2000)		
AUTHORS	3 Roest Crolius,H., Jalllon,O., Dasilva,C., Ozouf-Coataz,C., Fizesse,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetradodon nigroviridis Genome Res. 10 (7), 939-949 (2000)		
TITLE	Tetradodon nigroviridis DNA sequence		
JOURNAL	Nat. Genet. 25 (2), 235-238 (2000)		
MEDLINE	20296633		
PUBMED	10835645		
REFERENCE	3 Roest Crolius,H., Jalllon,O., Dasilva,C., Ozouf-Coataz,C., Fizesse,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetradodon nigroviridis Genome Res. 10 (7), 939-949 (2000)		
AUTHORS	3 Roest Crolius,H., Jalllon,O., Dasilva,C., Ozouf-Coataz,C., Fizesse,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetradodon nigroviridis Genome Res. 10 (7), 939-949 (2000)		
TITLE	Tetradodon nigroviridis DNA sequence		
JOURNAL	Nat. Genet. 25 (2), 235-238 (2000)		
MEDLINE	20296633		
PUBMED	10835645		
REFERENCE	3 Roest Crolius,H., Jalllon,O., Dasilva,C., Ozouf-Coataz,C., Fizesse,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetradodon nigroviridis Genome Res. 10 (7), 939-949 (2000)		
AUTHORS	3 Roest Crolius,H., Jalllon,O., Dasilva,C., Ozouf-Coataz,C., Fizesse,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetradodon nigroviridis Genome Res. 10 (7), 939-949 (2000)		
TITLE	Tetradodon nigroviridis DNA sequence		
JOURNAL	Nat. Genet. 25 (2), 235-238 (2000)		
MEDLINE	20296633		
PUBMED	10835645		
REFERENCE	3 Roest Crolius,H., Jalllon,O., Dasilva,C., Ozouf-Coataz,C., Fizesse,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetradodon nigroviridis Genome Res. 10 (7), 939-949 (2000)		
AUTHORS	3 Roest Crolius,H., Jalllon,O., Dasilva,C., Ozouf-Coataz,C., Fizesse,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetradodon nigroviridis Genome Res. 10 (7), 939-949 (2000)		
TITLE	Tetradodon nigroviridis DNA sequence		
JOURNAL	Nat. Genet. 25 (2), 235-238 (2000)		
MEDLINE	20296633		
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REFERENCE	3 Roest Crolius,H., Jalllon,O., Dasilva,C., Ozouf-Coataz,C., Fizesse,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetradodon nigroviridis Genome Res. 10 (7), 939-949 (2000)		
AUTHORS	3 Roest Crolius,H., Jalllon,O., Dasilva,C., Ozouf-Coataz,C., Fizesse,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetradodon nigroviridis Genome Res. 10 (7), 939-949 (2000)		
TITLE	Tetradodon nigroviridis DNA sequence		
JOURNAL	Nat. Genet. 25 (2), 235-238 (2000)		
MEDLINE	20296633		
PUBMED	10835645		
REFERENCE	3 Roest Crolius,H., Jalllon,O., Dasilva,C., Ozouf-Coataz,C., Fizesse,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetradodon nigroviridis Genome Res. 10 (7), 939-949 (2000)		
AUTHORS	3 Roest Crolius,H., Jalllon,O., Dasilva,C., Ozouf-Coataz,C., Fizesse,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetradodon nigroviridis Genome Res. 10 (7), 939-949 (2000)		
TITLE	Tetradodon nigroviridis DNA sequence		
JOURNAL	Nat. Genet. 25 (2), 235-238 (2000)		
MEDLINE	20296633		
PUBMED	10835645		
REFERENCE	3 Roest Crolius,H., Jalllon,O., Dasilva,C., Ozouf-Coataz,C., Fizesse,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetradodon nigroviridis Genome Res. 10 (7), 939-949 (2000)		
AUTHORS	3 Roest Crolius,H., Jalllon,O., Dasilva,C., Ozouf-Coataz,C., Fizesse,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetradodon nigroviridis Genome Res. 10 (7), 939-949 (2000)		
TITLE	Tetradodon nigroviridis DNA sequence		
JOURNAL	Nat. Genet. 25 (2), 235-238 (2000)		
MEDLINE	20296633		
PUBMED	10835645		
REFERENCE	3 Roest Crolius,H., Jalllon,O., Dasilva,C., Ozouf-Coataz,C., Fizesse		

QY	399	ACTAATTTTCATTGATTACTATCAACAATGTTACACACATCTTCACTTGACATGATGAG	455
Db	126	CGTCAATGTCATCGACTACTACTACACATGTTTCACTTCACTTCACTGACTACACCACTAG	67
QY	459	CGTGAACCGCTACATTGTCGGTGTGCCACCCCGGTGAAGCTTTGAGCTTCGACACCCCTT	518
Db	66	CGTGAACCCCTACGTGTGGCCGTGTGGCATCCGGTCAAAAGCGCTGACTTGAAGACGCCGCA	7
QY	519	GAAGCG 524	
Db	6	CAACGC 1	
RESULT 83			
LOCUS	CB557233	662 bp	mRNA linear EST 02-APR-2000
DEFINITION	AMGNNUC:URGP1-00001-All-A urgp1 (14349) Rattus norvegicus cDNA		
ACCESSION	CB557233		
VERSION	CB557233.1	GI:29496633	
KEYWORDS	EST.		
SOURCE	Rattus norvegicus (Norway rat)		
ORGANISM	Rattus norvegicus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
AUTHORS	1 (bases 1 to 662)		
TITLE	Amgen EST Program.		
JOURNAL	Amgen Rat EST Program		
COMMENT	Unpublished (2003) Contact: Dan Fitzpatrick Amgen, Inc One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA Tel: 805 447-4881 Plate: 00001 row: a column: 11.		
FEATURES			
source	location/Qualifiers		
	1..662		
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	/clone_lib="urgp1 (14349)"		
	/note="Vector: pSPORT1; Rat GPCR library rearrayed internal pSPORT vector"		
ORIGIN			
Query Match	13.1%;	Score 151;	DB 14; Length 662;
Best Local Similarity	69.5%;	Pred. No. 7, 6e-19;	
Matches	205;	Conservative 0;	Mismatches 90; Indels 0; Gaps 0;
QY	153	CGCGACATCTCCCGGCATCCCGGTATATATACAGCGGGCTTACTCCGATAGTGTGT	212
Db	368	CGCTTCTCGCCCTTGAGACTCAAGATCACATCGTGGGGCTTACTTGGCTGTGTGAT	427
QY	213	CGTGGGCTTGGTGGCAACTCGCTGTGATGTTCTGTATCATCCGATACACAAAGATGA	272
Db	428	CGGGGGGCTCTCGGGGAAGTGGCTGTGATGATATCTCTCGAGGACACCAAGATGA	487
QY	273	GACAGCAACAACATTATCATATTTTAACCTGGCTTGGCAAGTCTTATGTTACTTACAAC	332
Db	488	GACAGCTACCAACATTATCATATTTTAACCTGGCAAGTCTTATGTTACTTACAAC	547
QY	333	CATGCGCTTTAGAGTAGTACGCTCTATGTAATTCGCGCTTTGGGGATGTGCTGTG	392
Db	548	ACTGCGCTTCAAGGGCAAGACATCTTACTGGGCTTCTGGCCATTTGGGAATGACCTTG	607
QY	393	CAAGATAGTAATTTTCATGATTACTTACAACAATGTTCAACAGCATCTTACCTTG	447
Db	608	CAAGACTGTACTTGGTATCGACTACTTACAACAATGTTTACAGCACTTTTACTCTG	662
RESULT 84			
CD5359492/c			

LOCUS	CD55949.2	792 bp	mRNA	linear	EST 19-NOV-2003
DEFINITION	AGENCOURT_14496636 NIH_MGC_195 Homo sapiens cDNA clone IMAGE:6971826 5', mRNA sequence.				
ACCESSION	CD559492				
VERSION	CD559492.2	GI:38453541			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1 (bases 1 to 792)				
TITLE	NIH-MGC http://mgc.nci.nih.gov/ .				
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)				
COMMENT	On Jun 10, 2003 this sequence version replaced gi:31585560. Contact: Daniela S. Gethard, Ph.D. Office of Cancer Genomics National Cancer Institute / NIH Bldg. 31 Rm10A07 Bethesda, MD 20892 Email: cga9bs-remail.nih.gov Tissue Procurement: Narayan Bhat cDNA Library Preparation: Bhat Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov Plate: IRBK2 row: d column: 05 High quality sequence start: 12 High quality sequence stop: 726. Location/Qualifiers				
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	/cissue_type="mixed"				
	/lab_host="DH5A (TI phage-resistant)"				
	/clone_id="NIH_MGC_195"				
	/note="Vector: pDNR-Dual; Site 1: loxp-salI; Site 2: loxp-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxp sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK_prev.dat a Note: this is a NIH_MGC library."				
ORIGIN					
Query Match	13.0%;	Score 150.2;	DB 14;	Length 792;	
Best Local Similarity	55.0%;	Pred. No. 1.2e-18;			
Matches 382;	Conservative 0;	Mismatches 299;	Indels 13;	Gaps 4;	
QY	338	CGTTTCAAGATTAAGGTCTACTTGTATGAATTCCTGCGCTTTTGGGAGATGCTGTGCAGA	397		
DB	720	CCAGTCAATCGCGGAGACCTCTGTGAAGTACGCGCT-TCGGAGACCTCTGTGCAGC	662		
QY	398	TAGTAATTTCATTGATTACTACACATGTTCACAGACATCTTCACTTACCATGATGA	457		
DB	661	TGTGTCTGCGCGCTGCACCATTAACAATCTTCTCCAGCATCTAATTCTGACCGCTATGA	602		
QY	458	GGGTGACCGCTACATTGCGGTGTGCCACCCCGTGAAGG-----TTTGAATCTCCGA	511		
DB	601	GGGTGACCGCTACATTGCGGTGTGTCTGTGCGCACCGTGAAGTCTCCGCGCATATCCCTGTGCGCA	542		

OY	51.2	CAACCTTGAAGGCAAAAGATCATCATATCTGATCTGGCTGCTGTCATCTGTTGGCA	571
Db	54.1	CTTACCGGGGGGCAAGGTCGCCAGCTGTGTGTCTGGCTGGAGCGTCAGGTCCTGGTTC	482
OY	57.2	TCTCTGCATATAGTCCCTTGGAGGACACCAAGTACAGGGAAAGCCGATCGATGTTCATTTAGTGTCT	631
Db	48.1	TGCCCTTCTTCTCTTTCGCTGGCGCTCA---CAGCAAGACGTGCAAGTCCCAAGCTGTG	425
OY	63.2	CTTGCAGTTCGCCAGATGATGACTACTCTGTGTGGACCTTTCATGAAGATCTGCGTCT	691
Db	42.4	GAGTGAAGCTTCCCGTGGGCCGAGCAGGTCTGGT---TCAAGGCACGCGGTGTCTACAGCT	368
OY	65.2	TCATCTTTGGCTTTCGTGATCCTGTCTCTATCATCATGTCTGTCTACACCTGATGATCC	751
Db	36.7	TGTCCTGGGCTTCTGTGTGCTGCCCGCTGTGCACCATCTGTGTGCTCTACACAGACCTCTGC	308
OY	75.2	TGCGCTCAAGAGCGGTCCGGCTCTTTCTGGGCTCCCGAAGAAAGATGCCACCTGCGCTA	811
Db	30.7	GCAGGCTGGGGCCCGTGCGGCTCCGCTCTGGAGCCAAAGCTCTTAGGCAAGGCCAGCGGA	248
OY	81.2	GGATACACAGACTGTGTCTGTGTGTGTGGAGTCTTCTGCTCTGTGAGACTCCACTTC	871
Db	24.7	AGGTACCGCTCCTGTGCTCTCTGTGTGTGTGTGGCCGTGTCTCTCTGTGTGAGCCCTTTC	188
OY	87.2	ACATATTCATCTGTGTGAGAGCTCTGGGGAGACCTCCACAGCAACAGCTGTCTCTTCCA	931
Db	18.7	ACCTGAGCCTGTGTGCGGGCCGTGACACAGGACCTGGCCCAAGCCCACTGTGTATCAGTA	128
OY	93.2	GCTATTAATTCTGTGCATTCGCTTAAAGCTATACCAACAGTAGTACTGTAATCCCATTTCTTACG	991
Db	12.7	TGTCTCAAGTCAATCACAGCCCTCAGCTACGCCAACCTGTGCTGAAACCCCTTCTCTACG	68
OY	99.2	CCTTCTTGATGAAGAACTTCAGAGCGTGTTCGCG	1025
Db	6.7	CCTTCTTAGATGACAACCTTCGAAAGAACTTCGCG	34

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RESULT 85
BX390825
LOCUS
DEFINITION
BX390825 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
CDNA clone CS0DCK011YG11 5-PRIME, mRNA sequence.
ACCESSION
BX390825
VERSION
BX390825.1 GI:30623183
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1114)
Li, W.B., Gruber, C., Jesssee, J., and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
JOURNAL
COMMENT
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7532.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgl-bln/cluster.cgi?seq=CS0BAG049ZFO3_CS04630_1&cluster=7532.f.
Contact: Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paradey Avenue Genoscope sequence ID : CS0BAG049ZFO3_CS04630_1.
Location/Qualifiers
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FEATURES
source

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/cell_line="HELA"
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primer. Five prime end enriched, double-strand cDNA was
digested with NotI and cloned into the NotI and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

```

Query March	13.0%	Score 150;	DB 13;	Length 1114;
Best Local Similarity	59.7%;	Pred. No. 1.5e-18;		
Matches 252;	Conservative 0;	Mismatches 170;	Indels 0;	Gaps 0

OY	199	TCGGAGGTTGTCGTGGGCTTGGTGGGCACTGCGTGGTCAATGTTGGTATCATCCGA	258
Db	1	TCGGGTGTGCTGTGGGGCTGTGTGGAACTTAAGTATCTACGTGATCTCGGC	60
OY	259	TACACAAAGATGAGACAGCAACCAATTATCATATTTAACTGGCTTTGGCAGATGCT	318
Db	61	TATGCAAGATGAGAACGGCCACCAACATCTCAATCTCTAAATCTGGCAATGCTGATGAG	120
OY	319	TTAGTATACAAACATGCCCTTTGAGAGTACGGTCTACTTATGAAATTCCTGGCCTTT	378
Db	121	CTGCTCATGCTCAGGTGTCCTCTTCTTAAGTCACTTCACGTTGTGGCCATGGCCCTTC	180
OY	379	GGGAGTGTGCTGTGCAAGATAGTAATTTTCATTGATTAATCAACATGTTTCAACAGATC	438
Db	181	GGTGGCTGCTCTGCGGCTGTGTCTACAGCGTGAAGGGGTCAACATGTTACACAGCATC	240
OY	439	TTCACTTTGACCATGATGAGGGTGAACCGCTACATTTGCCGTGTGCCACCCCGTGAAGGCT	498
Db	241	TACTGTCTGACGTGTCTCAGGTGAGCCGCTACCTGCGGCGTGTGATCTCCATCAAGGGCG	300
OY	499	TTGGACTTCGGCAACACCTTGAAGGCAAGATCATCAATATCTGATCTGGGCTGCTGCG	558
Db	301	GCCGGCTACGGCGGCCACCGTGGCCAAAGTAGTAACCTGGGCTGTGGGTGCTATGCG	360
OY	559	TCATCTGTTGGCATCTCTGCAATAGTCTTGGAGGCCACCAAGTCAAGGAGACGTGAT	618
Db	361	CTGCTGTGATCTGTCGCATGATGATCTTCTCTCGACCCGGGGCAACAGCAGCGGACG	420
OY	619	GT 620	
Db	421	GT 422	

RESULT	86
LOCUS	BB632308
DEFINITION	BB632308 RIKEN full-length enriched, adult male hypothalamus Mus musculus cDNA A230027D20 5', mRNA sequence.
ACCESSION	BB632308
VERSION	BB632308.1
KEYWORDS	GI:16468911
SOURCE	EST.
ORGANISM	Mus musculus (house mouse)
REFERENCE	Mus musculus
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 643)
TITLE	Arkawa,T., Garrincci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hizumoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Kono,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shingawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toyai,T., Muramatsu,M. and Hayashizaki,Y.
JOURNAL	RIKEN Mouse ESTs (Arkawa,T., et al. 2001)
COMMENT	unpublished (2001) Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel.: 81-45-503-9222

Db	9	10CCACAGTACGTCGTCGTATCCAGCACTATTTCTGTATTG-CTGGGGAACCAAC	67
Qy	967	AGTACCGTGAATCCCATTTCTACGCGCTTTCTGTATGAAAACTTCAGCGGTTTCCGG	1026
Db	68	AGAGCGCTTCATCTCATCTTATGTCCTTT-TGATGAAAACTTCAGAGATGTTCAAA	126
Qy	1027	GACTTCTGCTTTCCACTGAAGTATGAGTGGAGCGGCAGAGCACTAGCAGAGTCCGAAT	10866
Db	127	GACTTCTGCTTTCCCGCTTTAAGATGAGATGGATAGGAGACACAGAGAGTTGAAAC	186
Qy	1087	ACAGTTCAAGATCCGCTTATCCCTGAGGGACATCGATGGGATGAAATAAACAGTATGACTA	1146
Db	187	ACCGTCAAGACCGCCTTATATGAGGGAGAGCAGATGGGACAAACAACTGTATGACTA	246
Qy	1147	GTCGTGA 1154	
Db	247	GTCGTGA 254	
RESULT 88			
LOCUS	AY400987	898 bp	DNA linear GSS 15-DEC-2003
DEFINITION	Pan troglodytes SSTR5 gene, VIRTUAL TRANSCRIPT, partial sequence,		
ACCESSION	AY400987		
VERSION	AY400987.1	GI:39756976	
KEYWORDS	GSS.		
SOURCE	Pan troglodytes (chimpanzee)		
ORGANISM	Pan troglodytes		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.		
AUTHORS	1 (bases 1 to 898) Clark,M.A.G., Gianowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.		
TITLE	Interfing nonneutral evolution from human-chimp-mouse orthologous gene trios		
JOURNAL	Science 302 (5652), 1960-1963 (2003)		
PUBMED	14671302		
REFERENCE	2 (bases 1 to 898) Clark,M.A.G., Gianowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.		
AUTHORS	Direct Submission		
TITLE	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA		
JOURNAL	This sequence was made by sequencing genomic exons and ordering them based on alignment.		
COMMENT	Location/Qualifiers		
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ORIGIN			
Query Match	12.8%;	Score 147.2;	DB 29; Length 898;
Best Local Similarity	51.3%;	Pred. No. 4.6e-18;	
Matches	425;	Conservative 0;	Mismatches 383; Indels 21; Gaps 3;
Qy	140	CGCAGCTGAGACCCCGGCACATCTCCCGGCATCCCGGTACATATCACCGCGGTACT	199
Db	83	CGCTGTGAGCGCGCGCCCTTCGGCGGAGCCCTGGCGGTCTGTGCGCCGTGTAC	142
Qy	200	CCGTAGTTCGTCTGTGGCTTGTGGGCAACTCGCTGTCATGTTCTGTATCATCCGAT	259
Db	143	TGCTGTGTGTGCGCGCGCGGCTGGCGGGAACACGCTGTATCTACGTGTGTCTGCGCT	202
Qy	260	ACACAAAGATAGAGCAGACCAACCAATTTACATATTTAACTGGCTTTGGCAGATGCTT	319

Db	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
Db	BUT08032										
Db	BUT08032	835 bp mRNA linear EST 15-JUL-2003									
Db	BUT08032	UI-M-FRO-cao-j-10-0-UI.r1 NIH BMP_FRO Mus musculus cDNA clone IMAGE:6415209 5', mRNA sequence.									
Db	BUT08032										
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REFERENCE 1 (bases 1 to 785)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: <http://image.llnl.gov>
 Plate: LLM11503 row: 1 column: 14
 High quality sequence stop: 728.
 Location/Qualifiers

FEATURES

source

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 /note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains; age range 23-27 yo. Library is oligo-dr primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NIH-MGC library."

ORIGIN

Query Match

Best Local Similarity 69.5%; Pred. No. 4.5e-17;
 Matches 235; Conservative 0; Mismatches 100; Indels 3; Gaps 3;

153 CGCGACATCTCCCGGCGCATCCGGTCATCATCAGCGGGTCTACTCGTAGTTCGT 212
 Db CGCCTTCCTCGGCGGCTCAAGGTACACATCGGGGCTCTACTGCGCTGTGTGT 363
 Qy 213 CGTGGCTTGGTGGGCAATCGCTGTGTCTTCTGATCATCCGATACAAAGTAA 272
 Db 364 CGAGGGCTCCCTGGGAACTGCTGTCTGATGATCGATCTCAGGACACCAAAATGA 423
 Qy 273 GACAGCAACCAATTTATATATTTAACTGGCTTGGAGATGCTTATTACTACAAC 332
 Db 424 GACAGCCACCAATTTATATCTTTAACTGGCCCTCGGC-GACACTGTGTCTGTGAC 482
 Qy 333 CATGCCCTTTCAGAGTACGCTCTACTTGAATTCCTGGCCTTTGGGGATGTGCTGTG 392
 Db 483 GCTGCCCTTCAGAGCAAGGACATCTCCCTGGGGCTTCTGCGTTGGGAATGCGCTGTG 542
 Qy 393 CAAGATATGAATTTCCATTGA-TTACTAGAACATGTTC-CCAGATCTTTCACCTTGACC 450
 Db 543 CAAGACAGTATGCTTACCTTACTTAACAATGTTCACCAAGCCTTTCACCCCTTA 602
 Qy 451 ATGATGAGCGGTGACCGCTACTATGCGCGTGTGCCACC 488
 Db 603 GCCATGAGTGTGGATGCTATGATGACATCTGCAACC 640

RESULT 92
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 DEFINITION UI-M-BG-bup-g-01-0-UI.r1 NIH_BMAP_EG0 Mus musculus cDNA clone
 IMAGE:5685144 5', mRNA sequence.
 ACCESSION BM951523
 VERSION BM951523.1 GI:19435113
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 714)
 AUTHORS Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
 TITLE NIH-MGC <http://mgc.nci.nih.gov/>.
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Dr. James Lin, University of Iowa
 CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: <http://image.llnl.gov>
 This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

FEATURES

source

Seq primer: pYX-5.
 Location/Qualifiers

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 /lab_host="DH10B (T1 phage resistant)"
 /clone_1lb="NIH BMAP EG0"
 /note="Organ: brain; Vector: pYX-AEC; Site 1: EcoR I; Site 2: Not I; The library was constructed according to Bonaldi, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured mRNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo-dr primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into pYX-AEC vector. The library tag sequence located between the Not I site and the polyA tail, is CAGCCACGAC. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Heman Chin, Ph.D., program coordinator."

ORIGIN

Query Match

Best Local Similarity 64.0%; Pred. No. 6.7e-17;
 Matches 213; Conservative 0; Mismatches 120; Indels 0; Gaps 0;

766 GTCCGGCTCTCTTCTGCTCCCGAGAGAAAGTGCACCTGCGATGACCAAGACTG 825
 Db 2 GTCCGGCTCTCTTCTGCTCCCGAGAGAAAGTGCACCTGCGATGACCAAGACTG 61
 Qy 826 GTCCGGCTCTCTTCTGCTCCCGAGAGAAAGTGCACCTGCGATGACCAAGACTG 885
 Db 62 GTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 121
 Qy 886 GTGAGAGCTCTGGGAGAGACCTCCACAGCAGCTGCTCTCCAGCATTAATCTTGC 945
 Db 122 GTTCAAGAGCTGGGATGATGATGATGATGATGATGATGATGATGATGATGAT 181
 Qy 946 ATCGCTTAGCTATACCAACAGTAGCTGAATCCATTTCTTACGCTTTTGTATGA 1005
 Db 182 ACAGCCCTGGGCTATGATCAACAGTGTCTCAATCCATTTCTTATGATGATGAT 241
 Qy 1006 AACTTCAGCGGTGTTCCGGGACTTCTGCTTTCACATGGAAGATAGAGTAGAGGCGAG 1065
 Db 242 AACTTCAGCGGTGTTGAAAGTTCTGCTGTGCTTCTGCTGACCGGAGATGACG 301
 Qy 1066 AGCACTAGCAGAGTCCGAATACAGTTCAAGAT 1098
 Db 302 GTTCTGATCGTGTGCGCAGCATTCGCAAGAT 334

RESULT 93
BM546464 1383 bp mRNA linear EST 20-FEB-2002
LOCUS AGENCOURT 6494036 NIH_MGC_124 Homo sapiens cDNA clone IMAGE:5729211
DEFINITION 5', mRNA Sequence.
ACCESSION BM546464
VERSION BM546464.1 GI:18779448
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE NIH-MGC <http://mgi.nci.nih.gov/>.
1 (bases 1 to 1383)
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Invitrogen
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLNL2726 row: c column: 04
High quality sequence start: 48
High quality sequence stop: 526.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5729211"
/tissue_type="hippocampus"
/lab_host="DH10B"
/clone_1lb="NIH_MGC_124"
/note="Torgan: brain; Vector: pCMV-SPORT6; Site_1: EcoRV
(destroyed); Site_2: NotI; RNA source male hippocampus,
age 27. Library is oligo-dT primed and directionally
cloned (EcoRV site is destroyed upon cloning). Average
insert size 1.4 kb, insert size range 0.9-4 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 012."

ORIGIN

Query Match 12.2%; Score 141; DB 12; Length 1383;
Best Local Similarity 70.2%; Pred. No. 8.7e-17;
Matches 203; Conservative 0; Mismatches 85; Indels 1; Gaps 1;
QY 153 CCGGCAATCTCCCGGCATCCGTCATCATCGCGGCTTACTCCGTAAGTTCGT 212
DB 373 CGCCTTCTGCCCCCTCGGCTCAAGTCAACATCGTGGGGCTCTTACGCGCGTGTGT 432
QY 213 CGTGGCTTGGGCACTGCTGTCATGTTGCTGATCCGATACCAAGATGATAA 272
DB 433 CGAGGGCTCTGCGGAAGCTGCTGTGATGATGATGATCTCTCAAGGCAACCAAAATAA 492
QY 273 GACAGCAACCAATTTATCATATTTACCTGGCTTTGGCAGATGCTTTAGTTACTACAC 332
DB 493 GACAGCAACCAATTTATCATATTTACCTGGCCCTGCGACACTCTGCTCTGCTGAC 552
QY 333 CATGCCCTTTTCAAGTACGCTCTACTGTATGATGATTCCTGGCCCTTTGGGAGTGTCTGTG 392
DB 553 GCTGCCCTTTTCAAGGCAAGCAATCTCTGCGGCTTCTGCGCTTTGGGAATGGCGTGTG 612
QY 393 CAAGTATGATTTTCCATGATTTACTATACACA-TCCTACAGCATCTT 440
DB 613 CAAGCCGCTATTCGCTATGACTACTACAAATGTTTCCAGACCTT 661

RESULT 94
CNS03GSG
LOCUS CNS03GSG 937 bp DNA linear GSS 01-SEP-2000
DEFINITION Tetradon nigroviridis genome survey sequence T7 end of clone
025E10 of library G from Tetradon nigroviridis, genomic survey
sequence.
ACCESSION AL243385
VERSION AL243385.1 GI:7964397
KEYWORDS GSS; genome survey sequence.
SOURCE Tetradon nigroviridis
ORGANISM Tetradon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
Tetraodontidae; Tetraodontidae; Tetraodon.
REFERENCE Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
1 Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
Estimate of human gene number provided by genome-wide analysis
using Tetradon nigroviridis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)
JOURNAL MEDLINE 20296633
PUBMED 10835645
REFERENCE 2
AUTHORS Roest Crolius,H., Jaillon,O., Dasilva,C., Ozouf-Coetaz,C.,
Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
Saurin,W. and Weissenbach,J.
Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetradon nigroviridis
Genome Res. 10 (7), 939-949 (2000)
JOURNAL MEDLINE 20359837
PUBMED 10899143
REFERENCE 3 (bases 1 to 937)
AUTHORS GenomeScope.
TITLE Direct Submission
JOURNALS Submitted (12-APR-2000) GenomeScope - Centre National de Sequenage :
BP 191 91006 Evry cedex - FRANCE (E-mail : seqrel@genomescope.cns.fr)
- Web : www.genomescope.cns.fr
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetradon nigroviridis
genome. For more information, please take a look at
<http://www.genomescope.cns.fr/Tetradon>.
Location/Qualifiers
1..937
/organism="Tetradon nigroviridis"
/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone="025E10"
/clone_1lb="ng"
/note="Genoscope sequence ID : COB025BC05LPI-end : T7"

ORIGIN

Query Match 12.1%; Score 140.2; DB 29; Length 937;
Best Local Similarity 57.0%; Pred. No. 1.1e-16;
Matches 256; Conservative 0; Mismatches 193; Indels 0; Gaps 0;
QY 111 CAGCAAGCGAGCGCGGCTTGGAGGACGCGAGCTGGAGCCCGCAATCTCCCGGC 170
DB 151 CACCTACAAAGGACGAGCAAGAACTTCTCACTCCGACCCCGAGATCCCAACCCGCGCT 210
QY 171 CATCCCGGTATCATACCGCGGCTTACTCCGTAAGTTCGTGTGTGGGCTTGTGGGCA 230
DB 211 GACCGGAGTTTATCCCTCTGTATTCAGGAGAGTGTGTGTGTGGCTCTGTGGGCA 270
QY 231 CTCGCTGTATGTTGGTATCATCCGATACCAAGATGAGAAGCAACCAATTTA 290
DB 271 CAGGTGTATCATATGATTTGTCCATACCAAGAAAGAGTCCGTACCAACTCTA 330
QY 291 CATATTTAATCTGGCTTTGGCAGATGCTTTAGTTACTACAAACCATGCCCTTTGAGATAC 350
DB 331 CATCTCAACTGGCATGCGGACGAGCTCTTCATGTGTGGCTGCCCTTCTGTGCGGT 390

QY 351 GGTCTACTGATGATTCCTGGCCCTTTGGGGATGCTGTGCAAGATGTAATTTCAT 410
 DB 391 GAGAAAGCTCTGCTCTCTGCGCCCTTCGAGCTGCTACATGTCGGCTGTGATACAGT 450
 QY 411 TGATTAACCAACATGTTGACAGCATCTTTCACCTTGACCATGATGAGCGTGAACGCTTA 470
 DB 451 GAGACGCATCAACAGTTCACAGCATCTTGTGCTGACAGATGTGCGTGGACCGCTTA 510
 QY 471 CATTGCGCTGTGCGACCCCGTGAAGGCTTTGACCTTCGACACACCTTTGAAGCAAAAGT 530
 DB 511 CTTGCTGTGTGACACCCCATCGCTCTCTGTGTGTGCGCGCGCGAGGTGGCAAGGC 570
 QY 531 CATCAATATCTGCATCTGCTGTGCTGCT 559
 DB 571 CATCAGACCAACGCTGTGGCGGGGCTCT 599
 RESULT 95
 CD559647 791 bp mRNA linear EST 26-NOV-2003
 LOCUS AGENCOURT_14496669 NIH_MGC_195 Homo sapiens cDNA clone
 DEFINITION IMAGE:6971826 5', mRNA sequence.
 ACCESSION CD559647
 VERSION CD559647.2 GI:38559005
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 791)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT On Jun 10, 2003 this sequence version replaced gi:31585715.
 Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Narayan Bhat
 cDNA Library Preparation: Bhat Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: IRBK2 row: d column: 05
 High quality sequence start: 4
 High quality sequence stop: 766.
 Location/Qualifiers
 1..791
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6971826"
 /csize_type="mixed"
 /lab_host="DH5A (71 phage-resistant)"
 /clone_1lb="NIH MGC 195"
 /note="Vector: PDNR-Dual; Site 1: loxp-Sall; Site 2:
 loxp-HindIII; Clones from this library have been
 PCR-amplified using gene-specific primers to contain the
 complete open reading frame (based on known gene sequences
 available from NCBI's RefSeq). Template for PCR is cDNA
 derived from either pooled cytoplasmic polyA RNA from 30
 cells lines or pooled total RNA from 10 different tissues
 (from BD Biosciences/Clontech and Washington University).
 PCR products are directionally cloned into the loxp sites
 of the PDNR-Dual vector. Library constructed by Dr.
 Narayan Bhat, Earl Bere III and Hongling Liao (Gene
 Expression Laboratory, Research Technology Program, SAIC
 Frederick, NCI-Frederick, Frederick, MD 21702). For
 information on which gene each clone represents, please

visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearranged_plates/IRBK.presv.dat
 a Note: this is a NIH_MGC Library."

ORIGIN
 Query Match 12.1%; Score 139.8; DB 14; Length 791;
 Best Local Similarity 54.8%; Pred. No. 1.2e-16;
 Matches 345; Conservative 0; Mismatches 272; Indels 12; Gaps 3;
 QY 166 CCGGCATCCCGGTATCATACGCGCGGTCTACTCCGTAGTGTGCTGCGGCTTGGTG 225
 DB 147 CCGTTCCTTATGCTCTCTTACCCCGGTGATCTCCGGATCTGTGTGCGGCTGACT 206
 QY 226 GCGAATCGCTGTGATGTCGTGATTCATCCGATACAAABAATGAAGCACCAACCAAC 285
 DB 207 GCGAACAAGCGCGGTATCTGTATATCTTAAGAGCGCGCCCAAGATGAAGCGGTGACCAAC 266
 QY 286 ATTACATATTTAACTGCTTTGGCAGATGCTTAGTTACTACAAACCATGCCCTTTCAG 345
 DB 267 GTGTTCAATCTGAACCTGCGCGCTCGCCAGCGGCTCTTCAACGCTGTACTGCCCTCAAC 326
 QY 346 AGTACGCTTACTTGTATGTAATTCCTGGCTTTTGGGAGTGTGCTGTGCAAGATGTAAT 405
 DB 327 ATCGCGGAGACCTGCTGAGTACTGGCCCTTCGCGGAGCTGCTGTGCAAGCTGTGTG 386
 QY 406 TCCATTGATTTACTAACAATGTCACAGCATCTTACCTTGAACATGATGAGCGGTGAC 465
 DB 387 GCGGTGACACTAACAATCTTCTTCAGCATCTTCTTACGCGGTATGAGCGGTGAC 446
 QY 466 CGCTACATTTCCGCTGTGCAACCCCGTGAAGC-----TTTGAATCTCCGACACCCCTTG 519
 DB 447 CGATACCTGTGTGTCTGTGCGACCGTGAAGTCCCGCACATGCTGTGGCGACCTACCGG 506
 QY 520 AAGGCAAAAGATCATATATCTGATCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGCA 579
 DB 507 GGGGCGAAGGTGTGCGACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 566
 QY 580 ATATGTCCTTGAAGGACCAAGTCAAGGAAGACGTGATGATGATGATGATGATGATGATG 639
 DB 567 TTCTCTTCTGCGGTGTGTA---CAGCAACGAGCTGCGAGTCCCAAGCTGTGGGCTGAGC 623
 QY 640 TTCCAGATGATGATCTCTGCTGTGGGACCTCTTCATGAAGATGCTGCTTTCATCTTT 699
 DB 624 TTCCGCTGCGCCGAGACAGTCTGTTCAGAGGACAGC---CGTGTACACGTTGGTCTTG 680
 QY 700 GCTTGTGATCTCTGTCTCTATCATCATCTGTGCTACACCCCTGATGATCTGTGCTTC 759
 DB 681 GCTTGTGATCTCTGTCTCTATCATCATCTGTGCTACACAGACCTCTGTGCGAGGCTG 740
 QY 760 AAGAGCTCCGCGCTCTTCTGTGCTCCG 788
 DB 741 CCGGCGGTGCGGCTCGCTGTGAGCCAG 769
 RESULT 96
 BE252309 642 bp mRNA linear EST 13-JUL-2000
 LOCUS 601114162P1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3354783 5',
 DEFINITION mRNA sequence.
 ACCESSION BE252309
 VERSION BE252309.1 GI:9122447
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 642)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
 Plate: LCM157 row: 1 column: 16
 High quality sequence stop: 630.

FEATURES

source

1..642
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
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 /cvsue_type="retinoblastoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_16"
 /note="Organ: eye; Vector: pOT7; Site_1: XhoI; Site_2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCAAGGAG(6). Library constructed by Ling Hong
 in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

ORIGIN

Query Match 12.1%; Score 139.4; DB 10; Length 642;
 Best Local Similarity 53.8%; Pred. No. 1.3e-16;

Matches 334; Conservative 0; Mismatches 281; Indels 6; Gaps 2;

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QY 155 CGCACATCTCCCGGCATCCGGTCATGACGCGGCTTACTCCGAGTGGTCTGC 214
DB 20 CCGTACTATGACCTGACCAAGCAATGACGCTCTCAATCATATTTTGGCTGCATCA 79
QY 215 TGGGCTGGTGGGCACTCGCTGTCATTTGTGATCATCCGATACCAAGATGAAGA 274
DB 80 TTGGGTGGTGGCAACACATTTGATCATCTCCGCTATGCGCAAGATGAAGA 139
QY 275 CAGCAACCAACATTTATATTTAACTGCTGGTGGAGATGCTTATGTTATACACCA 334
DB 140 CCATACCAACATTTATATCTTCAACTGCGCATGCGAGATAGCTTTTCATGCTGGGTC 199
QY 335 TGCCTTTTCAAGTACGCTCTACTTGAATTCCTGGCTTTGGGAGATGCTGTGCA 394
DB 200 TGCCTTTTCTGCTATGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 259
QY 335 AGATGATATTTCCATGATTTACTACACATTTTCAACAGCATTTTCACTTACCTTACCATGA 454
DB 260 GGGTGTCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 319
QY 455 TGAGCGTGAACCGCTACATTTGCGTGTGCAACCGCGTGAAGGCTTTGACCTTCCGCAAC 514
DB 320 TGAGCATGACCGGATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 379
QY 515 CTTGAAGGCAAGATCATCATATTCGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 574
DB 380 CCGGACCGGCAAGATGATCAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 436
QY 575 CTGCAATAGTCTTGGAGGACCAAGTCAGGAGAGACGTGATGATCATTTAGTGTCTCT 634
DB 437 TGCCATCATGATATATGCTGGGCTCCGAGCAACATGAGGAGGAGGAGGAGGAGGAGGAG 496
QY 635 TGCAATTCACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 694
DB 497 TCAACTGGCCAGGTGAATCTGGGGCTTGTACACAGGTTTCA---CATCTACACTTTTCA 553
QY 655 TCTTTGCTTGTGATCCCTGCTCTCATCATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 754
DB 554 TTTGGGGTCTCTGATACCCCTCAACATCATCTGCTTGTACCTGTTATATATATCA 613
QY 755 GTCTCAAGAGGCTCGGCTCC 775
DB 614 AGGTGAAGTCTCTGGAATCC 634

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RESULT 97
 BU317021 793 bp mRNA linear EST 28-NOV-2002
 LOCUS 603855026P1 CSEQCHN62 Gallus gallus cDNA clone CHEST85748 5', mRNA
 DEFINITION sequence.

ACCESSION BU317021.1 GI:25825022
 VERSION BU317021.1
 KEYWORDS EST.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

REFERENCE
 AUTHORS Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
 Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
 TITLE A Comprehensive Collection of Chicken cDNAs
 JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
 MEDLINE 2233534
 PUBMED 12445392

COMMENT
 Contact: Simon Hubbard
 Department of Biomolecular Sciences
 University of Manchester Institute of Science and Technology
 (UMIST)
 PO Box 88, Manchester, M60 10D, UK
 Tel: 01612008930
 Fax: 01612360409
 Email: Simon.Hubbard@umist.ac.uk.

FEATURES

source

1..793
 Location/Qualifiers
 /organism="Gallus gallus"
 /mol_type="mRNA"
 /strain="White Leghorn, H1sex"
 /db_xref="taxon:9031"
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 /dev_stage="36"
 /lab_host="DH10B"
 /clone_lib="CSEQCHN62"
 /note="Organ: heads; Vector: pBluescript II KS(+); Site_1:
 EcoRI; Site_2: NotI. This normalized library was
 constructed from 1 million independent clones. cDNA
 synthesis was initiated using an oligo(dT) primer, using
 methylated C in the first strand synthesis reaction.
 Following this first strand reaction, double-stranded cDNA
 was bluntended, ligated to NotI adapters, digested with
 EcoRI, size-selected, and cloned into the NotI and EcoRI
 compatible sites of a custom modified MCS of the
 pBluescript (KS+) vector. The library was normalized in 2
 rounds using conditions adapted from Soares et al., PNAS
 (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
 (1996): 791, except that a significantly longer
 reannealing hybridization was used."

ORIGIN

Query Match 12.1%; Score 139.4; DB 13; Length 793;
 Best Local Similarity 71.8%; Pred. No. 1.4e-16;

Matches 196; Conservative 0; Mismatches 76; Indels 1; Gaps 1;

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QY 159 CATCTCCCGCCGATCCGGTCAATCATCAAGCGGCTCTACTCCGATGTTCTGCTGGG 218
DB 89 CCGCGCGCTAGAGATCAAGATACCAATTTGGTGGCTTACTCCATTTGTGCACTTTGGG 148
QY 219 CTTGGTGGGCACTCGCTGTCATTTGTTGATCATCCATACCAAGATGAAGACAG 278
DB 149 GCTGTGGGCACTCGCTGTCATTTGTTGATCATCCATTCACCAAGATGAAGACAG 208
QY 279 AACCAATTTATATTTAACTGCTTTGGAGATGCTTATAGTACTACCAACCATGGCC 338
DB 209 AACCAATTTATATTTAACTGCTTTGGAGATGCTTATAGTACTACCAACCATGGCC 268
QY 339 CTTTCAGATGACGCTACTGATGATTCCTGGCTTTTGGGAGATGCTGCAAGAT 398

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Db 269 CTCGAGGGGTACAGACACGCTTCGGGCTTCGGCC-TTGGCAATGTCCTCGCAAGAT 327
 QY 399 AGTAATTCATTGATTACTTACACACATGTTTCAC 431
 Db 328 CGCTATCTCTATAGACTTACTTACAACTGTTTCAC 360

RESULT 98
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 LOCUS AGENCOURT_14740155 NIH_MGC_145 Homo sapiens cDNA clone
 DEFINITION IMAGE:6971895 5', mRNA sequence.
 CFI47826
 CFI47826.1 GI:33244094
 EST.
 KEYWORDS Homo sapiens (human)
 SOURCE
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 729)
 NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cga@dbp-r@mail.nih.gov
 Tissue Procurement: GPCR Consortium
 cDNA Library Preparation: GPCR Consortium
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: IRB102 row: b column: 02
 High quality sequence stop: 728.
 Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6971895"
 /tissue_type="mixed"
 /lab_host="DH10B"
 /clone_11b="NIH_MGC_145"
 /note="Vector: pCDNA3.1; Site 1: varies by clone; Site 2:
 varies by clone; ORFs were PCR-amplified and cloned into
 pCDNA3.1 by the GPCR Consortium. Cloning sites vary by
 clone and include the following: 5'-EcoRV-XbaI/XhoI-3',
 5'-EcoRV-XbaI/XhoI-3', EcoRV (TA cloned, non-directional).
 For information about which gene each clone represents,
 please visit our anonymous ftp site at
 ftp://image.llnl.gov/image/rearrayed_plates/IRB1_presv.dat
 a Note: this is a NIH_MGC Library."

ORIGIN

Query Match 12.1%; Score 139.2; DB 14; Length 729;
 Best Local Similarity 54.1%; Pred. No. 1.5e-16;
 Matches 329; Conservative 0; Mismatches 273; Indels 6; Gaps 2;

QY 155 CGCACATCTCCCGGCGGATCCGGTTCATCAAGCGGCTTACTCCGATGTTGCTCG 214
 Db 116 CGTACTATGACCTGACACAGCAATGACAGTCTCATCTATCTATTTTGGTCTGCATCA 175
 QY 215 TGGGCTGTGGGCAACCTGCTGATGTTGATGATCGATACACAAAGATGAAGA 274
 Db 176 TTGGGTGTGTGGCAACACATTTGATTAATGATCTCTCCGCTATGCCAAGATGAAGA 235
 QY 275 CAGCAACCAACATTTAATATTTAACTTGGCTTTGGCAGATCTTATGTTACTACACCA 334
 Db 226 CCATCAACCAACATTTAATCTCACTCACTGCGCATGCAATAGAGCTTCAATGCTGGGTC 295

QY 335 TGCCCTTTAGAGTACCGGCTACTTATGATATTCCTGCGCTTTGGGGATGTCCTGCA 394
 Db 296 TGCCCTTTCTGCTATGACAGTGGCTCTGGTCCATGCGCTTTGGCAAGCATTTGCC 355
 QY 395 AGATAGTAATTTCCATTGATTTACTTACACATGTTGACACGATCTTACCTTGACCATGA 454
 Db 356 GGGTGTATATGACTGTGATGATGGCATCAATCAATGATTTTCCAGCATCTTCTGCTGACGTCA 415
 QY 455 TGAGGTGAGACCGCTACATTTGCTGTGTCACCCCGTGAAGGCTTTGACCTTCCGACAC 514
 Db 416 TGAGCATCACCGAATACCTGCTGTGTGTCCACCCCATCAAGTCGCGCAAGTGAAGAGAC 475
 QY 515 CCTTAAGGCAAGATCATATATCTGATCTGCTGCTGTGCTGATCTGTTGGCATCT 574
 Db 476 CCGGACGCGCAAGATGATACCATGCTGTGTGTGGAGACTCTTCTGCTGTGATCTTGC 535
 QY 575 CTGCAATAGTCTTGGAGGACCAACAAAGTCAGGAAAGCTCGATGCTATGATGCTCTCT 634
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 QY 635 TCGAGTTCACAGATATGACTACTCTGCTGGGACCTTTATGAAGATCTGCTCTTCA 694
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 SOURCE
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 791)
 NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT On Jun 10, 2003 this sequence version replaced gi:31585714.
 Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cga@dbp-r@mail.nih.gov
 Tissue Procurement: Narayan Bhat
 cDNA Library Preparation: Bhat Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
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 PCR-amplified using gene-specific primers to contain the
 complete open reading frame (based on known gene sequences
 available from NCBI's RefSeq). Template for PCR is cDNA
 derived from either pooled cytoplasmic polyA RNA from 30
 cells lines or pooled total RNA from 10 different tissues
 (from BD Biosciences/Clontech and Washington University).
 PCR products are directionally cloned into the loxp sites
 of the pDNR-Dual vector. Library constructed by Dr.
 Narayan Bhat, Earl Bere III and Hongling Liao (Gene
 Expression Laboratory, Research Technology Program, SAIC
 Frederick, NCI-Frederick, Frederick, MD 21702). For
 information on which gene each clone represents, please
 visit our anonymous ftp site at
 ftp://image.llnl.gov/image/rearranged_plates/IRBK.presv.dat
 a Note: this is a NIH_MGC library."

ORIGIN

Query Match 12.0%; Score 138.6; DB 14; Length 791;
 Best Local Similarity 54.9%; Pred. No. 2e-16;
 Matches 342; Conservative 0; Mismatches 269; Indels 12; Gaps 3;

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 QY 226 GGCACATCGCTGTCATGTTGTCGATCATCCGATACAAAGATGAGACAGCAAC 285
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RESULT 100
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 LOCUS CD559648 792 bp mRNA linear EST 26-NOV-2003

DEFINITION AGENCOURT 14496622 NIH_MGC_195 Homo sapiens cDNA clone
 IMAGE:6971825 5', mRNA sequence.
 accession CD559648
 version CD559648.2 GI:38559007
 keywords EST.
 source Homo sapiens (human)
 organism Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 reference 1 (bases 1 to 792)
 authors NIH-MGC <http://mgc.nci.nih.gov/>.
 title National Institutes of Health, Mammalian Gene Collection (MGC)
 journal Unpublished (1999)
 comment On Jun 10, 2003 this sequence version replaced gi:31585716.
 Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Narayan Bhat
 cDNA Library Preparation: Bhat Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLU)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNLU at:
<http://image.llnl.gov>
 Plate: IRBK2 row: d column: 04
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 loxp-HindIII; Clones from this library have been
 PCR-amplified using gene-specific primers to contain the
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 Frederick, NCI-Frederick, Frederick, MD 21702). For
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ftp://image.llnl.gov/image/rearranged_plates/IRBK.presv.dat
 a Note: this is a NIH_MGC library."

ORIGIN

Query Match 12.0%; Score 138.2; DB 14; Length 792;
 Best Local Similarity 54.7%; Pred. No. 2.4e-16;
 Matches 344; Conservative 0; Mismatches 273; Indels 12; Gaps 3;

QY 166 CCGGCATCCCGCATCATCAGCGGCTCTCTCCGATGTTGTCGTGGGCTTGCTG 225
 Db 146 CCGTTCCTTATGTCCTGCTGCGCCGCTGATCCGGGATCTGTGCTGTGGGCTGACT 205
 QY 226 GGCACATCGCTGTCATGTTGTCGATCATCCGATACAAAGATGAGACAGCAACCAAC 285
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